

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 17:40:11 ; Search time 11860.7 Seconds
(without alignments)
19051.434 Million cell updates/sec

Title: US-10-786-065-3_COPY_20000_26200

Perfect score: 6201
Sequence: 1 caccatggcctcaggaacat.....aagagtaacgaagaatgrrg 6201

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	550.2	8.9	653	9 AG040253	AG040253 Pan troglodytes
2	413.6	6.7	710	4 BI091930	BI091930 602856713
3	412.8	6.7	517	6 CD522178	CD522178 AGENCOURT
4	412.8	6.7	583	5 BP871658	BP871658 BP871658
5	412.8	6.7	774	5 BU933084	BU933084 AGENCOURT
6	412.8	6.7	948	5 BU955838	BU955838 AGENCOURT
7	412	6.6	676	4 BI258333	BI258333 602968259
8	411.8	6.6	851	5 BU959722	BU959722 AGENCOURT
9	411	6.6	727	2 BE393340	BE393340 601311002
10	410.8	6.6	708	4 BI489733	BI489733 603032230
11	403.2	6.5	894	5 BU507729	BU507729 AGENCOURT
12	403	6.5	1180	3 BC005215	BC005215 Homo sapi
13	402.6	6.5	489	7 CN346858	CN346858 170005328
14	402.6	6.5	491	1 AI376271	AI376271 ta55h12.x
15	402.6	6.5	500	4 BM739173	BM739173 K-EST0008
16	402.6	6.5	599	1 AI148931	AI148931 tES2f08.x
17	402.6	6.5	601	4 BM753449	BM753449 K-EST0030
18	402.6	6.5	635	6 CB054131	CB054131 NISC_gm02
19	402.6	6.5	639	1 AI159762	AI159762 tn15907.x
20	402.6	6.5	673	7 CN346851	CN346851 170006001
21	402.6	6.5	675	7 CN346862	CN346862 170006000
22	402.6	6.5	690	7 CN346845	CN346845 170005328
23	402.6	6.5	693	4 BG700992	BG700992 602682170
24	402.6	6.5	702	7 CN346850	CN346850 170005831

25	402.6	6.5	710	7 CN346828	CN346828 170005325
26	402.6	6.5	720	6 CF132267	CF132267 UI-HR-F00
27	402.6	6.5	721	4 BF984014	BF984014 602306941
28	402.6	6.5	721	6 CA391711	CA391711 c618D04.Y
29	402.6	6.5	725	4 BM762609	BM762609 K-EST0043
30	402.6	6.5	737	7 CN346865	CN346865 170006000
31	402.6	6.5	740	4 BI222628	BI222628 602940118
32	402.6	6.5	754	7 CN346857	CN346857 170005999
33	402.6	6.5	770	7 CN346837	CN346837 170005977
34	402.6	6.5	795	5 BQ221377	BQ221377 AGENCOURT
35	402.6	6.5	812	4 BG819344	BG819344 602781541
36	402.6	6.5	814	1 AU117598	AU117598 AU117598
37	402.6	6.5	822	1 AU110030	AU110030 DKF2686P
38	402.6	6.5	828	1 AU117451	AU117451 AU117451
39	402.6	6.5	829	2 BE747955	BE747955 601580366
40	402.6	6.5	844	1 AU124576	AU124576 AU124576
41	402.6	6.5	845	4 BI909653	BI909653 603066683
42	402.6	6.5	854	5 BU153052	BU153052 AGENCOURT
43	402.6	6.5	857	5 BU156219	BU156219 AGENCOURT
44	402.6	6.5	869	5 BQ232770	BQ232770 AGENCOURT
45	402.6	6.5	875	1 AU124769	AU124769 AU124769

ALIGNMENTS

RESULT 1
LOCUS AG040253 653 bp DNA linear GSS 01-NOV-2001
DERIVATION Pan troglodytes DNA, clone: PTB-017017.F, genomic survey sequence.
ACCESSION AG040253
VERSION AG040253.1 GI:16568978
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
2 (bases 1 to 653)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenhiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKSI45
R Site 1 : SacI
R Site 2 : SacI
Location/Qualifiers
1.653
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-017017.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 8.9%; Score 550.2; DB 9; Length 653;
Best Local Similarity 98.4%; Pred. No. 2.6e-37;

	Matches	566;	Conservative	0;	Mismatches	8;	Indels	1;	Gaps	1;
Oy	3144	AAACTCCCAAGCTCAAAATTAATTTCCTCCACGCTGGCCTCCCAAAGTGTGGAATTAACAGT								3203
Dd	647	AACCCCCAAGCCTCCAAATTAATCTTCCCACGCTCGGCCTCCAAAGTGCTGGAATTAACAAGT								588
Oy	3204	GTGAGCCCAAAGGGTTTAATTGATGTGTGATGTGGGCTCTAGTGCCTCTCAAACTTAGTAgTg - AGCA								3262
Dd	587	GTGAGCCAAAAGGGTTTATTGACGTGTGGCTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT								528
Oy	3263	GACAAAGTGAACGGGGAACCTGACTCAACAAGTCTGGGTTTTAAAGCTTGAAGCTTCTGCAATTC								3322
Dd	527	GACAAAGTGAACGGGGAACCTGACTCAACAAGTCTGGGTTTTAAAGCTTGAAGCTTCTGCAATTC								468
Oy	3323	AACATGAGTCAAGCGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG								3382
Dd	467	AACATGAGTCAAGCGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG								408
Oy	3383	TCTAGTTAGCAATTAATGATAACAGGTTGATAATTATGATGATGATGATGATGATGATGATGATG								3442
Dd	407	TCTAGTTAGCAATTAATGATAACAGGTTGATAATTATGATGATGATGATGATGATGATGATGATG								348
Oy	3443	AATGGAAGAATACAGTAACAAAGAAAGTTCACTCTTGTTATGATGATGATGATGATGATGATGATG								3502
Dd	347	AATGGAAGAATACAGTAACAAAGAAAGTTCACTCTTGTTATGATGATGATGATGATGATGATGATG								288
Oy	3503	AAGATGAGGGCCAACATTAATCTGTTTTGTGTTTGACTGACGAGAGAGAAATGTAGTACTTA								3562
Dd	287	AAGATGAGGGCCAACATTAATCTGTTTTGTGTTTGACTGACGAGAGAGAAATGTAGTACTTA								228
Oy	3563	TTAACAGAAATATGAGAGAAAGATGGTTGGTTGGAGAGAAAGAGAGATCTGTTTTCACAGCTG								3622
Dd	227	TTAACAGAAATATGAGAGAAAGATGGTTGGTTGGAGAGAAAGAGAGATCTGTTTTCACAGCTG								168
Oy	3623	TTGAGAGTCCCAAGTGTGACAGAGATCTCCAAAGGGAATAAGACAGTAGCAACTTAAAG								3682
Dd	167	TTGAGAGTCCCAAGTGTGACAGAGATCTCCAAAGGGAATAAGACAGTAGCAACTTAAAG								108
Oy	3683	AAATCTGTCTCAGAAAGGAGCTGTGAGCTGCAGC								3717
Dd	107	AAATCTGTCTCAGAAAGGAGCTGTGAGCTGCAGC								73
RESULT 2										
Bt091930										
LOCUS										
DEFINITION	Bt091930	710 bp	mRNA		linear					EST 20-JUN-2001
LOCATION	602856713P1 NIH_MGC_10 Homo sapiens CDNA clone IMAGE:4998218 5',									
ACCSSION	Bt091930									
VERSION	Bt091930.1 GI:14510260									
KEYWORDS	EST.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
TITLE	NIH-MGC http://mgc.nci.nih.gov/.									
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)									
COMMENT	Unpublished (1999)									
	Contact: Robert Strausberg, Ph.D.									
	Email: cgsabds-remail.nih.gov									
	Tissue Procurement: ATCC									
	cDNA Library Preparation: Life Technologies, Inc.									
	cDNA Sequencing by: Incyte Genomics, Inc.									
	Clone distribution: MGC clone distribution information can be									
	found through the I.M.A.G.E. Consortium/LIML at:									
	http://image.llnl.gov									
	Plate: LRAM1026 row: i column: 03									
	High quality sequence stop: 707.									
FEATURES										
SOURCE	location/Qualifiers									
	1..710									
	/organism="Homo sapiens"									

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4998218"
/cell_line="MG36"
/lab_host="DH10B"
/clone_id="NTH_MGC_10"
/notes="Organ: caryix; Vector: pCMV-SPORT5; Site_1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Lite
Technologies."

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Query Match	6.7%	Score 413.6	DB 4	Length 710
Best Local Similarity	92.7%	Pred. No. 5,86-26		
Matches	434	Conservative	0	Mismatches 34; Indels 0; Gaps 0;
Qy	16	CAATTTATGAAAGCCAAATATATACGCTTTAAATAGAAATGTGACCTTAATATCCAGAAAG	75	
Db	178	CAATTTATGAAAGCCGAAATATACAGCTTTAAATAGAAATGTGACCTTAATATCCAGAAAG	237	
Qy	76	AACGCCCTTTGTAGATTGTGTACAAAATTTATATGAGTAGAGTTAATGTCTTAATG	135	
Db	238	CACCCCTTTGTAGATTGTGTACAAAATTTATATGAGTAGAGTTAATGTCTTAATG	297	
Qy	136	GAATGTGAAACCCAGAGCCATATCAGCGCTAGCAAAATGGCAGAAATTCATATATCA	195	
Db	298	GAGTGTGAGACCCAGAGCCATATCAGGTCTAGCAAAATGGCAGAAATTCATATATCA	357	
Qy	196	AAGTTATCCTTCAAGACCTTCAGGCGCTTAATGATGTCTTAAAGAAATGTGAAAGCCCTC	255	
Db	358	AAGTTATCCTTCAAGACCTTCAGGCGCTTAATGATGTCTTAAAGAAATGTGAAATCTCCTC	417	
Qy	256	AGCCATCTGAAAGCAGAGTTACAGCAATGATCAAAAGAAAGAAACCAAGGCCCTTCC	315	
Db	418	AGCCGCCGAAAGCAGAGTTACAGCAATGATCAAAAGAAAGAAACCAAGGCCCTTCC	477	
Qy	316	CTTCCCCCAATCTTGATGTAGACAGTCTTCAATTTCCATATGTATTAATTTCTAGATAC	375	
Db	478	CTTCCCCCAATCTTGATGTATACAGTCTTCAATTTCCAGATGTAAATTTCTAGATAC	537	
Qy	376	AGCTTTGAGAGCTCAAGTACTGGAAGAAAGCTCCCATTCAAAGAAATTTATCTTAAG	435	
Db	538	GCTCTTGAGAGCTCAAGTACCGGAAGAAAGCTCCCATTCAAAGAAATTTATCTTAAG	597	
Qy	436	ATACTGTAAATGATACTAATTTTGTATCATTTGGATATATTAAGTGT	483	
Db	598	ATACTGTAAATGATACTAATTTTGTATCATTTGGATATATTAAGTGT	645	

RESULT 3	CD522178	517 bp	mRNA	linear	EST 06-JUN-2003
LOCUS	CD522178				
DEFINITION	ABENECOURT1435240 NIH MGC 191 Homo sapiens cDNA clone				
ACCESSION	IMAGE:30410716 5', mRNA sequence.				
VERSION	CD522178				
KEYWORDS	CD522178.1 GI:31453896				
ORGANISM	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 517)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Daniela S. Gerhard, Ph.D.				
	Office of Cancer Genomics				
	National Cancer Institute / NIH				
	Bldg. 31 Rm10A07 Bethesda, MD 20892				
	Email: cgaas-remail.nih.gov				
	Tissue Procurement: Narayan Bhat				
	cDNA Library Preparation: CLONTECH Laboratories, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM201 row: F column: 05
 High quality sequence stop: 503.

FEATURES

source

1..517
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30410716"
 /issue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_191"
 /note="Vector: pDNR-Lib; Site 1: SfiI (ggccatcggcc);
 Site 2: SfiI (ggccgcgcgcgc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCCATTTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCCGACATG-(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.7%; Score 412.8; DB 6; Length 517;

Best Local Similarity 92.1%; Pred. No. 8.3e-26;

Matches 446; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

1 CACCATGGGCTCAGCAATTTATGAAAGCCAAATATACAGCCTTAAATGATGTGAC 60
 23 CACGAGGCTCGACAAATTTATGAAAGCCAAATATACAGCCTTAAATGATGTGAC 82
 61 CTAAATATCCAGAGAAATCCCTTTGTAGATTTGTAAACAAAATTAATATGATGAG 120
 83 CTAAATATCCAGAGAAATCCCTTTGTAGATTTGTAAACAAAATTAATATGATGAG 142
 121 TTAATAGTTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 143 TTAATAGTTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 202
 181 ATTCAATATCATCAAGTTATCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAG 240
 203 ATTCAATATCATCAAGTTATCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAG 262
 241 ATGTGAAAGCCCTCAGCATGTGAAGAGCAGTGTATACAGCAATGTATCAAAAAGAAA 300
 263 ATATGAAATCCCTCGACCGCCGGAAGAGCAGTGTATACAGCAATGTATCAAAAAGAAA 322
 301 CCACAGGCTTCCCTTCCCATCTGATGTAAAGAGCTTCAATTTCCATAGTAGT 360
 323 CCACAGGCTTCCCTTCCCATCTGATGTAAAGAGCTTCAATTTCCATAGTAGT 382
 361 AAATTTTCTAGATACAGCTTGTAGAGCTCAAGTATGAGAAAGAGCTCCCATTAAG 420
 383 AAATTTTCTAGATACAGCTTGTAGAGCTCAAGTATGAGAAAGAGCTCCCATTAAG 442
 421 GAAATTTATCTTAAGATCTGTAATGATGATGATGATGATGATGATGATGATGATG 479
 443 GAAATTTATCTTAAGATCTGTAATGATGATGATGATGATGATGATGATGATGATG 502
 480 TTGT 483
 503 TTGT 506

RESULT 4
 BP871658

LOCUS BP871658 583 bp mRNA linear EST 27-JUL-2004
 DEFINITION BP871658 Sugano cDNA library, embryonal kidney Homo sapiens cDNA
 clone HRR01130, mRNA sequence.
 ACCESSION BP871658
 VERSION BP871658.1 GI:50716151
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shirota M., Sakakibara Y., Chiba J.,
 1 (bases 1 to 583)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE
 JOURNAL
 COMMENT Database of Transcriptional Start Sites (DBTSS) for Comparative
 Studies of the Promoters of Human and Mouse Genes
 Unpublished (2004)
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRR01130"
 /issue_type="embryonal kidney"
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ORIGIN

Query Match 6.7%; Score 412.8; DB 5; Length 583;

Best Local Similarity 92.1%; Pred. No. 7.7e-26;

Matches 446; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

1 CACCATGGGCTCAGCAATTTATGAAAGCCAAATATACAGCCTTAAATGATGTGAC 60
 77 CACGAGGCTCGACAAATTTATGAAAGCCAAATATACAGCCTTAAATGATGTGAC 136
 61 CTAAATATCCAGAGAAATCCCTTTGTAGATTTGTAAACAAAATTAATATGATGAG 120
 137 CTAAATATCCAGAGAAATCCCTTTGTAGATTTGTAAACAAAATTAATATGATGAG 196
 121 TTAATAGTTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 197 TTAATAGTTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 256
 181 ATTCAATATCATCAAGTTATCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAG 240
 257 ATTCAATATCATCAAGTTATCTTCAAGAGCTTCAAGAGCTTCAAGAGCTTCAAGAG 316
 241 ATGTGAAAGCCCTCAGCATGTGAAGAGCAGTGTATACAGCAATGTATCAAAAAGAAA 300
 317 ATATGAAATCCCTCGACCGCCGGAAGAGCAGTGTATACAGCAATGTATCAAAAAGAAA 376
 301 CCACAGGCTTCCCTTCCCATCTGATGTAAAGAGCTTCAATTTCCATAGTAGT 360
 377 CCACAGGCTTCCCTTCCCATCTGATGTAAAGAGCTTCAATTTCCATAGTAGT 436
 361 AAATTTTCTAGATACAGCTTGTAGAGCTCAAGTATGAGAAAGAGCTCCCATTAAG 420
 437 AAATTTTCTAGATACAGCTTGTAGAGCTCAAGTATGAGAAAGAGCTCCCATTAAG 496
 421 GAAATTTATCTTAAGATCTGTAATGATGATGATGATGATGATGATGATGATGATG 479
 497 GAAATTTATCTTAAGATCTGTAATGATGATGATGATGATGATGATGATGATGATG 556
 480 TTGT 483
 557 TTGT 560

RESULT 5
BU933084

LOCUS
DEFINITION
AGENCOURT_10473040 NIH_MGC_127 Homo sapiens cDNA clone
IMAGE:6673789 5', mRNA sequence.

ACCESSION
BU933084

VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 774)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCM2956 row: h column: 13
High quality sequence stop: 549.
Location/Qualifiers

FEATURES
source

1..774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6673789"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_1ib="NIH_MGC_127"
/note="Vector: pDNR-Lib; Site 1: SfiI (ggccatcatgccc);
Site 2: SfiI (ggccgcgcgcgc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGGTGATCAACGACAGCGCATACGCGCG-3' and
5'-ATTCTAGAGCCGACGCGCGCATATG-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 1-2 kb
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_128). Library created in the laboratory of T.
Udell, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 6.7%; Score 412.8; DB 5; Length 774;
Best Local Similarity 92.1%; Pred. No. 6.4e-26;
Matches 446; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

1 CACCATGGGCTCAGGCAATTTATGAAAGCCAAATATACAGCCTTAATATGATGTGAC 60
2 |||||
3 30 CACCAAGGGCTCGCAATTTATGAAACCGAATATACAGCCTTAATATGATGTGAC 89
4 |||||
5 61 CTAATATACCAAGAAATCCCTTTGTAAAGTTTGTACAAAATTAATATGATGAG 120
6 |||||
7 Db 90 CTAATATACCAAGAAATCCCTTTGTAAAGTTTGTACAAAATTAATATGATGAG 149
8 |||||
9 Qy 121 TTAATAGTTCTAATGGAATGTGAACCAAGAGCCATATCAGCGCTAGCAAAATGGCAGA 180
10 |||||
11 Db 150 TAAATAGTTCTAATGGAATGTGAACCAAGAGCCATATCAGCGCTAGCAAAATGGCAGA 209
12 |||||
13 Qy 181 ATTCTATATCATCAAGTTATCTTCAAGAGCTTCAGGCGCTAATGATGTCTAAAGAA 240
14 |||||

Db 210 ATTCTATATGATCAAAAGTTTCTGCAAGAGCTTCGCGCCTTAATGATGTCTAAAGAA 269
Qy 241 ATGTGAAGAGCCCTCAGCCATCTGAAGAGACAGTGTATACAGCAATGATCAAAAAGAAAA 300
270 ATATGAAGATCCCTCAGCGCGCGCAAGAGCAATGTATACAGCAATTAATCAAAAAGAAAA 329
Qy 301 CCACAGGCGCTTCCTTCCTCCCAATCTGATGTAAGACAGTCTTCAATTTCCATATGAGT 360
330 CCACAGGCGCTTCCTTCCTCCCAATCTGATGTAAGACAGTCTTCAATTTCCACAGTGT 389
Qy 361 AAATTTCTAGATACAGTCTTGAAGCTCAAGTACTGGAAGAAAGCTCCCATTCAAAG 420
Db 390 AAATTTCTAGATACAGTCTTGAAGCTCAAGTACTGGAAGAAAGCTCCCATTCAAAG 449
Qy 421 GAAATTTCTAGATACAGTCTTGAAGCTCAAGTACTGGAAGAAAGCTCCCATTCAAAG 479
Db 450 GAAATTTCTAGATACAGTCTTGAAGCTCAAGTACTGGAAGAAAGCTCCCATTCAAAG 509
Qy 480 TTGT 483
Db 510 TTGT 513

RESULT 6
BU955838

LOCUS
DEFINITION
AGENCOURT_10621087 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6729290 5', mRNA sequence.

ACCESSION
BU955838

VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 948)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCM3052 row: e column: 01
High quality sequence stop: 592.
Location/Qualifiers

FEATURES
source

1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6729290"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_107"
/note="Organ: breast; Vector: pOT7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGAG(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.7%; Score 412.8; DB 5; Length 948;
Best Local Similarity 92.1%; Pred. No. 5.6e-26;
Matches 446; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY	1	CACCATGGGGCTCAGCGCAATTTATATGAAGCAAAATATAAGCTTTAAATATGAATGTGGAC	60
Db	43	CACCACGGGGCTCGGACAAATTTATGAAACCGCAATATACGCTTTAAATATGAATGTGGAC	102
QY	61	CTAAATATCCAGAAAGAACTCCCTTTGTATAGATTTTGTAACAAAAATTAATATGATGAG	120
Db	103	CTAATATATCCAGAAAGCAACCCCTTTGTATAGATTTTGTAACAAAAATTAATATGATGAG	162
QY	121	TTAATAGTTCTTAATGGAATGTTGAACCCAGAGCCATATCAGCGCTAGCAAAATGGCAGA	180
Db	163	TAAATAGTTCTTAATGGAATGTTGAACCCAGAGCCATATCAGTGTAGCAAAATGGCAGA	222
QY	181	ATTCAATATATCATCAAAAGTTAATCCCTTCAAGAGCTCAGCGGCTAATGATGTCTAAAGAA	240
Db	223	ATTCAATATATCATCAAAAGTTGTTCTTGTCAAGAGCTTCGGGCTTAATGATGTCTAAAGAA	282
QY	241	ATGTGAACAGCGCTTCAGCCATCTGACAGAGCAGTGTTTACAGCAATGATCAAAAAAGAAAA	300
Db	283	ATATGAACCTCCCTTCAGCGCCGCCAGAGACAGTGTTCAGCAATTAATCAAAAAAGAAAA	342
QY	301	CCACAGGCGCTTCCCTTCCCTCCCATCTGATGATGAGCAGTCTTCATTTCCATGATAGT	360
Db	343	CCACAGGCGCTTCCCTTCCCTCCCATCTGATGATGAGTCTTCATTTCCATGATAGT	402
QY	361	AAATTTTCTAATATACAGTTTGTATGAGCTCAAAAGTCTGAAAAAGAAAGCTCCCATTCAGAG	420
Db	403	AAATTTTCTAATATACAGTTTGTATGAGCTCAAAAGTCTGAAAAAGAAAGCTCCCATTCAGAG	462
QY	421	GAAATTTATCTTAAGATACGTGTGTAATGATGATCTAA-TTTTGTACATTTGGAATATATAG	479
Db	463	GAAATTTATCTTAAGATACGTGTGTAATGATGATCTAA-TTTTGTGTGTCATTGGAATATATATAG	522
QY	480	TTGT 483	
Db	523	TTGT 526	
RESULT 7			
LOCUS	BI258333		
DEFINITION	602968259P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5107598 5',		
ACCESSION	BI258333		
VERSION	BI258333.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 676)		
JOURNAL	NIH-MGC http://imgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: gsabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/BLML at: http://image.llnl.gov Plate: LLM11260 row: f column: 15 High quality sequence start: 8 Location/Qualifiers 1..676 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5107598" /ribose_type="cervical carcinoma cell line" /lab_host="DH10B"		
FEATURES			
SOURCE			

Query Match	6.6%	Score 412;	DB 4;	Length 676;
Best Local Similarity	92.5%	Pred. No. 8.2e-26;		
Matches 433;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;
<p> /clone_11b="NH_MGC_12" /clone_Torjan: c6rviX; Vector: pCW-SpOrt6; Site 1: Ncrl1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies." </p>				
ORIGIN				
Query	16	CAATTATGAAAGCCAAATATATACAGCCCTTAATAATAGATGAGACTTAATATCCAGAG	75	
Db	177	CAATTATGAAAGCCAAATATATACAGCCCTTAATAATAGATGAGACTTAATATCCAGAG	236	
Qy	76	AACCTCCCTTTGTAGATTGTGTAACAAAAATTAATATGAGTAGATTAGTTCTAATG	135	
Db	237	CACCCCTCTTTGTAGATTGTGTAACAAAAATTAATATGAGTAGATTAGTTCTAATG	296	
Qy	136	GAATGTGTAACCCCAAGAGCCATATACAGCCGTACGAAATGGCAGATTCATATATCATCA	195	
Db	297	GAGTGTGTGACCCCAAGAGCCATATACAGTGTACGCAAAATGGCAGAAATTCATATATGACATCA	356	
Qy	196	AAGTTATTCCTTCAAGAGCTTCAAGGCGCTTAATGATGTCTTAAGAAATGTGAAAGCGCCCTC	255	
Db	357	AAGTTATTCCTTCAAGAGCTTCAAGGCGCTTAATGATGTCTTAAGAAATGTGAAATGTGAAATG	416	
Qy	256	AGCCATCTGAAAGACAGAGTTTACAGCAATTGATCAAAAAGAAAACACAGAGCCCTTCC	315	
Db	417	AGCCGCGCGAAAGACAGAGTTTACAGCAATTATCAAAAAGAAAACACAGAGCCCTTCC	476	
Qy	316	CTTCCCTCCATATCTGATGTGAAGACAGCTTCTTCAATTTTCCATAGTAAATTTTCTAGATAC	375	
Db	477	CTTCCCTCCATATGATTTATATCATGTCTTCTTCAATTTTCCATAGTAAATTTTCTAGATAC	536	
Qy	376	AGCTGTGTAGACTCAAAAGTACTGGAAAGAAAGCTCCCATTCAAAGGAAATTTATCTTAAAG	435	
Db	537	GCTTTGTAGACTCAAAAGTACTGGAAAGAAAGCTCCCATTCAAAGGAAATTTATCTTAAAG	596	
Qy	436	ATACTGTAAATGATATCTAATTTTGTATCATTTTGGATATATATAAGTTGT 483		
Db	597	ATACTGTAAATGATATCTAATTTTGTATCATTTTGGATATATATAAGTTGT 644		
RESULT 8				
BUS95722	851 bp	mRNA	linear	EST 20-SEP-2002
LOCUS	AGNCNCURT_8908446	NIH_MGC_142	Homo sapiens cdna	IMAGE:6451603
DEFINITION	5', mRNA sequence.			
ACCESSION	BUS95722			
VERSION	BUS95722.1	GI:23247481		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 851) NIH-MGC http://mgs.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: NCI CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: http://image.lnl.gov plate: L1CM2624 row: b column: 20 High quality sequence stop: 455. Location/Qualifiers 1..851			
FEATURES				
SOURCE				

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6451603"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_142"
/note="Vector: pDNR-Lib; Site 1: SfiI (ggccatcatggc); Site 2: SfiI (ggccgcctggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAAGCAGAGTGGCCATTAAGCGCGG-3' and 5'-ATTCTAGGCGGAGCGGCGGACATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.6%; Score 411.8; DB 5; Length 851;
Best Local Similarity 91.9%; Pred. No. 7.3e-26;
Matches 445; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

QY 1 CACCATGGGCTCAGGCAATTATGAAAGCCAAATATACAGCTTAAATGAAATGTGAC 60
DB 30 CACCACGGGCTCGGACAAATTATGAAAGCCAAATATACAGCTTAAATGAAATGTGAC 89
QY 61 CTAATATACCGAAGAACTCCCTTTGTAAGATTGTGAACAAAATTAATATATAGTAG 120
DB 90 CTAATATACCGAAGAACTCCCTTTGTAAGATTGTGAACAAAATTAATATATAGTAG 149
QY 121 TTAATAGTTTAATGAAATGTGAACCAAGACCATATCAGCGCTAGCAAAATGGCAGA 180
DB 150 TAAATAGTTTAATGAAATGTGAACCAAGACCATATCAGCGCTAGCAAAATGGCAGA 209
QY 181 ATTCATATATCATCAAAATTAATCTTCAAGAGCTTCAAGCGCTTAATGATGTCTAAAGAA 240
DB 210 ATTCATATATCATCAAAATTAATCTTCAAGAGCTTCAAGCGCTTAATGATGTCTAAAGAA 269
QY 241 ATGTGAAGCGCTCAGCCATCTGAAGGACAGGTATACAGCAATGATCAAAAAGAAAA 300
DB 270 ATATGAAGCTCCCTCAGCGCCGGAAGGACAGGTATACAGCAATGATCAAAAAGAAAA 329
QY 301 CCACAGGCGCTCCCTCCCTCCCATCTTGATGTGAAGCAGTCTTCAATTTCCATAGTAGT 360
DB 330 CCACAGGCGCTCCCTCCCTCCCATCTTGATGTGAAGCAGTCTTCAATTTCCATAGTAGT 389
QY 361 AAATTTTCAATGATCAAGCTTTGAGCTCAAAATCTGAAAGAAAGCTCCATTCGAAG 420
DB 390 AAATTTTCAATGATCAAGCTTTGAGCTCAAAATCTGAAAGAAAGCTCCATTCGAAG 449
QY 421 GAAATTTATCTTAAGATCTGTAATGATCTAA-TTTTTGTACATTTGGAATATTAAG 479
DB 450 GAAATTTATCTTAAGATCTGTAATGATCTAA-TTTTTGTACATTTGGAATATTAAG 509
QY 480 TTGT 483
DB 510 TTGT 513

RESULT 9
BE393340 727 bp mRNA linear EST 21-JUL-2000
LOCUS 601311002F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632568 5',
DEFINITION MRNA sequence.
ACCESSION BE393340
VERSION BE393340.1 GI:9338801

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 727)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Plate: L1CM324 row: c column: 01
High quality sequence stop: 610.
Location/Qualifiers
1..727

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3632568"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
/note="Organ: uterus; Vector: POT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptors: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.6%; Score 411; DB 2; Length 727;
Best Local Similarity 92.5%; Pred. No. 9.4e-26;
Matches 432; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 16 CAATTTATGAAGCAAAATATACAGCTTAAATGAAATGTGACCTTAATACCGAGAG 75
DB 165 CAATTTATGAAGCAAAATATACAGCTTAAATGAAATGTGACCTTAATACCGAGAG 224
QY 76 AACTCCCTTTGTAAGATTGTGAACAAAATTAATATAGTAGAGTTAATAGTTCTAATG 135
DB 225 CACCCCTTTGTAAGATTGTGAACAAAATTAATATAGTAGAGTTAATAGTTCTAATG 284
QY 136 GAAATGTGAACCAAGACCATATCAGCGCTAGCAAAATGGCAGAAATCATATATCATCA 195
DB 285 GAGTGTGAGCAAGACCATATCAGCGCTAGCAAAATGGTGAATTCATATAGCATCA 344
QY 196 AAGTTATCTTCAAGAGCTTCAAGCGCTTAATGATGTCTAAAGAAATGTGAAGCGCTC 255
DB 345 AAGTTATCTTCAAGAGCGTTCGCGCCCTAATGATGTCTAAAGAAATGTGAAGCGCTC 404
QY 256 AGCATTGTGAAGACAGTGTATACAGCAATGTATCAAAAAGAAAAACACAGGCGCTTCC 315
DB 405 AGCATTGTGAAGACAGTGTATACAGCAATGTATCAAAAAGAAAAACACAGGCGCTTCC 464
QY 316 CTGCCCGCATCTGATGATGAGCAGTCTTCAATTTCCATAGTAGTAATTTCTAGATAC 375
DB 465 CTGCCCGCATCTGATGATGAGCAGTCTTCAATTTCCATAGTAGTAATTTCTAGATAC 524
QY 376 AGCTTTGAGAGCTCAAAATCTGAAAGAAAGAGCTCCCATTCGAAGAAATTAATCTTAAG 435
DB 525 GCTTTGTAGAGCTCAAAATCTGAAAGAAAGAGCTCCCATTCGAAGAAATTAATCTTAAG 584
QY 436 ATACTGTAAATGATCTAATTTTGTATCTTTGTAATTTGTAATTTGTAATTTGTAATTTG 482
DB 585 ATACTGTAAATGATCTAATTTTGTATCTTTGTAATTTGTAATTTGTAATTTGTAATTTG 631

RESULT 10
BI489733 708 bp mRNA linear EST 28-AUG-2001
LOCUS 60302230F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173398 5',
DEFINITION mRNA sequence.
ACCESSION BI489733
VERSION BI489733.1 GI:15328961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 708)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LLM11431 row: 1 column: 07
High quality sequence stop: 704.
Location/Qualifiers
1..708
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5173398"
/lab_host="DH10B"
/clone.lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 6.6%; Score 410.8; DB 4; Length 708;
Best Local Similarity 92.1%; Pred. No. 1e-25;
Matches 444; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
3 CCATGGGCTCAGGCAATTTATGAAGCCAAATATACAGCTTAATAATAGATGAGACT 62
1 CCAAGGCTCGACAAATTTATGAAGCCAAATATACAGCTTAATAATAGATGAGACT 60
63 AAATACCCAGAAAGAACTCCCTTTGTAGATTGTAAACAAATTAATATGATGAGATT 122
61 AAATACCCAGAAAGCAACCCCTTTGTAGATTGTAAACAAATTAATATGATGAGATT 120
123 AATAGTTCTTAATGAATGTGTAACCAAGAGCCATATACAGCGCTAGCAAAATGGCAGAT 182
121 AATAGTTCTTAATGAATGTGTAACCAAGAGCCATATCAGTCTAGCAAAATGGCAGAT 180
183 TCATATATCATCAAAATTTCTCTCAAGAGCTTCAGCGCTAATGATGTCTAAAGAAAT 242
181 TCATATATCATCAAAATTTCTCTCAAGAGCTTCAGCGCTAATGATGTCTAAAGAAAT 240
243 GTGAAAAGCCCTCAGCCATCTGAAGAGCAGTGTACAGCAATGTATCAAAAAGAAAAC 302
241 ATGAAAGCTCCCTCAGCGCCGAGAGAGCAGTGTACAGCAATTTATCAAAAAGAAAAC 300

QY 303 ACAGGCCCTTCCCTTCCCATCTGATGTAAAGAGCTTCATTTCCATAGTAGTA 362
DB 301 ACAGGCCCTTCCCTTCCCATCTGATGTAAAGAGCTTCATTTCCATAGTAGTA 360
QY 363 ATTTCTAGATACAGCTTTAGAGCTCAAGAGTACTGAGAAAGAGCTCCCATTCAGAG 422
DB 361 ATTTCTAGATACAGCTTTAGAGCTCAAGAGTACTGAGAAAGAGCTCCCATTCAGAG 420
QY 423 AATTATCTTAAGATACCTGTAATGATGATAA-TTTTGTACATTTGGAATATATAGTT 481
DB 421 AATTATCTTAAGATACCTGTAATGATGATAA-TTTTGTCCATTTGGAATATATAGTT 480
QY 482 GT 483
DB 481 GT 482

RESULT 11
BUS07729
LOCUS BUS07729 894 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT_10095740 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6501710
5', mRNA sequence.
ACCESSION BUS07729
VERSION BUS07729.1 GI:22813962
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LLM14056 row: 1 column: 15
High quality sequence stop: 621.
Location/Qualifiers
1..894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6501710"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

FEATURES
source

ORIGIN

Query Match 6.5%; Score 403.2; DB 5; Length 894;
Best Local Similarity 92.5%; Pred. No. 3.7e-25;
Matches 434; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
16 CAATTATGAAGCCAAATATACAGCTTAATAATAGATGTGACCTTAATACCAAGAG 75
DB 169 CAATTATGAAGCCAAATATACAGCTTAATAATAGATGTGACCTTAATACCAAGAG 228
QY 76 AACTCCCTTTGTAAAGATTGTACAAATAATTAATATGAGTAAATAGTTCTAATG 135
DB 229 CACCCCTTTGTAAAGATTGTACAAATAATTAATATGAGTAAATAGTTCTAATG 288
QY 136 GAATGTGAACCAAGAGCCATATCAGCGCTAGCAAAATGCGAGAAATCATATATACATCA 195
DB 289 GATGTGTGACCAAGAGCCATATCAGTGTAGCAAAATGCGAGAAATCATATATACATCA 348

QY 436 ATACTGTAATGACTAA-TTTTGTACATTTGGAATATATAAGTTGT 48
|||||
Db 61 ATACTGTAATGACTAA-TTTTGTCCATTTGGAATATATAAGTTGT 13
|||||

RESULT 15
 BM739173 500 bp mRNA linear EST 01-MAR-2002
 LOCUS K-EST0008565 S3SNUI6 Homo sapiens cDNA clone S3SNUI6-3-H01 5', mRNA
 DEFINITION
 ACCESSION BM739173
 VERSION BM739173
 KEYWORDS EST, GI:19060502
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 500)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,U.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 3 row: H column: 01
 High quality sequence stop: 500.
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S3SNUI6-3-H01"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="Top10P"
 /clone_1lb="S3SNUI6"
 /note="Organ: Stomach; Vector: pTZ19RP1; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10P by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 6.5%; Score 402.6; DB 4; Length 500;
 Best Local Similarity 92.5%; Pred. No. 6e-25;
 Matches 434; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
 16 CAATTATGAAAGCCAAATATACAGCCTTAAATAGATGTGACCTAAATACCGAGAAG 75
 16 CATTATATGAAAGCCAAATATACAGCCTTAAATAGATGTGACCTAAATACCGAGAAG 75
 76 AACTCCCTTTGTAGATTGTGACAAATATATATGATGAGTAAATAGTTCTTAATG 135
 76 CACCCCTTTGTAGATTGTGACAAATATATATGATGAGTAAATAGTTCTTAATG 135
 136 GAATGTGAACCCAAAGCCATATCGCGCTAGCAAAATGCGAAGTTATATATATCATCA 195
 136 GAGTGTGACCCAAAGCCATATCGCGCTAGCAAAATGCGAAGTTATATATATCATCA 195

QY 196 AAGTTATCTTCAAGAGCTTCAAGCCCTAATGATGTCTTAAAGAAATGTGAAACGCCCTTC 255
 DB 196 AAGTTGTCTTCAAGAGAGCTTTCGCGCCTTAATGATGTCTTAAAGAAATATGAAACTCCCTTC 255
 QY 256 AGCCATCTGAAGAGACAGTGTTCAGCAATTGATCAAAAAAGAAAAACAAGGCCCTTCCC 315
 DB 256 AGCCGCCGAGAGACAGTGTTCAGCAATTATCAAAAAAGAAAAACAAGGCCCTTCCC 315
 QY 316 CTTCCCCCACTGTGATGATGACAGTCTTCATTTTCCATAGTAGTAAATTTTCTAGATAC 375
 DB 316 CTTCCCCCACTGTGATGATGACAGTCTTCATTTTCCATAGTAGTAAATTTTCTAGATAC 375
 QY 376 AGCTGTATAGCTCAAGAGTCTGAGAAAGAAAGCTCCCATTTCAAGAAATTTATCTTAG 435
 DB 376 GTCTGTATAGCTCAAGAGTCTGAGAAAGAAAGCTCCCATTTCAAGAAATTTATCTTAG 435
 QY 436 ATACTGTAAATGATGACTTAA-TTTTGTACATTTGGAATATATAGTTGT 483
 DB 436 ATACTGTAAATGATGACTTAA-TTTTGTACATTTGGAATATATAGTTGT 484

Search completed: December 27, 2004, 10:56:48
 Job time : 11864.7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using ew model

Run on: December 26, 2004, 17:40:11 ; Search time 9563.51 Seconds
(without alignment)
19051.434 Million cell updates/sec

Title: US-10-786-065-3_COPY_1_5000

Perfect score: 5000
Sequence: 1 tataggccatgcgtgcgtc.....ctatcttcttctatcttgc 5000

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 1821986508 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	473.8	9.5	856	9	CL301570 gp808-CH2
C 2	440.2	8.8	483	8	AQ138494 HS_3076_B
C 3	433	8.7	819	8	BZ879668 CH240_195
C 4	402.8	8.1	482	8	AQ466201 HS_5157_A
C 5	401.4	8.0	431	8	AO052162 RPT11-50
C 6	374.8	7.5	436	8	B34439 HS_1024-B2-
C 7	359.4	7.2	676	8	BZ879665 CH240_195
C 8	325.2	6.5	5940	3	CR627133 Homo sapi
C 9	316.2	6.3	472	8	AQ709562 HS_5484_B
C 10	302.8	6.1	6146	8	AO839831 260L13-C4
C 11	292.8	5.9	1300	8	AF057104 AF057104
C 12	292.8	5.9	321	8	AQ072178 HS_3010_B
C 13	291.6	5.8	1279	3	BC037921 Homo sapi
C 14	284.8	5.7	647	4	BM559057 AGENCOURT
C 15	284.8	5.7	660	4	AL120269 DKEP2761K
C 16	282	5.6	564	5	BU860291 AGENCOURT
C 17	282	5.6	566	5	BU957747 AGENCOURT
C 18	281.2	5.6	1706	3	CR619443 full-length
C 19	279.2	5.6	515	8	AQ019248 CIT-HSP-2
C 20	279	5.6	1644	3	BC037923 Homo sapi
C 21	277	5.5	2100	3	AF289610 Homo sapi
C 22	276.4	5.5	669	3	AG155696 Pan trogl
C 23	276.4	5.5	714	6	CD363358 UT-H-F71-
C 24	276	5.5	576	6	CA427630 UT-H-DP0-

25	275.8	5.5	444	8	B89781	B89781 CIT-HSP-217
26	275.8	5.5	758	5	BQ708090	BQ708090 AGENCOURT
27	275.2	5.5	1029	4	BM471041	BM471041 AGENCOURT
28	274.6	5.5	513	5	BM42735	BM42735 DKEP2781P
C 29	274.4	5.5	3288	3	HS802613	AL161992 Homo sapi
C 30	274.2	5.5	3713	3	BC041839	BC041839 Homo sapi
C 31	274	5.5	924	5	BO674842	BO674842 AGENCOURT
C 32	273.8	5.5	709	6	CD359469	CD359469 AGENCOURT
C 33	273.8	5.5	736	7	CN280511	CN280511 170004241
C 34	273.8	5.5	772	5	BU928605	BU928605 AGENCOURT
C 35	273.8	5.5	882	5	BQ227019	BQ227019 AGENCOURT
C 36	273.4	5.5	701	5	BU615970	BU615970 UT-H-DFO-
C 37	273.2	5.5	3863	3	BC035034	BC035034 Homo sapi
C 38	273	5.5	664	8	AQ343449	AQ343449 RPT11-12
C 39	272.8	5.5	657	9	AG182991	AG182991 Pan trogl
C 40	272.6	5.5	822	4	BG249643	BG249643 602319736
C 41	272.2	5.4	514	8	AQ002001	AQ002001 CIT-HSP-2
C 42	272.2	5.4	541	6	CA437967	CA437967 UT-H-DHO-
C 43	272.2	5.4	727	6	CA440514	CA440514 UT-H-EDO-
C 44	272.2	5.4	1050	6	CD252308	CD252308 AGENCOURT
C 45	272	5.4	471	8	AZ695036	AZ695036 UP_396-2K

ALIGNMENTS

RESULT 1	CL301570/c	856 bp	DNA	linear	GSS 20-FEB-2004
LOCUS	gp808 CH257 PP0080Q4 SP6 A08CD726				CHORI-257 Lemur BAC library
DEFINITION	Microcebus murinus genomic clone CH257-8B16, genomic survey				
ACCESSION	CL301570				
VERSION	CL301570.1	GI:42718759			
KEYWORDS	GSS.				
SOURCE	Microcebus murinus	(gray mouse lemur)			
ORGANISM	Microcebus murinus				
REFERENCE	1 (bases 1 to 856)				
AUTHORS	Dore, C., Zhang, X., McKee, K.H., Forgetta, V., Lepage, P., Hudson, T.J.				
TITLE	MUGQ Lemur Physical Mapping Project				
JOURNAL	Unpublished (2004)				
COMMENT	Other GSSes: gp808-CH257_PP0080Q4_T7u_A08CD726				
	Contact: Dewar K				
	McGill University and Genome Quebec Innovation Centre				
	740 Dr. Penfield Room 7214, Montreal, QC, Canada, H3H 1A4				
	Tel: 514 398 3311 x00089				
	Fax: 514 398 1795				
	Email: ken.dewar@mcgill.ca				
	Plate: 8 row: B column: 16				
	Seq primer: SP6 : CTGGCCGTCGACATTAGG				
	Class: BAC ends.				
FEATURES	Location/Qualifiers				
source	1..856				
	/organism="Microcebus murinus"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:30608"				
	/clone="CH257-8B16"				
	/sex="female"				
	/cell_type="kidney"				
	/clone_lib="CHORI-257 Lemur BAC library"				
	/note="Vector: pTARBAC2.1 vector; Site 1: EcoRI; Site 2: EcoRI. The CHORI-257 mouse lemur BAC library has been constructed by Michael Medvedov in Pieter de Jong's laboratory at BACPAC Resources, Children's Hospital Oakland Research Institute. The preparation of the library followed the cloning approach developed in our laboratory (Osoegawa et al., 1998). Kidney was obtained from an adult female mouse lemur (Microcebus murinus) through John				

Allman, Division of Biology 216-76, Caltech, Pasadena, CA 91125. The local identification number for this animal is #8. A skin biopsy and a blood sample have been sent to the Coriell Cell Repositories to establish cell lines as part of the Integrated Primate Biomaterials and Information Resource (IPBIR) initiative. High-molecular-weight DNA was isolated from a kidney cell suspension prepared in a Dounce Homogenizer and the cells were embedded in agarose to stabilize the DNA. The embedded DNA was partially digested with a combination of EcoRI restriction enzyme and EcoRI methylase and size fractionated by pulsed-field electrophoresis. DNA fragments from the appropriate size fraction were cloned into the pTRBAC2.1 vector between the two EcoRI sites. The ligation products were transformed into DH10B (T1 resistant) electro-competent cells (Invitrogen). The library has been arrayed into 576 '384-well' microtiter dishes and also gridded onto twelve 22x22cm nylon high-density filters for screening by probe hybridization. Each hybridization membrane represents about 18,000 distinct mouse Lemur BAC clones, stamped in duplicate. Library characterization was performed by Qing Cao, Teresa Ren and Kazutoyo Osoegawa. This work was funded by NIH grant HG025323-01."

ORIGIN

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Query Match      9.5%; Score 473.8; DB 9; Length 856;
Best Local Similarity 80.3%; Pred. No. 8.5e-48;
Matches 614; Conservative 0; Mismatches 137; Indels 8; Gaps 5;

QY 3378 ATGCGACAGTTTACAGAGGATGAGAGTACATAGCTGGAGAGCTTTAGA 3437
    |||||
DB 856 ATCTCAGTTACAAAGGATTTAGCAGTGTAGTACTTTAGTGAAGAGCTTTAGA 797
    |||||

QY 3438 GATGAGATGCGGC-CCCCCAATTCATATTAAGCCAGGTGAGACATCAGAACT 3496
    |||||
DB 796 GATGAGGATGCCAGGCCCTTTATTTTACATTAAGCCAGGAGACATCAGAACT 727
    |||||

QY 3497 TCATACACACAGACCTGTGCAAGACATGCGCAGGAGAGAGACATGATTAAT 3556
    |||||
DB 736 TCACAGATTCAGACCTGTGCAAGACCTGCGCAATGAGAGAGAGGATGTT 677
    |||||

QY 3557 TAAACAGCCTTGAAGAAACAAACCTGCGCTTCAATTAATCAAGCCACTTAA 3616
    |||||
DB 676 TAAATAGCCTGGAAGAAACAAACCTG-CTTGCCCTATTTAAATCAGCAATCGAAA 618
    |||||

QY 3617 TGTTCATCAGCCTTTCCCTCTTCATTCAGAAATCAAGAAATAGACATTC 3676
    |||||
DB 617 TATTTATAGCCTTTCCCTCTTCATTCAGAAATCAAGAAATAGACATTC 558
    |||||

QY 3677 TCTACTACGACCCAAAGAAACATTTACCTTCAGGCGCTGTGGAGGACAGTTGTA 3736
    |||||
DB 557 TTTACTACTGACCCAAAGAAATGATTAACATCTGTAGGAGGTGGAGGACAGTTGTA 498
    |||||

QY 3737 AAGCGTCTTAACAGGTTTTTATATCCCTCCCTTAATCAATGACAGAGTTTGAAT 3796
    |||||
DB 497 AGGTATCTCTAAGAGATTTTATATATCCCTCCCTAATGATGACAGAGTTTGAAT 438
    |||||

QY 3797 GCGAACCCTGAATTTGCTGCTTATTCCTTCACCTGGCCTTTATAGAAGAACTGAAGT 3856
    |||||
DB 437 GCGAACCCTGAATTTGCTGCTTATTCCTTCACCTGGCCTTTATAGAAGAACTGAAGT 378
    |||||

QY 3857 GGTTCGCAAAATTAATGATCAAGAAAGATGATAAATCTGATATTTTATATTTGA 3916
    |||||
DB 377 GGTTCGCAAAATTAATGATCAAGAAAGATGATAAATCTGATATTTTATATTTGA 322
    |||||

QY 3917 AATATACAAATATGTCTGAGATTAATAATCTGTTATCAAAAGCTAGTACTAAT 3976
    |||||
DB 321 AATATACAAATATGTCTGAGATTAATAATCTGTTATCAAAAGCTAGTACTAAT 262
    |||||

QY 3977 TGGTAAACCAACCACTTTGTTAAATATATGTAAGATTCAGTAAT--CCCTTTAGT 4034
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DB 261 TGGTAAACCAACCACTTTGTTAAATATATGTAAGATTCAGTAATTCATCTTTAGC 202
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QY 4035 CAAGTGGGAAAGTTGATGATGCTTTTCTTTATGTTACTCCATAGAGAAAGT 4094
    |||||
DB 201 TAAGTGGGAAAGTTGATGATGCTTTTCTTTATGTTACTCCATAGAGAAAGT 142
    |||||

QY 4095 AATGCTCAATGCTGTTTAAATTAATTTTAAATAT 4133
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DB 141 AATGCTCAATGCTGTTTAAATTAATTTTAAATAT 103
    |||||

```

```

RESULT 2
A0138494
LOCUS
DEFINITION
HS_3076_B1_B01_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3076 Col=1 Row=D, genomic survey
sequence.
ACCESSION
A0138494
VERSION
A0138494.1 GI:3529147
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 493)
REFERENCE
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
9930589
PUBMED
10449764
COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3076 Row: D Column: 1
Class: BAC ends
High quality sequence strop: 483.
location/Qualifiers
1..483
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3076 Col=1 Row=D"
/sex="male"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

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ORIGIN
Query Match      8.8%; Score 440.2; DB 8; Length 483;
Best Local Similarity 99.3%; Pred. No. 1.2e-43;
Matches 442; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3665 AATAGACATTCCTACTACTGACCCAAAGAAATTAATCACTTCAGGCGCTGTGGAG 3724
    |||||
DB 39 AATAGACATTCCTACTACTGACCCAAAGAAATTAATCACTTCAGGCGCTGTGGAG 98
    |||||

QY 3725 GCAAGTTGTTAAGCGTCTCTACAGGTTTTTATATTCCTCCCTTAATCAATGACA 3784
    |||||
DB 99 GCAAGTTGTTAAGCGTCTCTACAGGTTTTTATATTCCTCCCTTAATCAATGACA 158
    |||||

QY 3785 GAGTTTGAATNGGAACCTGGAATTTGCTGCTTATTCCTCCACGCGCTTTAAGAA 3844
    |||||
DB 159 GAGTTTGAATNGGAACCTGGAATTTGCTGCTTATTCCTCCACGCGCTTTAAGAA 218
    |||||

QY 3845 GAAACTGAAGTTGTTTCTGCAAAATTAATGATGATCAAGAAAGATGATAATCTAGATT 3904
    |||||
DB 219 GAAACTGAAGTTGTTTCTGCAAAATTAATGATGATCAAGAAAGATGATAATCTAGATT 278
    |||||

```


QY 3905 TTATAATTTGGCAAAATACACAAAATGTCTGGAGAAATPAAAATACTGCTTATCCAAAAGCT 3964
DB 279 TTTATATTTGGCAAAATACACAAAATGTCTGGAGAAATPAAAATACTGCTTATCCAAAAGCT 338
QY 3965 AAGTACTAATTTTGGTAAACCAACCACTTGTAAATATATATGAAAAGATCCATGAAATTC 4024
DB 339 AAGTACTAATTTTGGTAAACCAACCACTTGTAAATATATGAAAAGATCCATGAAATTC 398
QY 4025 CCCTTTAGTCAGAGTGGAGAAAGTGGATGCTGCTTTTCTTTATGTTACTCCAAATAG 4084
DB 399 CCCTTTAGTCAGAGTGGAGAAAGTGGATGCTGCTTTTCTTTATGTTACTCCAAATAG 458
QY 4085 AGAGAAAAGTATGCTCAATAGTG 4109
DB 459 AGAGAAAAGTATGCTCAATAGTG 483

RESULT 3
B2879668/c 819 bp DNA linear GSS 18-MAR-2003
LOCUS CH240_195A22.TUB CHORI-240 Bos taurus genomic clone CH240_195A22,
DEFINITION genomic survey sequence.
ACCESSION B2879668
VERSION B2879668.1 GI:29107070
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 819)
Zhao,S., Shetty,J., Shateman,S., Tsegaye,G., Geer,K.,
Shavritsbeys,A., Gebregregis,E., Chen,D., Riggs,F., de Jong,P.,
Crawford,A.M. and McEwan,J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdjong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by AgResearch Ltd., New Zealand and The
Institute of Genomic Research (TIGR), USA.
Plate: 195 row: A column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_195A22"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull H Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match 8.7%; Score 433; DB 8; Length 819;
Best Local Similarity 78.9%; Pred. No. 7e-43;
Matches 651; Conservative 0; Mismatches 140; Indels 34; Gaps 10;

QY 2202 CCGAGAGTCAAGCTGAGACCAAGAGGCTGCTTCAAGATTTGTTATCCAGAGAGA 2261
DB 819 CAGAGAGAGTCCCTGCTGTATGACGAGGCTGGATCGATGATTCATATCCCG--GA 764
QY 2262 GCATCTTCTCTATTGATTAACCAAGAGTTCAGACCTCCCTTTTGTAGGGGATCTG 2321
DB 763 GCATCTTCTCTATTGATTAACCAAGAGTTCAGACCTCCCTTTTGTAGGGGATCTG 707
QY 2322 ATTCCTCTCGGTAGTCTTAAACCAATPAAAATGAAAATTCATTAAAGTCACAGAAAAT 2381
DB 706 CTTTCTCTCATTTAGACATPAGGCATPAAAATTCATTAAAGTCACAGAAAATG 647
QY 2382 TATGCTGTAGTATCAAAATTTGGGGAATTTCTGTAAACCAAGGAAAATTAATCT 2441
DB 646 TGTGCTGTGTATCAAAATTCGGGGAATTTCTTTTAAACCAAGGAAAATTAATCT 587
QY 2442 TGGCTTTGGGCTGCAGCAAACTCACTTGGCTGGAAGTCGAGAAAGTATCTCAAAAT 2501
DB 586 ATGCTTTGGGCTGCAGCAAACTCACTTGGCTGGAAGTATCTCTTGAAT 527
QY 2502 CTCTAAGTCTTAAATTAAGAGCTGAACTTAAAGCAAGCTGAGTATTAGTTGTA 2561
DB 526 CTCTGAAGTACGAATTAAGCAAGCTGAACTTAAAGCAAGCTGAGTATTAGTTGTA 470
QY 2562 TGTATGATTTGAACTTTAG-TAATTAATGATGATTTATTAAGCAATCCATAGA---- 2616
DB 469 TCTATGATTTGAACTTTAG-TAATTAATGATGATTTATTAAGCAATCCATAGA 410
QY 2617 -TTATTCCTTCAAGCAATTAATTAAGCAATGAAAGGAAAGGAAAGGAAAGGAAAGG 2674
DB 409 AGTTATTTCCCTTCAAGCAATTAATTAAGCAATGAAAGGAAAGGAAAGGAAAGGAAAGG 350
QY 2675 GAAAAGTGTGCAAAACATCAATCAAGAGATTTAGTTAGCTGAATG-TAAGACAC 2733
DB 349 GAAAAGTGTGCAAAACATCAATCAAGAGATTTAGTTAGCTGAATG-TAAGACAC 292
QY 2734 A-TTTTAGTGAAGAAAGATGATGATTTAGAGATTTAGCTGAATG-TAAGACAC 2791
DB 291 ATTTTATGATTTAGAGAAAGATGATGATTTAGAGATTTAGCTGAATG-TAAGACAC 232
QY 2792 -----CAGGATCTTCAAGAAAGGCTTTTGGGGGTACAGAAAGCTTAGAA 2840
DB 231 TTTTATTAAGGATCGATGTTCAAGAAAGGATTTAGAAAGTGTGGAAAGCTTAGAA 172
QY 2841 AACATTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2900
DB 171 AACATTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 113
QY 2901 CTTTACTTGCATTAATTTTATTTTCTGCTCTTTTCTTTTCTTCTTCTTCTTCTTCTT 2960
DB 112 CTTTACTTGCATTAATTTTATTTTCTGCTCTTTTCTTTTCTTCTTCTTCTTCTTCTT 53
QY 2961 AGAAGCATGATGATTCATGATTCATGATTCATGATTCATGATTCATGATTCATGATTC 3005
DB 52 AGAAGCATGATGATTCATGATTCATGATTCATGATTCATGATTCATGATTCATGATTC 8

RESULT 4
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LOCUS HS_5157_A2_B06_SPEE RPCI-11 Human Male BAC library Homo sapiens
DEFINITION genomic clone Plate=73 Col=12 Row=C, genomic survey sequence.
ACCESSION AQ466201
VERSION AQ466201.1 GI:4643296
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)
Mahira,G.G., Wallace,J.C., Smith,K., Shavritsbeys,A.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

TITLE	Hood, L.
JOURNAL	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED	99380589
COMMENT	10449764
	Contact: Mahairas GG, Wallace JC, Hood L

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High quality sequence stop: 482..
FEATURES
    source
    1..482
```

wallace@u.washington.edu
are derived from the human BAC library RPCT-11. For BAC
availability, please contact Pieter de Jong
resources (http://bacpac.med.buffalo.edu). Clones may be purchased from
Research h Genetics (info@resgen.com). BAC end Web Server:
www.hscg.washington.edu
33 row: C column: 12
er: SP6
BAC ends
ility sequence stop: 482.
Location/Qualifiers
1. .482
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=733 Col=12 Row=C"
/sex="male"
/clone_id="RPCT-11 Human Male BAC Library"
/note="(vector: BAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
BAC3.6 vector at EcoRI sites"

ORIGIN

Query Match	8.1%	Score 402.8;	DB 8;	Length 482;
Best Local Similarity	91.5%	Pred. No. 3.7e-39;		
Matches 439;	Conservative	0;	Mismatches 37;	Indels 4;
				Gaps 1;

QY	4301	ATGCTGTTATTATTATTTTCTGTTAAACAGAGATTGTAGGGGACATACAGTTTATT	4366
Db	481	ATGCTGTATCATTTATCTTTCTGTTACAGAGCTGTGAGGCCATACAGTTTATT	422
QY	4361	TTATTATTATTATTATA-----TTATTATTATTATTGGAATGGAATCTCTGACCC	4416

4417 ACGCTGAGTGCAGTGTGCGATCTCAGATGACTGCACACTCTGCTCCTGAGTTCAGGC 4476

Dp 361 AGGCTGGAGTGCAGTGTGGGATCTCAGATGATGCACCTCTGCTCTGAGTTCAGC 302

4477 AACCTCTGCCCCCTGACCTTATACCTTTCTTAATCTGTTTACGATGGTGACCTTA 4536

D_b 301 AACTCTCATGCCCCCTGGCCCTTATACTTCTTATCTGTATTAGTCATGGGTACCTTA 242

4537 ACTTTTTCATGCTGAGAACATCTGCAATAAAGACCACTTTTAATTCTAAGCT 4596

241 ACTTTTTCAGTCTGAGACATCTGCANATAGGACCACATTATGTGTATTCTAAGCT 182

7577 CCCCCAATACAAATAGGATACAGTTCATGAGTGGCTCGGACGGGGGCAACCT 4656

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001

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4717 CTTTGATTGTTCTGCACAGACCTTTCCAGCCGGAAGTTTACAACAATTCACTTAAATCTTTT 4726

Ddb
61 CTTTGATTGTTCTGCACAGACCTTCCAGCCCGAAGTTGACACAGAAATTCGAAATCCCTT 2

RESULT 5	431 bp	DNA	Linear	GSS 20-APR-1999
LOCUS	AC052162			
DEFINITION	RCF11-50K8.TK RPC1-11 Homo sapiens genomic clone RCF1-11-50K8, genomic survey sequence.			
ACCESSION	AC052162			
VERSION	AC052162.1	GI:349199		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE AUTHORS	TITLE JOURNAL COMMENT
1 (bases 1 to 431) Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venette, J. C.	Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998) Other GSSs: RPC11-50K8.TU	

TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: RPC111-50X8, TU
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel.: 301 838 0200
 Fax: 301 838 0208
 Email: mdamad@tigr.org
 Clones are derived from the human BAC library RPC1-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPIC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html
 Class: BAC end.

FEATURES	Location/Qualifiers
source	1. .431

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/sex="Male"
/cell_type="lymphocytes"
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RPC11 Human Male BAC Library"

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ORIGIN

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Best Local Similarity	98.5%;	Pred. No. 5	7e-39;	
Matches 405;	Conservative	0;	Mismatches 6;	Indels 0;
				Gaps 0;

3647 ATTGAGGATTTCAAGGAAATGACATTTCTACTACTGACCCAAAGAACATTATCAC 3706

Dd 21 ATCCGCGGATTCAAAGAAATAGACATTCTCTACTGACCCGAGAACAATTATCAC 80

3/0/ 1C1CAGGCC1G1G5AGGACAG1GG1AAAGCG1C1CAACAGG1T1TTATA1ACCT 3/66

01ACACAGCCGATGGAGCACAGTGGATTACAGCTCCTACACAGGTTTTTTATATCCCC 140

[illegible]

3827 CACCCTGGGCTTTTATTAAGAACTGAGCTTGGCTTTCTGGAAATTAATGCTACATGCAAAAG 3885

201 CACCTGCGCTTTATAGAAGAACTGAAGTTGTGTTCTGCAAA TTATGTTACATGCAAAAG 260

3887 ATGATAATCCTAGATTTTATATTTGCAAAATACACAAAATGCTCGAGATAAAAT 3946

Db 261 ATGATAAATCCTAGATTTTATATTGGCAAATACACAATAATGTCGAGAATAAAAAT 320

QY 3947 ACTGCTTATCCAAAGCTAAGTACTAATTTTGGTAAACACCACTTTGTTAATATATG 4006
 DB 321 ACTGCTTATCCAAAGCTAAGTACTAATTTTGGTAAACACCACTTTGTTAATATATG 380
 QY 4007 TAAAGATCATGATTTCCCTTTTGTGTCAGGTTGGAAAGTGTGATGTC 4057
 DB 381 TAAAGATCATGATTTCCCTTTTGTGTCAGGTTGGAAAGTGTGATGTC 431

RESULT 6
 B34439 436 bp DNA linear GSS 17-OCT-1997
 LOCUS HS-1024-B2-B02-MF.abi CIT Human Genomic Sperm Library C Homo
 DEFINITION sapiens genomic clone Plate=CT 803 Col=4 Row=D, genomic survey
 sequence.
 accession B34439
 version B34439.1 GI:2533808
 keywords GSS.
 source Homo sapiens (human)
 organism Homo sapiens
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 authors Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
 Tralcoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.B.
 title Construction of a Characterized Clone Resource for Genomic
 Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
 Tagged Connectors
 journal Unpublished (1997)
 comment Contact: Mahairas GG, Zackrone KD, Hood L
 University of Washington
 Seattle, WA 98195, USA
 Tel: (206) 616-8744
 Fax: (206) 685-7301
 Email: kzackroneu.washington.edu
 sequence tagged connector
 plate: CT 803 row: D column: 4
 class: BAC ends
 high quality sequence stop: 436.
 location/Qualifiers
 1. 436
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 /mol_type="genomic DNA"
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 /sex="M"
 /clone.lib="CIT Human Genomic Sperm Library C"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
 E-Coli DH10B"

ORIGIN
 Query Match 7.5%; Score 374.8; DB 8; Length 436;
 Best Local Similarity 99.0%; Pred. No. 8,9e-36;
 Matches 387; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2829 GGAAGCTTGAAGAACTTTGAAGAGTGAAGGAAATGAAGGAAATGAAGGAAATGCTTTTAC 2888
 DB 47 GCAGAGCTTGAAGAACTTTGAAGAGTGAAGGAAATGAAGGAAATGAAGGAAATGCTTTTAC 106
 QY 2889 CAGGCACTGAATTTTACTTGTGATTAATTTTCTGCTCTTTCTTTTCTCTAGCT 2948
 DB 107 CAGGCACTGAATTTTACTTGTGATTAATTTTCTGCTCTTTCTTTTCTCTAGCT 166

QY 2949 AACAGACTTAAAGAAAGATCATGTTCCATGACTTATTCACCCAGGGAGCTTCAAGC 3008
 DB 167 AACAGACTTAAAGAAAGATCATGTTCCATGACTTATTCACCCAGGGAGCTTCAAGC 226

QY 3009 TGGCCGTGCCAGAGTTCAAGAGTAAAGCCAGAGAGTAAAGAGTATTTTCAAGA 3068
 DB 227 TGGCCGTGCCAGAGTTCAAGAGTAAAGCCAGAGAGTAAAGAGTATTTTCAAGA 286

QY 3069 AGAGGATCTGAGGAGGTTTTCAGTGGGTGAGTGAAGCTAGTGTGATCAAGAAGAA 3128
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DB 287 AAGAGATCTGAGCAGAGGTTTTCAGTGGGTGAGTGAAGCTGATTCATGATCAAG-A 345
 QY 3129 TTTAATGAGCTTGTCTACGAGAGCCGCCCTTGTCTCAGGCAATTAATGAGCGAGC 3188
 DB 346 TTTAATGAGCTTGTCTACGAGAGCCGCCCTTGTCTCAGGCAATTAATGAGCGAGC 405
 QY 3189 CTTCCCAAGTCTGCTGCAATGCTGTCTA 3219
 DB 406 CTTCCCAAGTCTGCTGCAATGCTGTCTA 436

RESULT 7
 B2879665/7 676 bp DNA linear GSS 18-MAR-2003
 LOCUS CH240_195A22.TU CHORI-240 Bos taurus genomic clone CH240_195A22,
 DEFINITION genomic survey sequence.
 accession B2879665
 version B2879665.1 GI:29107067
 keywords GSS.
 source Bos taurus (cow)
 organism Bos taurus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 authors Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
 Shvartsbeyn,A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P.,
 Crawford,A.M. and McEwan,J.C.
 title Bovine BAC End Sequences from Library CHORI-240
 journal Unpublished (2003)
 comment Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@igr.org
 clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.chori.org).
 clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBMC) by AgResearch Ltd., New Zealand and The
 Institute of Genomic Research (TIGR), USA.
 plate: 195 row: A column: 22
 seq primer: SPE
 class: BAC ends.
 location/Qualifiers
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 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN
 Query Match 7.2%; Score 359.4; DB 8; Length 676;
 Best Local Similarity 79.6%; Pred. No. 5.3e-34;
 Matches 544; Conservative 0; Mismatches 111; Indels 28; Gaps 9;

QY 2389 GTAGTATCAAAATTTGGGAAATTTCTTGTAAACCAAGGAAATTAATCTTGCTTT 2448
 DB 676 GTAGTATCAAAATTTGGGAAATTTCTTGTAAACCAAGGAAATTAATCTTGCTTT 618
 QY 2449 GGGCTGCAAGAACTACTGCTTGAAGTCAAGGAAAGTCTCTCAAAATCTCTAAG 2508
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Db      617 GGGGTGACGAGAAATTCACCTTGCTTGACATCAAGAAAGTATTTCTTGAATCTCTGAA 558
Qy      2509 GTCTTAATTAACAGAGCTGAAACTTTAAAGGCAAGCTGACATTAAGTTGTAATGCTATG 2568
Db      557 GTACGAAATTAAGGAGCTGAACCTCAAAAAAACAAGCGCGGTAT---TTGTAATCTATG 501
Qy      2569 GATTGGAACCTTAG--TAATTAAGTCAATTAATTAAGCAATGACATGAGCA-----TTAAT 2621
Db      500 GATTAAATTTTCAAGTTAATTAAGTCAATGCTATCAAGCAATGCTATGACAGAAAGTAT 441
Qy      2622 CCCCTACAGCAATTAATTAAGTGAACATGAAAAAAGCACTTAATTAAGCAAAAAA 2681
Db      440 CCCCTAAAGAGTAAATTAAGGACAAAGAAAAAAGCTTAAGTTTAAGCAAAAAA- 382
Qy      2682 GTTGCAAAACATCTCAATTAAGAGATTAGTTAAGCTGAATGT-TAAAGACAA-TTTTT 2739
Db      381 -TTGGAACCCATCATCAGAGAAATTTAGGTTAACCTAAGTGTCTAAAGCAATTTTTT 323
Qy      2740 AGGTGAAGAAAGATGATGATTTTCAAGAGTTGATACCATTAATGCTTTTTCAGGGATC 2799
Db      322 AGGTAAAGAAAGATGTGTGTTTGAAGATGATATCATTAATGCGTTTGTGTTTTT 263
Qy      2800 T-----TTCAAGAAAGTGCTTTTGGGGGTACAGAAAGCTTAAGAAACATTT 2847
Db      262 AAAGAACTGATGTTCAGAAAGTACATTTTGAAGTGTGGAGCTTAAGAAACATTT 203
Qy      2848 GAAGAGTGAAGAAAGAGCAATTAAGAAAAATGCTTTTACAGGCACTGAATCTTATCT 2907
Db      202 GAAGAGTGAAGCAATCAGCAATTAAGAAAAAGCGTTTATGTAAGC-CATTTGCTTGAAGT 144
Qy      2908 TTGCAATAATTTTATTTCTGCTCTTTCTTTTCTCTAGTAAACAGACTTAAGAAAGCA 2967
Db      143 TTGCAATAATTTTATTTCTGCTCTTTCTTTTCTCTAGTAAACAGACTTAAGAAAGCA 84
Qy      2968 TCATGTTCCATGACTTCAATTTTCAACCCAGGGAAGCTTCAAGCTCCCGTCCGAAAGTT 3027
Db      83 TCATGTTCCATGACTTCAATTTTCAACCCAGGGAAGCTTCAAGCTCCCGTCCGAAAGTT 24
Qy      3028 AAGAGTAAAGGCGCAGGAGTAA 3050
Db      23 AAGAGTAAAGGCGCAGGAGTAA 1

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RESULT 8
LOCUS   CR627133.c 5940 bp mRNA linear HTC 03-AUG-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp686J154 (from clone DKFZp686J154).
ACCESSION CR627133
VERSION  CR627133.1 GI:50949747
KEYWORDS HTC.
SOURCE  Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 5940)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amlid, C., Osanger, A.,
Fob, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (13-JUL-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuenberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BWFZ (Biomedical Research Center at the
Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686J154) is available at the RZPD Deutsches Ressourcenzentrum
fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD
for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp686J154
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers

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DH10B; sites Sfi1A + Sfi1B"
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/note="unclassified"

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Best Local Similarity 66.5%; Pred. No. 2.9e-30;
Matches 546; Conservative 0; Mismatches 259; Indels 16; Gaps 5;

Qy      114 GTACAAATTAATTAAGAAATTTTCCAGGCAATGCTGCGTGCACCCAGTCCAGCTATTT 173
Db      4932 GTTAAAGAGTAAAGATTAATGCTGAACACAGCGGTCACTGTAAATCCAGC-ACCT 4874
Qy      174 GGGAGCTGAGGTAGAGGAAATGCTTGAAGCCAGAGTTGAAGACAGCTTAGGCAAT 233
Db      4873 AGGAGCTGAGGTGCTAGGACCAATTAAGCCCAAGATTCAAGACAGCTGAGCAACAT 4814
Qy      234 AGTGAACCCGTGCTATTAATA-----AATAATTAAGTGTGTTCTTGGACACAGGCTG 288
Db      4813 GGTGAACCCGTGCTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4754
Qy      289 CAG--CTAGCTCTCGAAGACTGAGTGGAGATCACTGAGCCAGAGGCTAGAGCT 346
Db      4753 TAGTCTCTGCTACTGAGGAGCTGAGTGGAGATCAATTAAGTGTGCTGAGCT 4694
Qy      347 GCAATGAACAGATGATCAACCACTGATTTCCAGCTGGAAGACAGAGGAACTCTGTTT 406
Db      4693 GCAATGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4634
Qy      407 CCAAAAAAAAAAAAAAAAAAATGCAAGAAAGACATCATTAATTAATTAATTAATTAATTA 466
Db      4633 CACATGAAGAAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4574
Qy      467 ACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 526
Db      4573 TATATTT-----TATGTTAAATATCTCAAGAGAGGATTAATAAATCATGAGATTA 4520
Qy      527 ATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 586
Db      4519 TAAAGACAGAGTAAAGATTTGAGAAACAAACATTTGATTTGTTCCATTAATTAATTAATTA 4460
Qy      587 ACTCTCTAGTTGTGAGTCAAAACTTTATATGATGTC--TTTGGCCGGGTGCGGTGCTACAG 644
Db      4459 ACTCTCACTGACTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4400
Qy      645 CCTGTAAATCCAGCACTTTGGAGGCGGAGCGGAGTATCAAGTTAGAGATTCAG 704
Db      4399 CCTGTAAATCCAGCACTTTGGAGGCGGAGCGGAGTATGAGTATGAGATTCAG 4340
Qy      705 ACCATCTCGCTAAACAGGTGAACCTGCTCTTAATAATAATAATAATAATAATAATAATAATA 764
Db      4339 ACCATCTCGCTAAACAGGTGAACCTGCTCTTAATAATAATAATAATAATAATAATAATAATA 4280
Qy      765 TGGGTGCGCAGACGCTGTAGTCCAGTGTCTCAGAGAGGCTGAGCAGAGATGATG 824
Db      4279 CGTGTGCGCGGCACTGTAGTCAAGTACTTAGAGAGGCTGAGGCAAGATATGCGT 4220
Qy      825 AACCGGAGAGCGAGGCTTGAAGTGAAGCGGAGTTGGCCCACTGACATCCAGCTGGGCG 884
Db      4219 AACCTGGAGGAGGAGCTTGAAGTGAAGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4160
Qy      885 ACAATGCGAGACTGTCTCAAAAAAAAAAAAAAAAAAAG 925
Db      4159 ACAAGACGAGACTGTCTCAAAAAAAAAAATCAATTGAGACAAAG 4119

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RESULT 9					
LOCUS	AQ709562/c	472 bp	DNA	linear	GSS 07-JUL-1999
DEFINITION	HS_5494_B2-B04-T7A RPCR-11 Human Male BAC Library Homo sapiens genomic clone Plate=1060 Col=8 Row=D, genomic survey sequence.				
ACCESSION	AQ709562				
VERSION	AQ709562.1 GI:5418988				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 472) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				
MEDLINE	99380589				
PUBMED	10449764				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dj.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hsc.washington.edu Plate: 1060 row: D column: 8 Seq primer: T7 Class: BAC ends High quality sequence stop: 472.				
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	/clone_lib="RPCI-11 Human Male BAC Library"				
	/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoII Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"				
ORIGIN					
Query Match	6.3%; Score 316.2; DB 8; Length 472;				
Best Local Similarity	99.1%; Pred. No. 9.6e-29;				
Matches 318:	Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
OY	4422	GGAGTGCAGTGCTGCAGATCTCAGATGATCGCAACTTCGTCCCTCTCGAATTCAAGCACTC	4481		
DB	359	GAAAGTCAGTGTGTGCAGATCTCAGATGATCGCAACTTCGTCCCTCGAATTCAAGCACTC	300		
OY	4482	TCCTGCCCTGAGCCCTTTATCTTTCTTAATCTGTGTTTAGTCATGATGATCCTTAACCTTT	4541		
DB	229	TCCTGCCCTGAGCCCTTTATCTTTCTTAATCTGTGTTTAGTCATGATGATCCTTAACCTTT	240		
OY	4542	TTTCATGCTGAAGAATCTGCATTAAGAACCAACATTTATTTTATTTCAAGCTTCTC	4601		
DB	229	TTTCATGCTGAAGAATCTGCATTAAGAACCAACATTTATTTTATTTCAAGCTTCTC	180		
OY	4602	ATATCAATTTGGCCATGTGTAATCTGTTTCAAGTGCGCTCGGAACGGGGGACCCTTGAAAC	4661		
DB	179	ATATCAATTTGGCCATGTGTAATCTGTTTCAAGTGCGCTCGGAACGGGGGACCCTTGAAAC	120		

QY	4662	ATTACTGGATATCAGGGGACCATGAGACACTTCTGATCTCTGAGTTCTTGACCTTTG	4721
Db	119	ATTACTGGATATCAGGGGACCATGAGACACTTCTGATCTCTGAGTTCTTGACCTTTG	60
QY	4722	ATTGTTCTGCACAGACCTTTTC	4742
Db	59	ATTGTTCTGCACAGACCTTTTC	39
RESULT 10			
AQ0839831			
LOCUS			
DEFINITION	260L13-C47 C1TB Homo sapiens genomic clone 260L13, genomic survey	6146 bp	DNA linear GSS 31-MAR-2000
ACCESSION	AQ0839831		
VERSION	AQ0839831.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 6146) Carpten,J.D., Makalowska,I., Robbins,C.M., Scott,N., Sood,R., Carpent,T.D., Bonner,T.I., Smith,J.R., Faruque,M.U., Stephan,D.A., Plakett,H., Morgenbesser,S.D., Su,K., Graham,C., Gregory,S.G., Williams,H., McDonald,U., Baxevanis,A.D., Klingler,K.W. and Lander,G.M.		
TITLE	A 6-Mb high-resolution physical and transcription map encompassing the hereditary prostate cancer 1 (HPC1) region		
JOURNAL	Genomics 64 (1), 1-14 (2000)		
MEDLINE	20175426		
PUBMED	10708513		
COMMENT	Contact: Carpten JD Cancer Genetics Branch National Human Genome Research Institute/National Institutes of Health Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD Tel: 301 435 5626 Fax: 301 435 5465 Email: jdc@nhgri.nih.gov Class: Shotgun.		
FEATURES			
Source	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol type="genomic DNA"		
	/db xref="taxon:9606"		
	/clone="260L13"		
	/clone_lib="C1TB"		
ORIGIN			
Query Match	6.1%;	Score 302.8;	DB 8; Length 6146;
Best Local Similarity	63.3%;	Pred. No. 1.4e-27;	
Matches 579;	Conservative 0;	Mismatches 297;	Indels 38; Gaps 6;
QY	109	TGTCGTGACAAATATATAAAGATTTTCCAGGCACTGGTGGCTGACACCCCACTGCCAG	168
Db	943	TATCATTAATTAATTTCTAATAAGAGGCTGGGACCGTGGCTCATGCTTAATCCAGC	1002
QY	169	TATTTGGGAGGCTGAGTGAAGGAATGCTTGAAGCCAGAGTTGAAGCAAGGCTAGGC	228
Db	1003	ACTTTGGAGGCGCAAGGCGAGGTGATTAACCTGAAGTCAAGGTTGAGAGCAAGCTGACC	1062
QY	229	AACATAGTAGAGCCCTGTGTCTATAAATAAT-----AATTAGCTGTGTGTTTGGACAG	283
Db	1063	AACATGTGTGAAGACCCCGTCTTACTATAAATAATGAAAAATTAGCCGGCGCTGATGCAAT	1122
QY	284	GCCTGCA--GCTAGCTACTGGAAGACTGAGGTGGAGAGATCAC--TAAAGCCAGAGGCT	340
Db	1123	GCCTGATATCCCACTACTCAGAGGCTGAGGCGAGAGAAATCTTGAACCTGGAGGCA	1182
QY	341	GAGGCTGACAGTGAACAGTATCAACCCAGCTGATTCAGCCTTGAAGACAGAGGAGACC	400
Db	1183	GAGGTGCAAGTGAACAGATTTGTGCAATTGCACTTCCAGCCTGGGTATGAGCAAACTC	1242

[illegible]

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/db_xref="taxon:9606"
/mab="6p21.3; HLA Class I region"
/clone="51R probe"
/clone_11b="Human"

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Query_Match      5.9%; Score 293.2; DB 8; Length 1300;
Best Local Similarity 66.2%; Pident.No. 3.7e-26;
Matches 564; Conservative 0; Mismatch 243; Indels 45; Gaps 8;

QY      102  AAACCTGCTGTGACAAATATATATAAATTTCCAGGCATGTGGCGTCCACCCCG 161
Dp      38  ATACAAATTTTATTCCAAAATACAAATATATATGGGCTGGGCGCGTGTGACGCTGTA 97
QY      162  TGCAGCTATTTTGGAGGCTTGAGGTAGAGGAATGCTTGAAGCCAGAGTTGAAGACAG 221
Dp      98  TCTTAGCACTTTGGCAGGCGGAGCGGCGAGAGA--TCAGAGGTGACAGAGTTCAAGCAC 155
QY      222  CCTTAGGCAACAATATGAGACCCCTGTGCTATATAAAAT-----AATTAGTGTGCTT 275
Dp      156  CTTGGCCAAACATGTGTGAAGCCCTGTCTCTACTATAAAATACAAAAAATTAGCTGGCGT 215
QY      276  TGGACACAGGCTGGA--GCTAGTACTCGGAAGACTAGGTGGAGGATCAC-TGAGCCC 332
Dp      216  TGGGCGGAGCTGTATATCCAGCTACTCCGAGACTAAGCACAAAGATCCCTTGAACCC 275
QY      333  AGAGGCTGAGGCTGCACTGACATGATACCCAGCTGATTCAGCTTGAAGACAGA 392
Dp      276  GGGAGGCGGAGGTTGCACTGAGTGCAGATGCGACCACTGACATCCAGCTTAGCGGACAGA 335
QY      393  GGGAGCCCGTGTCCAAAAAATTTTTGCAAGAAATGCAAGAAAGATCATTAAC 452
Dp      336  GTGAGACTGTGTCTCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAATAT 395
QY      453  TGACCTGGGACATTAACCTTTATGTGATGAATTAACA---CATCTTTAGGAAGAAATTAG 509
Dp      396  TTTGCCCTTAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 455
QY      510  CATTTCGATTAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 554
Dp      456  CTAAATTAATTTTGAATATGATGCTTTTAACAATTTGTAATGACAGACATTTGATGCTG 515
QY      555  -TGGAAATTAATATTTGAGAAACTAGCTTCTGCACTCTCAGTTGTCAGTCAAACTTT 613
Dp      516  TTCTATTTAGATTCAATGTTGATTAATCTTGCTTTAAGACAGTTAGAGCTATTAATAA 575
QY      614  AATGTCCTTTGGCGCGGCTGCGGTGAGCTCAGCCTGTAAATCCAGCACTTTGGAGGCC 673
Dp      576  CTGTGTGATTAACCAAGGCGCGGTGAGCTCAGCCTGTAAATCCAGCACTTTGGAGTCTGA 635
QY      674  GGGGGGTGATTCACAAGGTTAGGAAGATCGAGACATCTCGGCTTAACACCGGTGAACCT 733
Dp      636  GGGGGGGGATTCACGAGATAGGAAGATGAGACATCTCGGCTTAACACCGGTGAAGCCCG 695
QY      734  TCTCTACTAAAAATAC--AAAAAATTAGCCGGGTGCGGTGCCAGACGCGCTGTAGTCC 791
Dp      696  TCTCTATTAATAATTAACAAAAAATTAAGCAGAGTGGGTGGAGGACCTGTAGTCCAG 755
QY      792  CTGCTCAGAGGCTGAGGCGCAGAGAAATGTTGTGAACCCGGAGGCGAGAGCTTGACGTAG 851
Dp      756  CTACTTTGGAAGGCTGAGGCGCAGAGAAATGTTGTGAAC-----CTTGCACTGTAG 802
QY      852  CCAGATTGGCCACATGCACTCCAGGCTGGGCGACAGTGCAGAGCTCTGTCTCAAAAAA 911
Dp      803  CCGAGATCAAGCCACTGCACTACAGCTTGGGCAACAGAGCAAAACCCGCTCTCAAAAAA 862
QY      912  AAAAAAAAAAAAA 923
Dp      863  AAAAAAAAAAAAA 874

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RESULT	12
AQ072178/c	
LOCUS	321 bp DNA linear GSS 05-AUG-1998
DEFINITION	H5_3010_B2_H02_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=4 Row=P, genomic survey sequence.
ACCESSION	AQ072178
VERSION	GSS. AQ072178.1 GI:3391027
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 321) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L. Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
TITLE	JOURNAL MEDLINE PUBMED COMMENT
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3010 row: P column: 4 Class: BAC ends High quality sequence atop: 321. Location/Qualifiers 1..321 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="plate=3010 col=4 Row=P" /sex="male" /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pbeloBAC11; BAC Clones in E-Coli DH10B"
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SOURCE	
ORIGIN	
Query Match	5.9%; Score 292.8; DB 8; Length 321;
Best Local Similarity	94.4%; Fred. No. 7.3e-26;
Matches 303; Conservative	0; Mismatches 18; Indels 0; Gaps 0;
D	4322 CTTGTTAAACAGCATGTGTAAGGGGCATACAGTTTATTATTATTATTATTATTATATATTT 4381
D	321 CTTGTTAACAAGATTGTAGCGACATACAGTTCTATTTCATTCTATTATTATTATAACT 262
D	4382 TATTATTATTATTGGAAATGAATCTGTGCACCAGCGCTGAGTGCAATGAGTGGTGGATCT 4441
D	261 CACGATTCATTNTEGAATGAATCTGTGCACCAGCGCTGAGTGCAATGAGTGGTGGATCT 202
D	4442 CAGATGATGGAACCTCTGCCCTCCGATTTCAAGAATCTTCCTGCCCCCTGACCTTAT 4501
D	201 CAGATGATGGAATCCTCTGCCCTCTGGAATTCAGAACCTCTGAGCCATGGCCCTGTAT 142
D	4502 ACTTCTTAATCTGTTTAGTCATGSGTACCTTAACCTTTTTTCAATGCTGAGAACATCT 4561
D	141 ACTTCTTAATCTGTTTAGTCATGSGTACCTTAACCTTTTTTCAATGCTGAGAACATCT 82
D	4562 GCATTAAGAACCACATTTTATTATTCTAAGCTTCTCATATCAATTTGGCCATGSTA 4621
D	81 GCAATTAAGAACCACATTTTATTATTCTAAGCTTCTCATATCAATTTGGCCATGSTA 22
D	4622 ACTGTTTCAAGGTGGCTGG 4642
D	21 ACTGTTTCAAGGTGGCTGG 1

LOCUS	BC037921	1279 bp	mRNA	linear	HTC 04-MAR-2003
DEFINITION	Homo sapiens, clone IMAGE:5278633, mRNA.				
ACCESSION	BC037921				
VERSION	BC037921.1 GI:23138806				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1279)				
TITLE	Strausberg,R.				
JOURNAL	Direct Submission				
REMARK	Submitted (16-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbe-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bisset, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutische, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven Ness, Pawan Pandoh, Anna-Lilja Prabh, Parvaneh Saedi, Jacqueline Scheidt, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Nataja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.				
FEATURES	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: http://image.lnl.gov Series: IRAX Plate: 75 Row: m Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: Excellent library of origin This clone has the following problem: retained intron.</p> <p>Location/Qualifiers</p> <p>1..1279</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:5278633"</p> <p>/tissue_type="Brain, hypothalamus"</p> <p>/clone_id="NH_MGC_96"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pBluescript"</p>				
ORIGIN	<p>Query Match 5.8%; Score 291.6; DB 3; Length 1279; Best Local Similarity 66.1%; Pred. No. 5.8e-26; Matches 522; Conservative 0; Mismatches 219; Indels 49; Gaps 5;</p> <p>139 GGCATGTGCGCGTGCACCCCGACGTCAGCATTTTGGAGGCTAGGTAGAGGAATGCT 198 531 GGCACTGTGCTACCCCTGTAAATCCAGTAATCTTGGGAGGCTAGGTGGATGATCAC 590 </p> <p>199 TGAAGCCAGAGATTGAAGACAAGCTTAGGCACTAGTGAAGACCTGTGTATATAAAA 258 </p> <p>591 TGAAGTCAGAGATTCAAGACAGCAGCTGTCACTAGTGTGAATCCCATCTCTACTATAAAA 650 </p> <p>259 T-----AATTAGCTGCTGTGCTTGGGACAAGGCCCGCA--GCTAGCTCTCGGAAGACTGA 311 </p> <p>651 TGCATAAATTAATGACGAGTGTGTGGCGCTGCTGTATATCCCACTACTACAGAGGCTGG 710 </p>				

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QY 312 GGTGGAGGATCAC-TGAAGCCAGAGAGCTGAGCTGCACTGAAACAGTATCACTCCAGCT 370
Db 711 GACATGAGAAATCGTTGGATCTTTGTAGCAGAGGTTCAGCGAGCTGAGATTGTGCCACT 770
QY 371 GGATTTCCAGCTTGAGAGCAGAGGAGACCTGTTTCCAAAAAATAAAAAAAAAAAT 430
Db 771 GCATCTCCAGCTTGAGAGCAGAGGAGACCTGTTTCCAAAAAATAAAAAAAAAAAT 830
QY 431 GCAAGAAAAAGCATCATTAATCTTGAAGCTGAGACATTAATTTATGTATGTAATTCACAA 490
Db 831 ACCGACCCCAAAAGCAAAAC-----AAA 854
QY 491 TCTTTTGAAGAAATTAAGCATTTCTGATATAATATTAATTAATTAATTAATTAATTAAT 550
Db 855 ACAAACCAAAAAACCGAAGTCTTCACTGATCTTTGTACATCTCTCGAAGATC 914
QY 551 CAATGGAATTAATTAATTTGAGAACTAGCTTCTCACTCTCACTGTCAGTCAAAAC 610
Db 915 CTGAGGCATGATGATTTCTGCAACTGATCTAATGTTGATCAAC-----TAGAAG 969
QY 611 TTTATGCTCTTTGGCCGGTGCCTGCTCAAGCTGTAATCCAGCACTTTGGAGGC 670
Db 970 ACATTAAGTTCTGGCCGGAGTGTGCTCACTGTAATCTAGCACTTTGGAGGT 1029
QY 671 CGAGCGGGTGAATCAAGGTTAGAGATCGAGACATCTGCTTAACCGGTGAAC 730
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QY 731 TCGTCTTACTAAAAATACAAAAATTAAGCCGGTGCCTGAGAGCGCTGATGCCA 790
Db 1090 CCGTCTTACTAAAAATACAAAAATTAAGCCGGTGCCTGAGAGCGCTGATGCCA 1149
QY 791 GCTGCTAGAGAGCTGAGAGAGAGATGCTGTAACCCGGAGGGAGCTTGACGTGA 850
Db 1150 GCTACTCAGAGGCTGAGAGAGAGATGCTGTAACCCGGAGGGAGCTTGACGTGA 1209
QY 851 GCGGAGTTGCGGCATCGCATCTCAAGCTGGGAGAGCGAGACTGCTCAAAAAA 910
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QY 911 AAAAAAAAAA 920
Db 1270 AAAAAAAAAA 1279

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RESULT 14
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LOCUS AGENCOURT 6598315 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5474291
DEFINITION 5', mRNA Sequence.
ACCESSION BM559057
VERSION BM559057.1 GI:18802313
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 647)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM1987 row: e column: 12
High quality sequence stop: 603.

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                /clone_1ib="NIH MGC 41"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."

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ORIGIN
Query Match 5.8%; Score 288.2; DB 4; Length 647;
Best Local Similarity 68.0%; Pred. No. 2e-25;
Matches 431; Conservative 0; Mismatches 199; Indels 4; Gaps 2;

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QY 351 TGAACAGTATGATCCAGCTGATTCAGCTGGAAGACAGAGGAGACCTGTTCCAA 410
Db 68 TAGGTGAGATTTGTCATTTGATCTCCAGCTCGGTGACAGAGTGTGACCTGTCAAA 127
QY 411 AAAAAAAAAAAAAAAAAATGCAAAAGACATATAAATTGACCTGGACATPACTT 470
Db 128 AAAAAAAAAATTTTAAACAAGTTGACAGAGGATTTTAAAGTATTTTCCATTGTAT 187
QY 471 TATGTGATGAATTCACATCTTTAGAGAAATTAAGATTTGATTAATTAATTAAT 530
Db 188 CAAAGTTAAACCAAGCAAGTAAAGCATCTTTTAAAGGTGACAGATTAACAGTGA 247
QY 531 TAATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 590
Db 248 GAAGTATGAGAGCTATTTGACAAAGTTAAGTTTGGGGTGGAGACATTAATGAGGAT 307
QY 591 TCTCAGTTGTAGTCAAAACCTTAATGCTTTGGCCGGGTGCGGTGCTCAAGCTGTA 650
Db 308 GGGCACACAAAGCTTGAAGTTAGTG--TAGGGCCGGGGCGGTGCTCAAGCTGTA 364
QY 651 ATCCAGACATTTGGAGAGCGAGGCGGTGATCAAGAGTTAGAGATGAGACATC 710
Db 365 ATCCAGACATTTGGAGAGCGAGGCGGTGATCAAGAGTTAGAGATGAGACATC 424
QY 711 CTGCTTAAACAGGTGAAACCTGCTCTTAATAAATAAATAAATAAATTAATTAATTAAT 770
Db 425 CTGCTTAAACAGGTGAAACCTGCTCTTAATAAATAAATAAATAAATTAATTAATTAAT 484
QY 771 GCCAAGCCCTGTATGCTCCAGTGTCTGAGAGCTGAGAGCGAGAAATGCTGAACCG 830
Db 485 GCGGGGCGCTGTATGCTCCAGTGTCTGAGAGCTGAGAGCGAGAAATGCTGAACCG 544
QY 831 GGAGGCGAGCTTGAAGTGAAGCCAGATGAGCCAGTCACTGCAAGCTTGGGCGACAGT 890
Db 545 GGAGGCGAGCTTGAAGTGAAGCCAGATGAGCCAGTCACTGCAAGCTTGGGCGACAG 604
QY 891 CGAGACTCTGTCTCAAAAAAAAAAAAAAAAAA 924
Db 605 CGAGACTCTGTCTCAAAAAAAAAAAAAAAAAA 638

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RESULT 15
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LOCUS DKFZp761K027_g1 761 (synonym: hamy2) Homo sapiens cDNA clone
DEFINITION DKFZp761K027_3', mRNA sequence.

ACCESSION AL120269
 VERSION AL120269.1 GI:5926168
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 660)
 Koehler, K., Beyer, A., Mewe, H. W., Gassenhuber, J., and Wiemann, S.
 EST (Koehler, et al.)
 Unpublished (1999)
 JOURNAL
 COMMENT
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 3' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Charite,
 Berlin/Germany) within the cDNA sequencing consortium of the German
 Genome Project.
 r1 sequence also available.
 This clone (DKFZ761K027) is available at the RZPD in Berlin.
 Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 1..660

FEATURES
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ORIGIN

Query Match 5.7%; Score 284.8; DB 1; Length 660;
 Best Local Similarity 69.7%; Pred. No. 5e-25;
 Matches 463; Conservative 0; Mismatches 182; Indels 19; Gaps 5;

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QY 262 TTAGCGGTGTTCTTGACACAGGCGCTGCA--GCTAGTACTGGAGAGACTGAGGTGGAG 319
DB 648 TAAAGACGACGCTGACACATGCTGTAAACCCACGCTATTGGAGGCTGAGGTGGAG 589
QY 320 GATCAC-TGAGCCAGAGAGGCTGAGGCTCAGTGAACAGTGAACCCAGCTGATTCCA 378
DB 588 GATCGCTTGAAGCCAGAGATTGAGGCTCGGTGAGCTTAATATGCGACTGCACTCCA 529
QY 379 GCCTGAGACAGAGAGGAGACCTGTTCCAAAAAAGAGAGAGAGAGAGAGAGAGAG 438
DB 528 GCTTGGGTGACACAGTAAGAGCCCATCTC--TTAAAAAGTTAAAAATTAATGAAT 471
QY 439 AGACATCAATACTGACCTGGGACATACTTTATGTATGTAATGAATTCACAACTTTAG 498
DB 470 AATCACTCACTTAATGAATAAGTGTATATTA---AATCATATGCTATTTAGGT 415
QY 499 GAAGAAATTAGCATTTCTGATAAATGTATTAATTAATTAATTAATTAATTAATGA 558
DB 414 TATTTTTCATATCTTTATTAACATGTAATCTCACTGATGATGATGATGATGATGAT 355
QY 559 ATTAATATTTGAGAACTAGCTTCACTCTCTCAGTTGTCAGTCAAAACTTTAATGG 618
DB 354 ATCTATTAACCAATATATGTATGATATACGTTTGCACTTGAATACTAT-----T 305
QY 619 TCTTTGGCGGGGTGGGCTGAGGCTGATATCCAGACCTTTGGAGGCGGAGGCGG 678
DB 304 TACTAGGCTGGGGGCGCTGCTCAGCTGTATATCCAGACCTTTGGAGGCGGAGGCTG 245
QY 679 GTGATCACAAGATTAGAGATGAGACCATCTGCTAAACAGGTGAACCTGCTCTCT 738
DB 244 GCGGATCACAAGGTGACGAGATGAGATCATCTGCTAAACAGGTGAACCTGCTCTCT 185

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QY 739 ACTAAAAATATACAAAAAATTAGCCGGTGGGGTGGCCAGAGCCCTGTAGTCCAGCTGTCTCA 798
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QY 799 GGAGGCTGAGGAGAGAAATGTTGTAACCCGAGAGGCGGAGCTTGCACTGAGCCGAGAT 858
DB 124 GGAAGCTGTGGCAGAGAAATGGCGTGAACCCGAGAGGCGGAGCTTGCACTGAGCTGAGAT 65
QY 859 TCGCCACTGCACTCCAGCTGCGGCGACAGTGCAGACTTGTCTCAAAAAAAGAGAGAG 918
DB 64 CGCTCCACTGCACTCCAGCTGCGGCGACAGAGTGAATTTGTCTTAAAAAAGAGAGAG 5
QY 919 AAAA 922
DB 4 AAAA 1

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QY 421 AAAAAAAAAATGCAAGAAAGACATCATTAACCTTGACGACATTAATTATGATG 480
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QY 481 AATTACAAATCTTTTAAAGAAATTAAGCATTTCTGATTAATAATATATATAT 540
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QY 541 AATTAAATTTCAATGGAATTAATAATTTCTGAGAAATCTAGCTTCTCACTCT 600
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Qy	4861	TCCATTTATATGATTTTCTCTCTGATATGTTGAAATGCTGCAGATATATATTAG	4920
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RESULT 2
US-10-224-562-3
; Sequence 3, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERMOF
; FILE REFERENCE: CLO01098D1V
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-562-3

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Query Match	100.0%	Score 50000;	DB 4;	Length 53332;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Qy	241	CCCTGTGTCTATATAAAATAATTAAGTGTGTCTTGGCAAGAGCTGCAGTAGCTACT	300	
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DB 2761 TTTGAGAGATGATATACATATTAATGATTTTCAAGGAGATCTTTCAAGAAAAATGCTTTTG 2820
QY 2821 GGGGTACAGAGAGCTTGAAGAAATTTGAAGAGTGAAGAAATGAGGCAATTAAGAAAAAT 2880
DB 2821 GGGGTACAGAGAGCTTGAAGAAATTTGAAGAGTGAAGAAATGAGGCAATTAAGAAAAAT 2880
QY 2881 GGTTTTACAGAGAGCTGATATCTTTATCTTTGATTAATTTTATTTTCTGCTTTTCTTTT 2940
DB 2881 GGTTTTACAGAGAGCTGATATCTTTATCTTTGATTAATTTTATTTTCTGCTTTTCTTTT 2940
QY 2941 CTCTAGCTTACAGAGCTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3000
DB 2941 CTCTAGCTTACAGAGCTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3000
QY 3001 CTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
DB 3001 CTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
QY 3061 TTTTACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
DB 3061 TTTTACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
QY 3121 AAGAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
DB 3121 AAGAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
QY 3181 GAGCGAGCTTCCCAAGTGTGCTGTGCAATGCTGTAAATTTCTGAGGAAAAAAGT 3240
DB 3181 GAGCGAGCTTCCCAAGTGTGCTGTGCAATGCTGTAAATTTCTGAGGAAAAAAGT 3240
QY 3241 CAACACTAATAAAGATGTTCTTTCTCTTCCCTTCCAGGCTCTTTTCCCAATTC 3300
DB 3241 CAACACTAATAAAGATGTTCTTTCTCTTCCCTTCCAGGCTCTTTTCCCAATTC 3300
QY 3301 CCTAGAGAGAGAGAGAGAGCTCCTTTTGGGAGAGCTCATCTTACTTGAACCTTGAGAA 3360
DB 3301 CCTAGAGAGAGAGAGAGAGCTCCTTTTGGGAGAGCTCATCTTACTTGAACCTTGAGAA 3360
QY 3361 GCTGGGTGAAGCTCTTATGCGACAGTTTACAAAGGAGATTTAGCAGGTGATGACATAG 3420
DB 3361 GCTGGGTGAAGCTCTTATGCGACAGTTTACAAAGGAGATTTAGCAGGTGATGACATAG 3420
QY 3421 CTGGGAGAGAGCTTGAAGATGAGAGTCCGCCCCCAATTTCAATTTAAGCCAGGT 3480
DB 3421 CTGGGAGAGAGCTTGAAGATGAGAGTCCGCCCCCAATTTCAATTTAAGCCAGGT 3480
QY 3481 GAGACATCATATGAGAGTTCATGACATGAGAGCTGAGCAACCATGAGCGAGAGAG 3540
DB 3481 GAGACATCATATGAGAGTTCATGACATGAGAGCTGAGCAACCATGAGCGAGAGAG 3540
QY 3541 GAGAGCATGATTAATTAACAGCTTGAAGAAAAAAGAAACAACTGCGCTGCTTAATTA 3600
DB 3541 GAGAGCATGATTAATTAACAGCTTGAAGAAAAAAGAAACAACTGCGCTGCTTAATTA 3600
QY 3601 AATCAGCCCACTTAAATGTTTATCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3660
DB 3601 AATCAGCCCACTTAAATGTTTATCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3660
QY 3661 AAGAAAAATGACATTTCTACTAGTGAAGCAAGAAACAAATTAATCTTCAAGGCTGTG 3720
DB 3661 AAGAAAAATGACATTTCTACTAGTGAAGCAAGAAACAAATTAATCTTCAAGGCTGTG 3720
QY 3721 GAGAGCAAGTTGATTAAGAGCTCTTAACAGAGTTTATATCCCTTCAATCAAT 3780

3721 GGAGGACAGTGGTAAAGCTCTCTAAACAGTCTTAAATCCCTCCCTAAACACAAT 3780
3781 GACAGAGTTTGTATGGCAACCTGGAATTTGCTGCTCAATCTCCACCGGCTTAT 3840
3781 GACAGAGTTTGTATGGCAACCTGGAATTTGCTGCTCAATCTCCACCGGCTTAT 3840
3841 AGAAGAACTGGAAGTTGTTCTGCAATTATGCTACATGCAAAAGATGATAAATCTAG 3900
3841 AGAAGAACTGGAAGTTGTTCTGCAATTATGCTACATGCAAAAGATGATAAATCTAG 3900
3901 ATTTTATATTTTGCAGAAATGCAAGAAATGCTGAGAAATAAATCTGCTTATCCAA 3960
3901 ATTTTATATTTTGCAGAAATGCAAGAAATGCTGAGAAATAAATCTGCTTATCCAA 3960
3961 AGTAAGTACTAATTTTGTAAACCAACCACTTGTAAATATATGTAAGATCCATGA 4020
3961 AGTAAGTACTAATTTTGTAAACCAACCACTTGTAAATATATGTAAGATCCATGA 4020
4021 ATTCCCTTTTATGCAAGGTGGGAAAGTTGATGCTGCTTTTCTTTATGTTACTCA 4080
4021 ATTCCCTTTTATGCAAGGTGGGAAAGTTGATGCTGCTTTTCTTTATGTTACTCA 4080
4081 ATAGAGAGAAAGTAATGCTCAATAGTGTAAATATATATTTTAAATATATGCTAT 4140
4081 ATAGAGAGAAAGTAATGCTCAATAGTGTAAATATATATTTTAAATATATGCTAT 4140
4141 CCGAGTCAAGTGTGTTTAACTACTGTTATCAACACAGTTTCTTTGTTCT 4200
4141 CCGAGTCAAGTGTGTTTAACTACTGTTATCAACACAGTTTCTTTGTTCT 4200
4201 TCTCCACTCCCACTGCTCACTTAACCTGGCCAAAGAAAGAAATTTTATATTA 4260
4201 TCTCCACTCCCACTGCTCACTTAACCTGGCCAAAGAAAGAAATTTTATATTA 4260
4261 CTACTACAGACTAATATATTTATTTATTTATTTATTTATTTATTTATTTATTT 4320
4261 CTACTACAGACTAATATATTTATTTATTTATTTATTTATTTATTTATTTATTT 4320
4321 ACTTGTAAAAAGAGATTGTAGGGGACATACAGTTTATTTTATTTATTTATTTAT 4380
4321 ACTTGTAAAAAGAGATTGTAGGGGACATACAGTTTATTTTATTTATTTATTTATTT 4380
4381 TTAATTTATTTATTTGATGATATCTGTCAACCAACCTGAGAGTGGGATC 4440
4381 TTAATTTATTTATTTGATGATATCTGTCAACCAACCTGAGAGTGGGATC 4440
4441 TCAAGTACTGCAACCTGTGCTCTGAGTTCAAGCAACTCTGCCCCCTGCTTTA 4500
4441 TCAAGTACTGCAACCTGTGCTCTGAGTTCAAGCAACTCTGCCCCCTGCTTTA 4500
4501 TACTTCTTAACTGTTTGTATGATGCTTAACCTTTTCAATGCTGGAACATC 4560
4501 TACTTCTTAACTGTTTGTATGATGCTTAACCTTTTCAATGCTGGAACATC 4560
4561 TGCATTAAGAGACACATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4620
4561 TGCATTAAGAGACACATTTTATTTATTTATTTATTTATTTATTTATTTATTTAT 4620
4621 AACTGTTTAAAGTGTGGAACGGGGGCACTGGAACATATCTGGATCATGAGCA 4680
4621 AACTGTTTAAAGTGTGGAACGGGGGCACTGGAACATATCTGGATCATGAGCA 4680
4681 CCATGACATTCGATTCCTCTCTGAGTGTGATGCTTGTGCAAGACCTT 4740
4681 CCATGACATTCGATTCCTCTCTGAGTGTGATGCTTGTGCAAGACCTT 4740
4741 TCCAGCCGGAAGTTTACAGAGATTCATTTCTTTCTTCTAGTACTTATGTTTCT 4800
4741 TCCAGCCGGAAGTTTACAGAGATTCATTTCTTTCTTCTAGTACTTATGTTTCT 4800
4801 TTTTCAATTTACTTTTCACTTCTGGAATTTATTTGTAATTTCAATCACCACG 4860
4801 TTTTCAATTTACTTTTCACTTCTGGAATTTATTTGTAATTTCAATCACCACG 4860

4801 TTTTCAATTTACTTTTCACTTCTGGAATTTATTTGTAATTTCAATCACCACG 4860
4861 TCCATTTATTAATTTTCTTTCTGATGCTTGAAGTGGCAATGATTTATTTAG 4920
4861 TCCATTTATTAATTTTCTTTCTGATGCTTGAAGTGGCAATGATTTATTTAG 4920
4921 ATCTCAAGATATCTGAAATTTCTTCTGTTCTTAATCTTTTAAATCATGTTTCTTAAT 4980
4921 ATCTCAAGATATCTGAAATTTCTTCTGTTCTTAATCTTTTAAATCATGTTTCTTAAT 4980
4981 CTATCTTTCTTATTTTGT 5000
4981 CTATCTTTCTTATTTGT 5000

RESULT 3
US-09-679-299A-18
; Sequence 18, Application US/09679299A
; Patent No. 656135
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Wale
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 6 EXPRESSION
; FILE REFERENCE: RTS-0187
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 18
; LENGTH: 17000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-679-299A-18

Query Match 6.7%; Score 336.2; DB 4; Length 17000;
Best Local Similarity 68.6%; Pred. No. 9.8e-63;
Matches 555; Conservative 0; Mismatches 238; Indels 16; Gaps 6;

120 ATATATTAAGAAATTTTCCAGCATGCTGTCACCCCACTGCACTATTTGGAGG 179
6897 ATTAATTTCTTTTGGCCAGGTGTGTGTCATGCTGTAATCCAGCACTTTGGAGG 6956
180 CTGAGGTGAGAGAAATGCTGGAAGCAGAGTTGAAGCAAGCTTACGATATGAG 239
6957 CCAAGTGGAGAGATCACTTAAGCAAGAGTTTGAACAGTCTGGGCAACAGTGGAG 7016
240 ACCCTGTCTATTAATAATTAATAGTGTGCTTGGCAAGGCTGCAAG--CTAGCT 297
7017 ACTGCTCTCTACAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7076
298 ACTCGAAGACTGAGTGGAGATCAC-TGAGCCAGAGGCTGAGCTGCAATGAAACA 356
7077 ACTCGAGGCTGAAGGGGAGATGCTTGAATCCAGAGTTCAAGGCTGCAAGGCT 7136
357 GTGATCACCCAGCTGATTTCCAGCTGGAAGACAGAGGAGACCTGTTTCAAAAAAA 416
7137 GTGATCACCCAGCTGATTTCCAGCTGGAAGACAGAGGAGACCTGTTTCAAAAAAA 7196
417 AAAAAAATGCAAGAAAGATCATTAACCTTGAACCTGGAACATTAATTTATGT 476
7197 AAAAAAATTAATTTT---TTTCCATGTTTCCAAATGAAGATTAATAATTAAT 7252
477 GATGAATTCACAACTTTTGAAGAAATTAAGCATTTCTGATTAATATTAATTA 536
7253 TAAAAAATTCAGACTTCTGATGTAAGGAAAGTTAAT---CATTAATGTC 7306
537 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 596
7307 AACACTAATAGGTAAACAAGATCAAGAGTGTGAGACATGGGCTTTGATGAG 7366
597 TTGTAGTCAAAACCTTAATAGTCTTTGGCGGGGTGCGGTGCTCAAGCTGTAAATCCA 656
7367 CCTCCCTTAAGAACTTGCTG--AGTTGGCGGGGATGTTGGCTCACTCTGTAATCCG 7424


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QY 657 GCACCTTGGAGGCCGAGGGGTGATCAAGATTAGAGATTCAGACCATCTGGCT 716
DB 7425 GCACTTTGGAGGCTGAGGGGTGATCATTAAGTCAGAGATTAAGCATCTGGCT 7484
QY 717 AACAGGTGAAACCTGTCTCTACT--AAAATACAAAAATTAGCCGGGTGGTCCAG 775
DB 7485 AACATGTGTAACCTGTCTCTCTTAATAAAATCAAAAAATTAGCCGGGTGGTCCAG 7544
QY 776 AGCCCTGTAGTCCCACTGCTCAGAGAGCTGAGGAGAGATGTGTGAACCCGGAGG 835
DB 7545 GAGCCTGTAGTCCCACTGCTCAGAGAGCTGAGGAGAGATGTGTGAACCCGGAGG 7604
QY 836 CGAGAGCTTGAGTGAAGCCGAGATTCGCACTGCACTCCAGCCTGGGCGACAGTGGAG 895
DB 7605 CGAGAGCTTGAGTGAAGCCGAGATTCGCACTGCACTCCAGCCTGGGCGACAGTGGAG 7664
QY 896 CTCTGTCTCAAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 924
DB 7665 CTCTGTCTCAAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 7693

RESULT 4
US-09-797-906-3/C
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: ZIANGHE YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84495
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(84495)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 6.7%; Score 334.4; DB 3; Length 84495;
Best Local Similarity 61.8%; Pred. No. 4.4e-62;
Matches 656; Conservative 0; Mismatches 386; Indels 20; Gaps 7;

QY 119 AATAATTAAGAATTTTCAGAGCATGTGCGCTGACACCCCAAGTGCAGCTATTTGGAG 178
DB 38013 AATAATTAAGAATTTTCAGAGCATGTGCGCTGACACCCCAAGTGCAGCTATTTGGAG 37954
QY 179 GCTGAGGTGAGAGGATGCTTGAAGCCAGAGAGTTGAAGACAGCCCTAGGCAATATGTA 238
DB 37953 ACAGAGGTGAGAGGATGCTTGAAGCCAGAGAGTTGAAGACAGCCCTAGGCAATATGTA 37894
QY 239 GACCCGTGTCTATAAATAAT--AATTAGCTGTGTCTTGGCA--CAGGCTGCAGC 292
DB 37893 GACTCTGTCTATAAATAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 37834
QY 293 TAGCTACTCGAAGAGTGAAGTGAAGATCAC-TGAGCCCAAGAGAGCTGAGGCTCAGT 351
DB 37833 CAGCTACTCGAAGAGTGAAGTGAAGATCAC-TGAGCCCAAGAGAGCTGAGGCTCAGT 37774
QY 352 GAACAGTATCAACCCAGCTGATTCAGAGCTGGAAGACAGAGGAGAACCTGTTCCAAA 411
DB 37773 GAGCTGTGATCAAGCAGCTGATTCAGAGCTGGAAGACAGAGGAGAACCTGTTCCAAA 37715
QY 412 AAAAAAAAAAAAAAAAAATGCAAGAAAGACATCATTAACCTGAGGACATAACTTT 471
DB 37714 CAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 37658

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QY 472 TATGATGTAATTTCAATCTTTTAGAAGAAATTTAGCATTTCTGATAAATGATAT 531
DB 37657 AAGGTAAACCAAGAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 37599
QY 532 AATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
DB 37598 ----AAGATTTTGGCTGGGAGAAACATGACAGAGTTTCTGAGTCTGCTGATAT 37543
QY 592 CTCAGTTGTCAATCAAACTTTAATGATCTTTTGGCCGGGTGGGCTCAAGCCCTGTA 651
DB 37542 CTGATTTTCTTAATAACAGATACAG---TAGGCGGGGGGTGGGCTCAACCTGTA 37487
QY 652 TCCAGCACTTTGGAGGCGGAGGCGGTGATTCACAGATTAGAGATGAGACCATCC 711
DB 37486 TCCAGCACTTTGGAGGCGGAGGCGGTGATTCACAGATTAGAGATGAGACCATCC 37427
QY 712 TGGCTTAACAGGAGTGAACCTGCTCTACTAATAAATAATAATAATAATAATAATAATA 771
DB 37426 TGGCTTAACAGGAGTGAACCTGCTCTACTAATAAATAATAATAATAATAATAATAATA 77367
QY 772 CCAGAGCCTGTAGTCCCACTGCTCAGAGAGCTGAGGAGAGATGTGTGAACCCGG 831
DB 37366 GCGGCGCCTGCAAGTCCCACTGCTCAGAGAGCTGAGGAGAGATGTGTGAACCCGG 37307
QY 832 GAGGCGGAGCTTGCAGTGAAGCCGAGATTCGCACTGCACTCCAGCCTGGGCGACATGC 891
DB 37306 GAGGCGGAGCTTGCAGTGAAGCCGAGATTCGCACTGCACTCCAGCCTGGGCGACATGC 37247
QY 892 GAGACTGTCTCAAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 951
DB 37246 GAGACTGTCTCAAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 37187
QY 952 TTCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1011
DB 37186 GTTACATAGATTTGCTCATATCATTCATTAATGATATTTCTTTACAGTTTC 37127
QY 1012 GAATGAGCTTAAGTCTCTCTCTGTCGCAATTTGAAATGAAATATCATGCTATTA 1071
DB 37126 TCTCTACATATTTCAATTAATAATGCTGGAGTTGAGAGAAATGAGCCAGAAAT 37067
QY 1072 TTAATTAACCTGAACATTTTAAACATCATGAGGCTCAATATTAATTAATTAATA 1131
DB 37066 AAAAAATTAACATCAAAAAAATTAATAATAATAATAATAATAATAATAATAATAATA 37007
QY 1132 TATGTTGTGATTAATGACATTAATTTATTTTCCCTTAA 1173
DB 37006 TATTTGAAGAAATTAATTAATTAATTTATTTGATGTGTTAA 36965

RESULT 5
US-09-146-053-6
; Sequence 6, Application US/09146053A
; Patent No. 619349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 6.7%; Score 333.8; DB 3; Length 45546;

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Best Local Similarity 66.7%; Pred. No. 4,7e-62;
Matches 540; Conservative 0; Mismatches 257; Indels 12; Gaps 4;

QY 136 CCAGGACATGGTGGGCTGACCCCGAGTGCAGTATTGGAGGCTGAGTAGAGGAAT 195
Db 36453 CCGGGTGCATGGCTTACCTGTAATTGACGACCTTTGGAGGTAGAGCAGAGGATC 36512
QY 196 GCTTGAAGCAGAGATTGAAGACAAAGCTTAGGCAACATAGTGAAGCCCTGTCTATMAA 255
Db 36513 ACTTGAGGCCAGAGGTTCAAGATCAGCCTGAGCAACATAGGCAAA-----AAAAAAA 36566
QY 256 AATTAATTAGCTGGTGTCTTTGGACAGGCTGAG--CTAGCTACCTGGAAATCGAGG 313
Db 36567 AAAAATTTAGCCAGGAATGGTGGACGTGCTGTGATCCAACTACCCGGAGGCTGAGG 36626
QY 314 TGGAGAGATCACTGAGCCCGAGAGGCTGAGGCTGACAGTGAACAGTATCAACCAAGCTGA 373
Db 36627 TGGAGAGATCATGAGCCCGAGAGGTTGAAGCTGACAGCTGTGACACACACTGCA 36686
QY 374 TTCCAGCTTGAAGACAGAGGAGACCTGTGTTCCAAAAAATAAATAAATGCA 433
Db 36687 TTCAGGCTGGGCAACAGAGGAGACCTGTCTCAATTAATTAAATTAATTAATTA 36746
QY 434 AGAAAGACATCATTAACCTTGACCTGGGACATTACTTTATGTGAATTAATCAATCT 493
Db 36747 ATTAAATTAACCTTAAGAAATCTTTTGG--GAGGTTTTCCGATTAATGATCTCTCA 36803
QY 494 TTTAGAGAAATTAAGCATTTCTGATTAATTAATTAATTAATTAATTAATTAATTA 553
Db 36804 CTATCCAACTCTTACTATCTCAAAATTAAGAAATATATATCATTCAGAGAGTGAAGATGCT 36863
QY 554 ATGGAATTAATTTCTGAGAAACTAGCTTCTCACTCTCACTGTCACTGCTCAAACTTT 613
Db 36864 TTTGTACATGCTGTGATCTTACCTGCCCCAAATATCCACTCATGATCATCTAATAAT 36923
QY 614 AATGCTCT--TTGGCCGGGCTCGGCTGAGCTCAGCCTGTAAATCCAGACCTTTGGAGGCG 672
Db 36924 AAGAAATTTCTGGCTGATGATGATGCTGCTCAGCTGTAAATCCAGACCTTTGGAGGCG 36983
QY 673 AGCGGGGTGATCAACAAGTTAGAGATGAGACCATCTGCTGATTAACAGCGTAAACCTTC 732
Db 36984 AGGTGGGCAAGATCAGAGAGTCAAGAGATCAAGACATCTGCTGATTAATGATGTAACCC 37043
QY 733 GTCTCACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 792
Db 37044 GTCTCACTAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 37103
QY 793 TGCTCAGAGGCTGAGGCAAGAAATGTTGAACCGGAGGCGGAGCTTGCAGTGAGC 852
Db 37104 TACCGAGAGGCTGAGGCAAGAAATGTTGAACCGGAGGCGGAGCTTGCAGTGAGC 37163
QY 853 CGAGATTGGCCACTGCTGACTCCAGCCTGGGCGACAGTGCAGACTGTGTCTCAAAAAAA 912
Db 37164 CGAGATCGCCTCACTGACTCCAGCCTAGGCAACAGATGAAGCTCAAAAAAATAAATA 37223
QY 913 AAAAAAAAAAAGTGAATGCTTTGAG 941
Db 37224 TTAAATTAAATTTAAAAAATACTTGAG 37252

RESULT 6
US-09-801-052-3
; Sequence 3, Application US/09801052
; Patent No. 6368842
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001045
; CURRENT APPLICATION NUMBER: US/09/801, 052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16063
; TYPE: DNA
; ORGANISM: Human
US-09-801-052-3

Query Match
Best Local Similarity 67.7%; Pred. No. 4.5e-59;
Matches 540; Conservative 0; Mismatches 243; Indels 15; Gaps 6;

QY 136 CCAGGACATGGTGGGCTGACCCCGAGTGCAGTATTGGAGGCTGAGTAGAGGAAT 195
Db 10451 CCGGGGTGTGTGCTTCAACGCTGTATCCAACTTTGGGAGCTGAGGTGGTGTATC 10510
QY 196 GCTTGAAGCAGAGATTGAAGCAAGCCTAGGCAACATAGTGAAGCCCTGTCTATAAA 255
Db 10511 ACTTGAGCTCAGAGAGTTCAAGACAGCCTGCTAATCATGTGAATCCATCTCTCTTA 10570
QY 256 AAT-----AATTAGCTGTGTCTTTGGACAGGCTGCA--GTTAGCTTCTGGAAAGC 308
Db 10571 AATACAAAAAATTAAGCCGGGCTGTGTGACAGCTGTGTAATCCAGCTACTTGAAGAGC 10630
QY 309 TGAGGTGGAGGATGAC--TGAGCCAGAGGCTGAGGCTGACGTGAACAGTATGATACCA 367
Db 10631 TGAGGTGGAGGATGATGCTTGAACCTGGAGGTGAAGGTTGACGTGAGTGTGAGATGCGGC 10690
QY 368 GCTGATTCACCTGAGAGACAGAGGAG--ACCTGTTTCCAAAAAATAAATAAATAAATA 425
Db 10691 ACTGCTCTCAGCTCTGTGCAAGACAGAGCAAGACTGTCTCAAAAAAACAACAAAA 10750
QY 426 AAAATGCAAGAAAGACATCATTAACCTGACCTGGACATTAACCTTTATGTGATGAATT 485
Db 10751 AAAAGAGAGGCTCAGAAATTTGGGTTGAGGCGAGAAAGCTGAGGCGGCTGACAGA 10810
QY 486 CAAATCTTTTGAAGAAATTAGCATTTCTGATTAATAATTAATTAATTAATTAATTA 545
Db 10811 TGTGGATTTGGAGAGTGAAGGCAATGGGCTGAGAAACAGATGAGGGCTTTGGGAGATG 10870
QY 546 AATTCAAATGGAATTAATAATTTCTGAGAACTAGCTTCTCACTCTCAAGTTGTCAATC 605
Db 10871 GGGACTAATAAATGATTTG--GGTTAGGGTACAGACTTGGGAGTTTGTGATCTTGGGATA 10928
QY 606 AAAAATTAAATGCTTTTGGCGGCTGAGGCTGCTCAAGCTGTAAATCCAGACCTTTGG 665
Db 10929 AAAAAATTAACAAC--GGCGGAGGCTGTGCTCAACCTGTAAATCCAGACCTTTGG 10985
QY 666 GAGGCGAGGCGGCTGATCAACAAGTTAGAGATGAGACCATCTGCTTAACAAGGTTG 725
Db 10986 GAGGCTGAGGCGGCTGATCAAGAGTCAAGAGATGAGACCATCTGCTTAACAAGGTTG 11045
QY 726 AAACCTGCTCTACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 785
Db 11046 AAGCCCCGCTCTACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 11105
QY 786 TCCAGCTGCTCAAGAGGCTGAGGCAAGAAATGTTGAACCGGAGGCGGAGCTTGC 845
Db 11106 TCCAGCTCACTTGGAGGCTGAGGCAAGAAATGTTGAACCGGAGGCGGAGGCTTGC 11165
QY 846 AGTGAAGCAGATTCGCGCACTGCACTCAAGCTGAGGCAAGTGCAGAGACTGTCTCA 905
Db 11166 AGTGAAGCAGATTCATGCACTGCACTCAAGCTGAGGCAAGGAGGAGGAGCACTTCTCA 11225
QY 906 AAAAAAAAAAAAAAAAAA 923
Db 11226 AAAAAAAAAAAAAAAAAA 11243

RESULT 7
US-10-020-121-3
; Sequence 3, Application US/10020121
; Patent No. 6638747
; GENERAL INFORMATION:
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APPLICANT: BEASLEY, Ellen et al.
 TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEIN,
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 FILE REFERENCES: CL001045DIY
 CURRENT APPLICATION NUMBER: US/10/020,121
 CURRENT FILING DATE: 2001-12-18
 PRIOR APPLICATION NUMBER: US 60/255,386
 PRIOR FILING DATE: 2000-12-15
 PRIOR APPLICATION NUMBER: US 09/801,052
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PasteSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 16063
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-020-121-3

Query Match 6.4%; Score 319.2; DB 4; Length 16063;
 Best Local Similarity 67.7%; Pred. No. 4.5e-59;
 Matches 540; Conservative 0; Mismatches 243; Indels 15; Gaps 6;

136 CCAGGATGTCGTCGACCCAGTCAGCTATTTGGAGGCTGAGGATGAGGAT 195
 10451 CCGGGCGTGTGCTCAGCCCTGTATCCACATTTTGGGGCTGAGGTGGATC 10510
 196 GCTTGAGCCAGAGTTGAAGACAGCCCTAGGCAATAGTAGAGCCCTGTCTATAA 255
 10511 ACTTGAGTCAGAGTTCAAGACAGCCCTGTGCTAACATGTTAAATCCATCTCTTA 10570
 256 AAT-----AATTAGTGTGTCTTGGCAAGGCTGCA--GCTAGTACTGGAAGAC 308
 10571 AATATCAAAATATGACCGGCGCTGTGGCACTGTATATCCAGTACTTGAAGAGC 10630
 309 TGAGGTGGAGGATAC--TGAAGCCAGAGGCTGAGGCTGAGTGAACATGATCCCA 367
 10631 TGAGGAGAGAGATTCCTTGAACCTGGAGAGTGAAGTTGACGTGAGTTCGCCGC 10690
 368 GCTGATTCAGCTGGAAGACAGAGGAG--ACCTGTTTCCAAAAA 425
 10691 ACTGCTCTCAGCTGTGGAGACAGACAGCAAGATCTGTCTCAAAAAACAACAAAA 10750
 426 AATATGCAAGAAAGACATCATTAATTGACTGGACATTAATTATGTGTAATT 485
 10751 AAAAAAGAGGCTCAGAAATATTTGGGTTGAGGCAAGAACCTGAGGAGGATG 10810
 486 CACAATCTTTAGAGAAATTAAGCATTTCTGATAAATATTAATTAATTAAT 545
 10811 TGTGGATTGGGAGGTAGAGGAGTGGGCTGGAAACAGATGAGGGCTTGGGGATG 10870
 546 AATTCATAATGAATTAATTAATTTCTGAGAACTAGCTTCTCACTCTCAAGTTGTCAGT 605
 10871 GGGACTTAAGATTTG--GTTTGGGTTGCAAGCTTGGGATTTGTATCTTGGGATA 10928
 606 AAAATCTTAATGTCCTTTGGCGGGGTGGCTGCAAGCTGTAAATCCAGCATTTGG 665
 10929 AAGAGATTAACAAC--GGCGGAGTGTGGCTCAACCTGTATCCAGCATTTGG 10985
 666 GAGGCGGAGCGGGTGGATCACAAGTTAGAGATGAGAACCATCTGTGCTAACAGGTG 725
 10986 GAGGCTGAGCGGGTGGATCAGAGGTGAGAGATGAGAACCATCTGTGCTAACAGGTG 11045
 726 AATCTCTCTCTACTAATAAATAAATAAATTAAGCGGGTGGCTGAGAGCGCTGTAG 785
 11046 AAGCCCCGTCTACTAATAAATAAATAAATTAAGCGGGTGGCTGAGAGCGCTGTAG 11105
 786 TCCAGCTCTCTAGAGGCTGAGGACAGAGATGTGTGAACCCGGAGCGGAGCTTGC 845
 11106 TCCAGCTCTCTGAGGCTGAGGACAGAGATGTGTGAACCCGGAGCGGAGCTTGC 11165
 846 AGTGGCGGAGATGTCGCACTGCACTCAAGCTGGGCGACAGTGGAGATCTGTCTCA 905

Db 11166 AGTGGCGGAGATGTCGCACTGCACTCAAGCTGGGCGACGAGGAGACACCTTCTCA 11225
 QY 906 AAAAAAAAAAAAAAAAAA 923
 Db 11226 AAAAAAAAAAAAAAAAAA 11243

RESULT 8 US-09-792-616-1/C

Sequence 1, Application US/09792616
 Patent No. 6780587
 GENERAL INFORMATION:

APPLICANT: PKE International, Inc.
 TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
 TITLE OF INVENTION: Pseudoxanthoma Elasticum
 FILE REFERENCE: PKE-001
 CURRENT APPLICATION NUMBER: US/09/792,616
 CURRENT FILING DATE: 2001-02-23
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 107820
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: "n" can be an A or a T or a G or a C

Query Match 6.3%; Score 317; DB 4; Length 107820;
 Best Local Similarity 64.0%; Pred. No. 2.8e-58;
 Matches 620; Conservative 0; Mismatches 315; Indels 34; Gaps 8;

13 CTGTGCTCAGCGGTGTATTTCCAGACATTTGGAGG-----CAGAGATGCTTGAG 66
 Db 89369 CAGTGGCTACACCATTAATCCCAACCTTTGGAGGCCAACCCCTGACGATCATTGAG 89310
 67 CTCAGGAATTGAGACCAAGCTTACGTAATAGTGAACCTGTGTGTAAATAATA 126
 Db 89309 GCCGGAGTTGAGACACACCTGCGCCACATGAGCAATATCCA--TCTACTATAAACA 89251
 127 AAGATTTTCCAGGATGTTGGCGTGCACCCCAAGTCCAGATTAATTTGGAGGCTGAGT 186
 Db 89250 AAAAAATTAGCCAGGTGTGTGCTTACCGCTGTAGCTTGAACATTTGGAGGCTGAGT 89191
 187 AGGAGGAATGCTTGAAGCCAGAGGTTGAAGACAGGCTTGAAGACATAGTGAACCTGT 246
 Db 89190 GGGAGGATTTCTTGAAGCCAGTGAAGTCAAGACCAAGCTTGGCAGATGATACCAAT 89131
 247 GTCTATAAAAATAATTAAGTGTGTCTTGGACAGGCTTCAAGTACTACTCGGAAG 306
 Db 89130 CCAAAAAACAAAAATTAAGCAGGTGTATGG--TGGCTGTATTAATTTCACTACTCAGAA 89072
 307 ACTGAGGTGAGGATCAC--TGAAGCCAGAGGCTGAGGCTGAGTGAACAGTGTACAC 365
 Db 89071 GCTGAGGCTGAGATTCGCTTGAAGCCAGGAGGAGGTTCAAGTGAACCCAGATCA 89012
 366 CAGCTGATTCAGGCTGGAAGACAGAGGAGACCCGTGTTCCAAAAA 425
 Db 89011 TCACTGCTTCAAGCTTGAAGCAAGATGAGATTCATCTCAAAAAAATAATTAAT 88952
 426 AATATGCAAGAAAGACATCAATTAATTAAGTGAACCTGGAACATTAATTTA--TGTATGAAA 483
 Db 88951 TAAATAAAAAAGCTGAGGAGAGAGTCAAGCTTCTTCAATGATGATTTTGGTCAAC 88892
 484 TTCACAAATCTTTAGAGAAATTAAGATTTGTGATTAATTAATTAATTAATTTAATTT 540
 Db 88891 GGAATTTGATTTCCAGGAAATGTCTGTTTCTTCCAGAGGCTTATCTTGGTTAG 88832
 541 -----ATTATTAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 583
 Db 88831 CCACTGAATCTCTGCACTTCTATTTCTTCCCATCTGTAAATGATTAATTAAT 88772

QY	584	CTCACTCTCAGTTCGACGCAAAATTAAATGCTTTTGGCCGGGTGCGGTGCTCAC	643
Db	88771	ATACTCATACATTATATACAAATTATATAACTATCAATTTACAGGCTGGGCTGGTGCTCAT	88712
QY	644	GCCCTGATATCCAGACATTTTGGAGGCGCAGCGCGGGTGATCAC--AAGTTTAGAGATC	701
Db	88711	GCCTGATATCCAGCACTTTGGGAGGGTGAGGCAAGGTGATCATCCTGAGGTCAAGAGTTTC	88652
QY	702	GAGACCATCTCTGGCTAAACACGGTGAAAACCTCGTCTCTACTAAAAATACAAAAATTAGCC	761
Db	88651	GAGACCATGCTGGCGCAACATGTGAAATCTCATCTCTACAAAAATAC--AAAAATTAGCC	88593
QY	762	GGGAGGGGTGCGAAGCCTCTGTAGTCCCACTCTCTCAGAGGGCTGAGGCAAGAAATGCT	821
Db	88592	GGGATATGTGGTGGTCTCCTGTATCCCACTATCCAGAGGGCTGAGGTGGAGAAATCCG	88533
QY	822	GTGAATCCCGGAGGCGGAGCTTGCAGTGAAGCCAGATTTGGGCGACATCGCATCCAGGCTGG	881
Db	88532	TTGAATCTGGGAGGTGAGGTTCAGATGAGCCAGAGATTGCAACATCTGCATCTCGAGCTTGG	88473
QY	882	GCGACAGTGGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGTTGAATGGTCTTTTGAAG	941
Db	88472	GAGACAGAAACAAGCTCATCTCAAAACAAACATATATTAACCTTAAGGGTCAATGTA	88413
QY	942	CCAAAGTAGT	950
Db	88412	AGAAATTAAAT	88404

```

RESULT 9
US-10-118-328-3
; Sequence 3, Application US/10118328
; Patent No. 6773904
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001220
; CURRENT APPLICATION NUMBER: US/10/118,328
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30350
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-118-328-3

```

Query Match	6.2%;	Score 309;	DB 4;	Length 30350;
Best Local Similarity	65.4%;	Pred. No. 9e-57;		
Matches 633;	Conservative 0;	Mismatches 270;	Indels 66;	Gaps 10;
QY	15	GTGGCTCAGCGCGTGTATTCCTCCAGCACTTTGGG-----AGCGAGAGAGATCGCTTGAAGCT	68	
Db	25156	GTGGCTCACAACAGTATATCCAGCACTTTGGGAGGTCAAGGTGGGTGTGATTTGTCTGAGACT	25215	
QY	69	CAGGAATTGGAGACACAGCCTACCTACATATAGTAAACCTCTGCTGTCAATATATATAAA	128	
Db	25216	CAGGAGTTTGAAGCCAGCCTCTGGGCAACATAGAGAGACC-CCATCTATACAAAAATTAGAG	25274	
QY	129	GAATTTTCCAGGCATGTGGC-GTGCACCCCAGTGCACGTATTTTGGAGGCTGAGTAA	187	
Db	25275	AAATTTGGCTGGGGGCGGTGGCTTCAGGCTGTATATCCCGGCACTTTGGGAGGCCCCAAACG	25334	
QY	188	GGAGGATGCTGTTCAACCCAGAGATTCAACACAAGCCTTAGGCAACATATGTGAGACCTGTG	247	
Db	25335	GGTGGATCACTTGAAGTCAAGGATTCGAGATTCGACACAGCCTGGCCAAACATGTGTGAAGCCCCGTG	25394	
QY	248	TCCT-----ATPAAAAATATATTAAGCTGCTTGTCTTGGACAGGCGCTCGAG--CTAGCTA	298	

Db	25395	TCCTCTAAAAATACAAAAAAATTTAGCTGGGCATGTGGCATGCTCTGATGTCTCAGCTA	2545
QY	299	CTCGAAAGACTGAGGTGGAGGATCAC-TGAGCCAGAGAGGCTGAGGCTTCGATGAAACAG	357
Db	25455	CTCGGAGAGGCTGAGGCGAAGAAATCCGCTTGAACCCAGAGAGCGGAGGTTGCAGTGAGCCG	25514
QY	358	TGATCACCACGCTGGATTCACGCTTGAAAGACAGAGGAGACCCCTGTCTTCCAAAAAAA	417
Db	25515	AGATGCAACCATCGCACTCCAGCTTG3-CGACTGAGCAAGACTCTGTCTCAAAAAAAA	25573
QY	418	AAAAAAAAAAAAATGCAGAAAAAGACATCATTAACCTGACCT-----	458
Db	25574	AAAAAAAAAAAAAAAAAGCCATATATATATATATATATATATAGAGAGAGAGAGNA	25633
QY	459	-----GGGACATACTTTATGTGTGAATAATTCACAATCTTTAGAGAAATTA	508
Db	25634	GAGAGAGAGAGAGAGAGATTGCTGAGCATGCTGGCATGTGCTCTATCCCACTCC	25693
QY	509	GCATTTGCTGAATAAAGTATATATATATATATATATATTAATAATCAATGGAATTAATAT	568
Db	25694	AACACTGCGGAGAGGCTGAGTGGAGAGATCATTTGAGCCTAGAGGTGAGGCTGCACGC	25753
QY	569	CTGAGAAACTAGGCTTCTCACTCTCTCAGTTTCAGTCAAA-----A	609
Db	25754	AGCTAGATACGCCCATCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCAATTA	25813
QY	610	CTTTAATGCTCTTTGGCCGGGTGCGGTGCTCACGCTGTATATCCAGACATTTGGAGG	669
Db	25814	AAAAAAAAAAAAAGGGGCGGGGATGTGTCTCACGCTGTATATCCAGACATTTGGAGG	25873
QY	670	CCGAGCGGCTGTGATCACAAGTTAGAGATCGAGACATCTCTGTCTAACACGCTGAAC	729
Db	25874	CCGAGCGGCTGTGATCACGAAGTCAAGAAATGAGACATCTCTGTCAACATGTGAAGC	25933
QY	730	CTGTCTCTACTTAAAAATCAAAAAATTTGCGGGGTGCGGTGTCAGACGCTGTGTGCC	789
Db	25934	CTGTCTCTACTTAAAAATCAAAAAATTTGCGAGGATGTGTGCGCGCCCTATATGTCCC	25993
QY	790	AGCTGCTCAGAGGCTGAGGACAGAAATGTGTGAAACCCGGGAGGCGAGCTTGACAGT	849
Db	25994	AGCTACTCAGAGGCTGAGGACAGAAATCACTTGAAACCCAGAGAGTGAAGTTGCACTG	26053
QY	850	AGCCGAGATTGCGCCACTGCACTCCAGCCTGAGCGCAAGTGCAGACTTGTCTCAAAA	909
Db	26054	AGCCAGATTGCGCCACTGCACTCCAGCCT-GGCGACAGATGGAATCTCGCTCAAAAA	26112
QY	910	AAAAAAAAAAAAAAGT	926
Db	26113	AAAAAAAAAAAAATGATT	26129

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RESULT 10
US-09-817-180-3
: Sequence 3, Application US/09817180
: Patent No. 6340584
: GENERAL INFORMATION:
: APPLICANT: GAN, Weiniu et al.
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CL001183
: CURRENT APPLICATION NUMBER: US/09/817,180
: CURRENT FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 15297
: TYPE: DNA
: ORGANISM: Human
US-09-817-180-3
Query Match      6.1%; Score 303.6; DB 3; Length 15297;

```

Best Local Similarity 65.0%; Pred. No. 1e-55;
Matches 603; Conservative 0; Mismatches 289; Indels 36; Gaps 9;

Qy	13	CTGTGGCTCTCAGCGGTGATTTCCAGACACTTTGGGAGGC-----AGAGGATGCTTTGAG	66
Db	11700	CAGTTGCTCAGCGCTGTTCATCCAGACACTTTGGGAGGCTGAGCTGGGTGGATTCACCTTGGAG	11755
Qy	67	CTCAGGAATTTGAGACACAGCCTTACGTAACTAGTGAACCTCTGTCTGTACAAATATATA	126
Db	11760	CCGAGGAGTTCAAGATCAGCTTGGACAAACACAGTGAAA--CTCCATCTGTATCAAAAAATAC	11818
Qy	127	AAGAAATTTCCAGGCATGTGGGGGTGACCCCGACGCTGATTTGGGAGGCTGAGGT	186
Db	11819	AAAAATATGACTGGGCACGGTGGCTCACACTGTATATCCACGACCTTTGGGAGGCCAGAGC	11878
Qy	187	AGGAGGAATCTTGAAGCCAGAGTTGAAAGACAAGCCTAGGACAACTATGAGAACCTGTG	246
Db	11879	AGGTGGATTCACCTGTGGTCAAGAGTTTGAGACCAAGCCAGACCAACTATGTGAAACCCCAT	11933
Qy	247	GTCATATAAAAAT-----AATTAGCTGTGTGCTTGGCACAGGCTTGA--GCTAGCTAC	299
Db	11939	CTCTACTATAAAAATACAAAAATTTAGCCAGGACATGGTGCACTGTCTGTATATCCACCTAC	11998
Qy	300	TCCGAAATCTGAGGTGGGAGGATTCAC--TGAGCCCAAGAGCTGAGGCTGCATGTGAACAGT	358
Db	11999	TTGGGAGGCTGAGGTGGGAATTTGCTTGAACCCAGAGGCGGAGGCTGCATGTGAGACCA	12058
Qy	359	GATCACCCAGCTGGATTTCCAGCCTGGAAAGAC--AGAGGGAAGCCTGTGTTCAAAAAAAA	417
Db	12059	GATTTGTCCACTGCATCTCCAGCCTGGGCGCAAGAGTGAATCTCATCTCAAAAAAAAACC	12118
Qy	418	AAAAAAAAAAAAATGCAAGAAAAGACATCATTAATCTGACCTGGGACATTACTTTATGTG	477
Db	12119	AAAAAAAAAAAAATACAAAAATTTAGCTGGGTGTGTGACATGGGCGCTGTATGTCCCTGCTA	12178
Qy	478	ATGAAATTCACATCTTTTGGAGAATTTGCACTTTCTGATTAATATTAATTAATTAAT	537
Db	12179	CTGGGAGGCTGAGGTGGGAGATTCCTGAGGCCGGGAGGTGAGGTTGCACGTGACGTG	12238
Qy	538	ATTATTTATTAATTCAAATGGAATTAATAATTCGAGAACTAGCTCTCACTCTCCAGT	597
Db	12239	A-----GATCATGCCACTGCACCCCAACCTTGGGTGACAGAGAGAA	12281
Qy	598	TGTCAGTCAAAACTTTATATGCTCTTTGGCCGGGTGGGTTGCTCAGCGCTGTATATCCAG	657
Db	12282	GAGACCTTGACTGGAABAAAABAAAAAACCTGGGGCGCAGTGGCTCAGCGCTGTATATTTCA	12341
Qy	658	CACTTTGGAGGCCGAGGCCGGGTGATCAC--AAGTTAGAGATCGAGCAATCTCTGCT	715
Db	12342	CATTTTGGAGGCGCTGAGGAAGGTGATCACTTGATGCTAGGAATTTGACACTAGCTGCGC	12401
Qy	716	TAAACGGGTGAACCTGTCTCTAATTAATAATCAAAAAATTTAGCCGGGTGGCGGTGCCAG	775
Db	12402	CAACATAGGCAAAACCT--GTCTCTAATTAATAATCAAAAAATTTAGCGAGGTGATGTGTGC	12460
Qy	776	ACGCTGTATCTCCAGCTGCTCAGAGAGCTGAGAGCAGAGAAATGTGTGAACCCGGGAGG	835
Db	12461	AAGCTGTATATCCAGTACTTTGGAGGCTGAGGCAAGAAATCGCTTGAACCTGGGAGG	12522
Qy	836	CGAGACTTGCAGTAGCCGAGATTTGGGCCACTGCACTCCAGCTGGGCGACAGTGGGAGA	895
Db	12521	TGGAGGTTGCAGTAGAGCTGAGATCACACCACTGCATTTCCAGCTGGGTGACAGAGCAAGA	12580
Qy	896	CTCTGTCTCAAAAAAAAAAAAAAAAAA 923	
Db	12581	CTCCATCTCAAAAAAAAAAAAAAAAAA 12608	

```

1  APPLICANT: GAN, Weiniu et al.
2  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
3  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
4  TITLE OF INVENTION: THEREOF
5  FILE REFERENCE: C0001183D1V
6  CURRENT APPLICATION NUMBER: US/10/003,295
7  CURRENT FILING DATE: 2001-12-06
8  NUMBER OF SEQ ID NOS: 4
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 3
11 LENGTH: 15297
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 US-10-003-295-3

```

Query Match	6.1%;	Score 303.6;	DB 4;	Length 15297;
Best Local Similarity	65.0%;	Pred. No. 1e-55;		
Matches 603;	Conservative	0;	Mismatches 289;	Indels 36;
				Gaps 9;

Oy	13	CTGAGGCTCAGCGGTGATATCCAGACCTTTGGAGAGC-----AGAGAGATGCTTGA	66
Db	11700	CAGTTGCTCAGCGCTGTCACTCCAGACCTTTGGAGAGCTGAGCTGGGTGATCACTTGA	11755
Oy	67	CTCAGGAATTGGAGACAGAGCTTACGTACATAGTGAAACCTCTGTCTGTACAAATATTA	126
Db	11760	CCAGAGAGTTCAAGATCAGCTTGAGACACAGGTGAA-CTCATCTGTACAAAATAATAC	11811
Oy	127	AAGATTTTTCAGGCAATGCTGGCGTGCACCCAGTGCACAGCTATTTGGAGGCTGAGT	186
Db	11819	AAAAATGAGCTGGGCGACGGTGGCTCACCTGTAACTCCAGACCTTTGGAGGCGCAAGCG	11876
Oy	187	AGAGGAATGCTTGAAGCCAGAGGTTGAAGACAAAGCTGAGGCAATAGTGAGACCTGT	246
Db	11879	AGGTGATCACCTGTGGTCAAGAGTTTGAGACCAAGCAAGCAATGTGAAACCCCAT	11933
Oy	247	GTCATATTAATAAT-----AATTAGCTGTGTCTTGGSCACAGGCTCGCA--GCTACTAC	299
Db	11939	CTCTACTTAAAAATACAAAAATTAGCAGAGCATGTGTGGCATGTGCTGTAACTCCAGCTAC	11999
Oy	300	TCGGAAGACTGAGTGGAGAGATCAC-TGAGCCAGAGAGCTGAGGCTSCAGTGAACAGT	358
Db	11999	TTGGAGAGCTGAGTGGAGAAATTGCTTGAAACCAAGAGGCGGAGCTCAGATGAGCCGA	12058
Oy	359	GATCACCAGCTGATTTCCAGGCTGGAAAGC-AGAGGAGAGCCCTTTTCCAAAAAAA	417
Db	12059	GATTGTGCCACTGCACTCCAGGCTGGGCGACAGAGTGAATCCACTTCCAAAAAAAACC	12118
Oy	418	AAAAAAAAAAAAATGCAGAAAGAACATCACTAACTGACCTGGGACATTAACCTTTATGTG	477
Db	12119	AAAAAAAAAAAAATACAAAAATTAGCTGGGTGTGTGACATGGGCTGTAGTCCCTGCTA	12176
Oy	478	ATGAAAATTCACATCTTTTGAAGAAATTAGCATTTCTGATTAATAATGATTAATTAAT	537
Db	12179	CTGGGAGGCTGAGTGGGAGATCACTGAGGCCGGAGGTGAGAGTTGACAGTGAGCTG	12233
Oy	538	ATTATTAATAATTCAAATGGAATTAATAATTCTGAGAAACTAGACTTCTCACTCTCACT	597
Db	12239	A-----GATCATGCACTGCACCCCAACTGGGTGAGACAGAGAGAGA	12281
Oy	598	TGTCAGTCAAAACTTTAATGTGCTTTGGCCGGGTGGGCTGAGCTCAAGCTGTAAATCCAG	657
Db	12282	GAGACCTTGCTCGAAGAAAGAAAAAAACCTGGCGGAGTGGCTCAGAGCTGTAAATTTCAA	12341
Oy	658	CACATTGGGAGCGGAGGCGGTGATCAC--AAGGTTAGAGATGCAACCATCTGTGC	715
Db	12342	CATTTTGGAGGCTGAGAAAGTGAATCACTTGAGTCTGAGATTTGAACATAGCTGGC	12401
Oy	716	TAAACAGGTGAAAACCTGTCTCTACTTAAATAATCAAAAAATTAGCCGGGTGGCGTCCAG	775
Db	12402	CAACATGGCAAAACCT-GTCTTACTAAATAATCAAAAAATTAGCAGGCTGTAGTGTGC	12460
Oy	776	AGCGCTGTAGTCCCACTGTCTCAGAGGCTGAGGCAAGAGAAATGTGTGAACCCGGGAG	835

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Db      12461 AAGCGTGAATCCAGGCTACTTGGGAGGCTGAGGACACAAGATGCTTGAACCTGGAGG 12520
Qy      836 CGGAGCTTGCAGTGAAGCCGAGATTGGCCCACTGCACTCCAGCTGGGCGACAGTGCAGAG 895
Db      12521 TGAAGGTTGAGAGTGAAGTGCATGATCACACCACTGCTTCCAGCGTGGTGAACAGCAAGA 12580
Qy      896 CTCGTCTCAAAAAAAAAAAAAAAAAAAAA 923
Db      12581 CTCATCTCAGAAAAAAGAAAAAAGAAAAA 12608

RESULT 12
US-09-780-172-18
; Sequence 18, Application US/09780172
; Patent No. 6607916
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASHIN KINASE 2-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0159
; CURRENT APPLICATION NUMBER: US/09/780,172
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 63000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-172-18

Query Match      5.8%; Score 292.4; DB 4; Length 63000;
Best Local Similarity 67.0%; Pred. No. 4.6e-53;
Matches 549; Conservative 0; Mismatches 236; Indels 35; Gaps 8;

Qy      136 CCAGGATGCTGGCGTGCACCCCACTGCTATTTGGGAGCTGAGTGAAGAAAT 195
Db      38747 CCGGGTGCCTGGCTCAGCGCTGTAATCCAGCACTTTGGAGGCCAAGCGGCGGGA-- 38804
Qy      196 GCTTGAAGCAGAGTGAAGACACCTTGAAGCAATAGTGAACCTGCTCTTAA 255
Db      38805 TCACAAAGTGAAGATCGAGACATCTGGCTTAAACGGTGAACCCGCTTTTACTAA 38864
Qy      256 AAT-----AATGAGTGTGCTCTGGCAAGGCTGCGAG--CTAGTACTGGA-A 305
Db      38865 AATAACAAAAAATTTGCGGGGCTGTGTGGCCCTGTAGTCCCACTTGAAGGGA 38924
Qy      306 GACTGAGTGGGAGATCAC-TGAGCCAGAGAGCTGAGGCTGCACTGAACAGTATCAC 364
Db      38925 GGTGAGGAGGAGATGCGTGAACCTGGAGGCGGGCTTGCAAGCGAGATCAC 38984
Qy      365 CCAGCTGATTCAGGCTGGAAGACAGAGGAGACCCCTTTTCCAAAAAAGAAAAA 424
Db      38985 GCCACTGCACTCAGGCTGGGCGACAGACAGACTCCGCTCTCAAAAAAAGAAAAA 39044
Qy      425 AAA-----AATGCAAGAAAAAGACATCACTAAACCTGACCTGGACATA 467
Db      39045 AAAAAATTAATCTCTTGGGAAAGCTGTCTCTTGTGGAGACAAAGTATTTAGAACAA 39104
Qy      468 CTTTATATGATGAATTAATCAATCTTTTGAAGAAATTAAGATTTGATTAATGTA 527
Db      39105 CCTTATATCAAGCAGCTCATGTCAATGCAATTAAGATTAACAGTTGGGATTAG 39164
Qy      528 TTATATATATATATATTAATTAATGAATGAATTAATTTCTGAGAAACTGACTTCTCA 587
Db      39165 AAAGATTAATTTGAAGATTAAGTTTCTTAAATCTGAGATTTGAACACACGTAATTTA 39224
Qy      588 CTCCTCAGTGTCACTCAAACTTAAATGCTCTTTGCGCGGAGTGGGCTCAGGCT 647
Db      39225 ATTGCGCTAATTTAA--AAAAAAGAAAAATTAAGAGGCGCAGGCGGCTCAGGCT 39282
Qy      648 GTAAATCCGCACTTTGGAGGCGGAGGCGGTGATCAAGATTAAGATGAAGACC 707
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Db      39283 GTAAATCCGCACTTTGGAGGCGGAGGCGGAGAAATCAAGAGTCAAGATTCAGAGACC 39342
Qy      708 ATCTGGCTTAACAGCT---GAAACCTGCTCTTAATAAATAAATAAATAAATAAATAAATAA 764
Db      39343 ATCTGGTTAAACAGGCTGAGAGACCGGCGCTCTCTAATAAATAAATAAATAAATAAATAA 39402
Qy      765 TGGGTCGCAAGACGCTTAAGTCCCAAGCTGCTCAGAGGCTGAGGCAAGATGATGTG 824
Db      39403 CATGTGGAAGCGCTGTGTGTCACAGCTGCGGAGGCTGAGGCAAGATGATGTG 39462
Qy      825 AACCCGAGAGCGGAGCTTGCAGTGAAGCCAGATTTGCGCACTGCACTCAGCTGAGCG 884
Db      39463 AACCCGAGAGGCTGAGAGCTGCACTGCAAGATGCGGCACTGCACTTACCTGAGCG 39522
Qy      885 ACAGTGCAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAA 924
Db      39523 ACAGAGTGAAGTCACTCCATAAATAAATAAATAAATAA 39562

RESULT 13
US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match      5.8%; Score 292; DB 4; Length 70000;
Best Local Similarity 63.2%; Pred. No. 5.8e-53;
Matches 550; Conservative 0; Mismatches 305; Indels 15; Gaps 6;

Qy      93 AACATAGTGAACCTGCTGTCTGTACAAATTAATAAAGATTTCCAGGCACTGTGCGTG 152
Db      14313 AAAATTAATTAATCAATTAATAATTAATAAAGCAAAAGCCGCGCATGTGATCA 14254
Qy      153 CACCCAGTGCAGCTTATTTGGAGGCTGAGGTAAGAAATGCTTGAAGCAGAGATT 212
Db      14253 TGCTGTAACTCCAGCACTTTGGAGGCGCAAGGCGAGCA--TCAGAGGTCAAGAGTT 14196
Qy      213 GAAGCAAGCTTGAAGCAATAGTGAACCTGTGTCTAATAA-----AATAATTAGC 266
Db      14195 CAAGACATCTGCTTACACAGTGAACCTGTCTCTAATAAATAAATAAATAAATAAATAA 14136
Qy      267 TGTGTCTTGGACAGGCTGCGAG--CTAGTACTGGAAGACTGAGGTGGAGATCA 324
Db      14135 CAGGTATGTGCGACGACCTGTAGTCACTCGGAGGCTGAGGCGGAAGATAG 14076
Qy      325 C-TGAGCCAGAGAGCTGAGGCTGCAAGTGAACAGTGAACCCAGCTGAGATTCCAGGCTG 383
Db      14075 CTTGAACCCAGAGAGGAGAGGTTGCTTAAAGCAAGATCAAGCACTGCACTCCAGGCTG 14016
Qy      384 GAAGCAGAGAGAGACCTGTGTTCAAAAAAAAAAAAAAAAAAAAAATGCAAGAAAGCA 443
Db      14015 GGCAACAGAGCAAGA-CTTAACGCTCAAAAAAATAATATACATACATACATGAGAA 13957
Qy      444 TCATTAACCTTGAAGTGAATCTTTATATGATGAATTCACATC---TTTGAAGA 500
Db      13956 CAACACAGCAGCAAGAAATGAATTTGGAAACCAAGACACATGATTCGTGTTCTTCAAC 13897
Qy      501 AGAAATTAAGCATTTCTGATTAATAATGATTAATTAATTAATTAATTAATTAATTAATGAAT 560
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Db	13896	TGCTTCCTGTATTAAGTGGAGTAATCACTTATCATCCAGGCTATTTTCTCATGCAT	13833
Qy	561	TAAATATTCTGAGAACTAGCTTCTCACTCTCTCAGTGTCACTCAAAACTTTAATGTC	620
Db	13836	AAATGGAAATACGTCTTCTCTTCCCACTCCAGGATTTGGCAGAGAAATGTCTAACCA	13777
Qy	621	TTTGGCCGGGTGGGGTGCTCAGCCCTGTAAATCCAGCACTTTGGAGGCCAGGGGGGT	680
Db	13776	ACATCTCTAAAAATCCTCTGTAAATTTGATATCCAGCACTTTGGAGGCCAGGGGAGGC	13717
Qy	681	GGATTCACAGGTATAGAGATCGAGACCATCTCGGCTTAACAAGGTGAACCTCGTCTTAC	740
Db	13716	GGATTCAGAGGTCAAGAGATTGAGACCATCTTGGCTTAACATGTGTGAACCCATCTTTC	13655
Qy	741	TAAAAATACAAAAATTTAGCCGGGTGCGGTGCCAGACGCTGTAGTCCAGCTGCTCAG	800
Db	13656	TAAAAATACAAAATATTAGCCAGGCGTGGTGGGGGTGCTGTAGTCCAGGTACTTTGG	13597
Qy	801	AGGCTGAGGCAAGAGAAATGCTGTGAACCCGGGAGGCGAGACTTGCAGTGAACCGAGATTG	860
Db	13596	AGGCTGAGGCAAGAGAAATGCGTGAACCTTGGGAGGCGGAGCTTGCAGTAAAGCCGAGATCG	13537
Qy	861	CGCACATGCACTCAGGCTGGGGGAGACAGTGCAGACTTCTGTCAAAAAAATTTTTAAAAA	920
Db	13536	CGTCACATGCACTCAGGCTGGGGGAGACAGACGAGACTTGTCTCAAAAAAATTTTTAAAAA	13477
Qy	921	AAAGTTGAATGGCTTTTGAAGCCAGAGAT	950
Db	13476	GAATAACAAAAATCTCTGAATATATAAGT	13447

RESULT 14

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US-09-544-398B-11
; Sequence 1B, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carnull, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3.
; FILE REFERENCE: 013796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 66933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-11

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Query Match	5.7%;	Score 287;	DB 4;	Length 66933;
Best Local Similarity	66.8%;	Prod. No. 6.8e-52;		
Matches 528;	Conservative	0;	Mismatches 230;	Indels 33; Gaps 7;
QY	155	CCCCAGTGCACGCTATTGTTGGAGGCTGAGGTGAGAGATGCTTAAGCCCGAGGATTGA	214	
Db	37990	CCTCTAATCCACACATTTTGGGAGTCCGAGGTGGGAGATCACTTAGGTCCAGGAGTTTG	38049	
QY	215	AGACAAAGCCTAAGGCAACATAGTAGAGCCCGGTGCTCTATAAAAA---ATAATTAGCTGT	270	
Db	38050	AGACACGCTGGGCAACATAGTAAACCTGGCTCTACTTAAAGTACAAATAATTAGCTGGG	38109	
QY	271	TGCTTGGGCAAGGCGCTGCA--GCTAGCTACTCGGAAGA CTGAGGTGGAGGATCAC-TG	327	

Db	38110	TGTGTGTGGCCGCGCACCTGTAAATCCAGTTACTACAGAGGCTAGAGCGAGAGAATCGCTTG	38169
Qy	328	AGCCACGAGAGGCTGAGGCTGCGAGTGAACAAGTATCAACCGAGCTGAGTTCCACCTCGGAAG	387
Db	38170	TACCCCGGAGGCGAGAGATGTGCAGTGAACCAAGATTGTGCTCTGCACTCCACCTCGGGTA	38229
Qy	388	ACAGAGGGAGAC--CCGTGTTCMAAAAAAAAAAAAAAAAAAAAAAAAAATGCAGAAAGAATC	445
Db	38230	ACAGAGTGAAGACTTCTGTCTCAAAAAAAAAAAAAAAAAATCATCGGATGGATGAGCGGACAC	38289
Qy	446	ATTAACCTTGACCTGGGACATTACTTTATGTGATGAATTCACAACTTTTAGAAGAAA	505
Db	38290	TTCCTGTGATTTATTCATCCACGCGGCTAGAGTTCCTCCACCTTGGTGTGCGTAATA	38349
Qy	506	TTAGCACTTCTGATTAATAATGATATTAATATTAATTAATTAATCAAA-----	554
Db	38350	AGGCCACTATGAACATTTCCCTCCGCTGCGGAAGTTTGTACTAGTGAAGAAAAGCCGCG	38409
Qy	555	-----TGGAATTAATAATTTCTGAGAAACTAGCTTCTCACTCTCACTTGTCACT	604
Db	38410	TTTGTGTGTGTGCATAGGATTTCTGATGAAGAAAGTTTGCACTAACATAGTATTTGTACT	38469
Qy	605	CAA--AACTTTATGTGCTTTTGGCGGGGCGGTGGCTCAGCCCTGATATCCACAGACTT	662
Db	38470	ACATTTAAATGAAGCTCAGGGGCGGGGCGGGTGGCTCAGCCCTGTATATCCAGACATT	38529
Qy	663	TGGAGAGCGGAGGCGGGTGGATCACAAGGTTAGAGATGAGAACCATCCTGGCTAACG	722
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Qy	723	GTAAGAACTGTCTCTTACTTAATAAAT-CAAAAAATTAGCCGGGTGGCGGTGCCAGACGCT	781
Db	38590	GTAAGAAACCCGCTCTTACTTAATAAATACAAAAAATCAGCAAGTGTGTGTGGGGCACCT	38649
Qy	782	GTAAGTCCACAGCTGCTCAGGAGGCTGAGGCAAGATGGTGTGAACCCCGAGGCGGAGC	841
Db	38650	GTAAGTCCACAGCTACTTGGGAGGCTAGAGGAGAGAAATGGCGTGAACCCCGGAGGCGGAGC	38709
Qy	842	TTGCAAGTGAAGCGAGATTGGCGCACTGCACTCAGCCTGGGCGACAGTGTGCGAGACTTGT	901
Db	38710	TTTCGGGTGAGCCGAGATGCTCTTCACTGCACTCGAGCTGGGCAAGACAGACAGACTTCGT	38769
Qy	902	CTCAAAAAAAAA 912	
Db	38770	CTCAGCGCAAAA 38780	

RESULT 15

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US-09-543-771-11
Sequence 11, Application US/09543771
Patent No. 6780609
GENERAL INFORMATION:
APPLICANT: John F. Carroll et al.
TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3.
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/543, 771
CURRENT FILING DATE: 2000-04-05
EARLIER APPLICATION NUMBER: US 09/229,319
EARLIER FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: US 60/071,449
EARLIER FILING DATE: 1998-01-13
EARLIER APPLICATION NUMBER: US 60/105,511
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 11
LENGTH: 66933
TYPE: DNA
ORGANISM: Homo sapiens
US-09-543-771-11

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Query Match Similarity	5.7%	Score	287	DB 4	Length	66933
Best Local Similarity	66.8%	Pred. NO.	6	8e-52		
Matches 528; Conservative	0	Mismatches	230	Indels	33	Gaps

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QY      155  CCCCAGTGCAGTATTGGAGGCTGAGTAGAGGAATGCTTGAAGCCAGAGTTGA 214
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Db      37990  CCTTATATCCAGATATTTGGAGTCCGAGGTGGGCAATCAGTGAATCAGAGTTTG 38049
QY      215  AGACAAGCCTAAGGCATATAGTAGAGCCCTGTGTCTATAAAA----ATAATTAGCTGT 270
      |||
Db      38050  AGACAGCCTGGCCAAATAGTAGAAACCTGGCTCTATTAAGTACAAAATTAGCTGGG 38109
QY      271  TGTCTTGGCACAGGCTGCA--GCTAGCTACTGGAAAGTGAAGTGGAGATCAC-TG 327
      |||
Db      38110  TGTGTGGCCGCGCACCTGTATCCAGTTACTCAGAGGCTGAGGCGAGAAATCGCTTG 38169
QY      328  AGCCAGAGAGCTGAGGCTCAGTGAAACATGATCACCCAGCTGGAATCCAGCCTGGAAG 387
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QY      388  ACAAGAGGAGAC--CCTGTTCCAAAAAATGCAAGAAAAATGCAAGAAAAAGACATC 445
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Db      38230  ACAGAGTGAACATTCCTGTCTCAAAAAAATGCAAGAAAAATCATCGGATGGAAGGACAC 38289
QY      446  ATAACTTGACCTGGGACATAACTTTATGTGATGAATTCACATCTTTTAGAAGAA 505
      |||
Db      38290  TTCTGTATTATTCATCCACGAGGTCTAGGTTCTTCCACCTTGGTGTGTGATATA 38349
QY      506  TTAGCATTTCTGATAAAATGATATTATATATTATTAATAATCAAA----- 554
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QY      555  -----TGAATTAATAATTTCTGAGAACTAGCTTCTCACTCTCAGTTGTCAGT 604
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QY      605  CAA--AACTTATAGCTTTTGGCCGGGTGCGGTCAAGCTGTAAATCCAGCACTT 662
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Db      38470  ACATTAATAAGAAAGCTCAGGAGCGGCGGTGCTCAAGCTGTAAATCCAGCACTT 38529
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QY      723  GTGAAACCTGCTCTACTTAATAATA-CAAAAAATTAGCCGGGTGCGGTGCCAGCGCT 781
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Db      38590  GTGAAACCCCGTCTACTTAATAATAACAAAAAATAGCCAGGTGTGTGGCGGCACT 38649
QY      782  GTAGTCCGAGCTGTCAAGAGGCTGAGGCGAGAAATGTGTGAACCCGGAGAGCGGAGC 841
      |||
Db      38650  GTAGTCCGAGCTACTTGGAGGCTGAGGCGAGAAATGTGTGAACCCGGAGAGCGGAGC 38709
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      |||
Db      38710  TTGCGGTGAGCCGAGATCGCTTCACTGCACTCGAGCCTGGGCAACAGAGCAAGATCCGT 38769
QY      902  CTCAAAAAAA 912
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Db      38770  CTCACGCAAAA 38780
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Search completed: December 27, 2004, 11:07:41
Job time : 268.615 sec8

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QY 241 CCCTGTCTATAAAAAATAATTAGTGTGTCTTGGCAAGGCTGACAGTACT 300
Db 241 CCCTGTCTATAAAAAATAATTAGTGTGTCTTGGCAAGGCTGACAGTACT 300
QY 301 CGGAAGCTGAGGTGGAGGATCACTAGCCAGAGGCTGAGGCTGAGGAACAGTGA 360
Db 301 CGGAAGCTGAGGTGGAGGATCACTAGCCAGAGGCTGAGGCTGAGGAACAGTGA 360
QY 361 TCACCCAGCTGAGATTCAGGCTGGAGAAGAGGAGAACCCGTCTTCCAAAAA 420
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QY 421 AAAAAAATGCAAGAAAGACATCATAACTTGACCTGGGACATACTTTATGTATG 480
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QY 4561 TGCATTAAGAGCACTTTTATTTATTTCTAAGCTTCTCATATCAATTTGGCATGT 4620
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Db 4621 AACTGTTTCAAGGTGGCTGGAAACGGGGGCAACCTGGAACATCTTGATATACAGGCA 4680
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QY 4741 TCCAGCCCGAGTTTACAGAAATCTATCTTTCTCTGATTAATCTTTATTTGTTTCT 4800
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Db 4981 CTATCTTTCTTATTTTGT 5000

RESULT 2
US-10-224-562-3
/ Sequence 3, Application US/10224562
/ Publication No. US200302229A1
/ GENERAL INFORMATION:
/ APPLICANT: YAN, Chunhua et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ FILE REFERENCE: CL001098DIV
/ CURRENT APPLICATION NUMBER: US/10/224,562
/ CURRENT FILING DATE: 2002-08-21
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 53332
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-224-562-3

Query Match 100.0%; Score 5000; DB 14; Length 53332;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATAGCCCAATGCTGTGGCTCAAGCGCTGATTTCCGACACTTTGGAGGAGGAGATCG 60
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Db 301 CGGAACACTGAGTGGGAGGATCTAGACCCAGAGAGGCTGAGGCTGAGTGAACGTGA 360
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Db 361 TCACCCAGCTGATTCACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Db 1261 AGTGTGATTTGAAGACTACAGACTGCAACCAATTTTAACCTGATTCCTTGACATGTT 1320

QY 1321 GTCCTGTTAATAGTACTTTACATATAGTAAATTATTACATATATGTGAGAG 1380
DB 1321 GTCCTGTTAATAGTACTTTACATATAGTAAATTATTACATATATGTGAGAG 1380
QY 1381 CAAGCAAGAAAGAGAAAGATATTTTCATTCAACTCCTCTCTCCATCAGCAATGGCTA 1440
DB 1381 CAAGCAAGAAAGAGAAAGATATTTTCATTCAACTCCTCTCTCCATCAGCAATGGCTA 1440
QY 1441 ATATCATCTTTGTACAGTTAAGAACAACTAGGTGCTCAACATATGTTTTGAATAAA 1500
DB 1441 ATATCATCTTTGTACAGTTAAGAACAACTAGGTGCTCAACATATGTTTTGAATAAA 1500
QY 1501 TGAATGAATGGCAACCTTTCTAGACATATGATGATCTATTTGTAAGGCAAGAT 1560
DB 1501 TGAATGAATGGCAACCTTTCTAGACATATGATGATCTATTTGTAAGGCAAGAT 1560
QY 1561 GCAGTAGATATTTTCAACTTTTCTGTTTATGATTTCTGTGTTCTTTGACTATA 1620
DB 1561 GCAGTAGATATTTTCAACTTTTCTGTTTATGATTTCTGTGTTCTTTGACTATA 1620
QY 1621 AAGTAGCTAGTAGCAAAATTTGTTTAAAGTCTGAAACCAAAATGCTTTCAGATAAA 1680
DB 1621 AAGTAGCTAGTAGCAAAATTTGTTTAAAGTCTGAAACCAAAATGCTTTCAGATAAA 1680
QY 1681 GGTAGGAGAAAAATCTCTCAACATGTCACCTTTAGCAACAGAAACCTTAATGCA 1740
DB 1681 GGTAGGAGAAAAATCTCTCAACATGTCACCTTTAGCAACAGAAACCTTAATGCA 1740
QY 1741 TATCACCATCATGATATCATATTAATATCATTTGATGATGATGATGATGATGAT 1800
DB 1741 TATCACCATCATGATATCATATTAATATCATTTGATGATGATGATGATGATGAT 1800
QY 1801 AAACATATGATACCAATAGCACTACTGTGCGCAAGAACCAAACTTTAATGCGCAA 1860
DB 1801 AAACATATGATACCAATAGCACTACTGTGCGCAAGAACCAAACTTTAATGCGCAA 1860
QY 1861 TTTTATTTTATTAATTAACAGCTGCTCTGTTTCACTGTGCAATCTGATGATGCA 1920
DB 1861 TTTTATTTTATTAATTAACAGCTGCTCTGTTTCACTGTGCAATCTGATGATGCA 1920
QY 1921 TCCCTGCTGATGATGAGTTCTTTGCACTGATTAAGGAAAACTGTAAGTTGAGGCT 1980
DB 1921 TCCCTGCTGATGATGAGTTCTTTGCACTGATTAAGGAAAACTGTAAGTTGAGGCT 1980
QY 1981 GCTCAGGAGAGCACTCATGTGATCATATGAAAGCTCCAGCTGCTGCTGCA 2040
DB 1981 GCTCAGGAGAGCACTCATGTGATCATATGAAAGCTCCAGCTGCTGCTGCA 2040
QY 2041 AAAGGAGAGAACAAAGATAGAGAGAGCAATGGGGAAGGTTCAAGTGGGGTTTTCTC 2100
DB 2041 AAAGGAGAGAACAAAGATAGAGAGAGCAATGGGGAAGGTTCAAGTGGGGTTTTCTC 2100
QY 2101 CTTGAACCTTAACAAGATTTATGGGTCAAGAGCTGTGTGCAAAAGCTGTACAGCTGATGCA 2160
DB 2101 CTTGAACCTTAACAAGATTTATGGGTCAAGAGCTGTGTGCAAAAGCTGTACAGCTGATGCA 2160
QY 2161 GCTGCTACCATTTGTTCAAGAGAGAGGAGGACACAGCTGTGAGAGAGTCAAGCTGAGA 2220
DB 2161 GCTGCTACCATTTGTTCAAGAGAGAGGAGGACACAGCTGTGAGAGAGTCAAGCTGAGA 2220
QY 2221 CCACGAGAGCTGCTTCAAGATTTTGTATCCCAAGAGAGAGATCTTTTCTATTTGAT 2280
DB 2221 CCACGAGAGCTGCTTCAAGATTTTGTATCCCAAGAGAGAGATCTTTTCTATTTGAT 2280
QY 2281 AACCAAGAGATTGAGACATCTCTTTTGTGAGGAGGATCTGATTTCTTCTGAGTGGTCT 2340
DB 2281 AACCAAGAGATTGAGACATCTCTCTTTTGTGAGGAGGATCTGATTTCTTCTGAGTGGTCT 2340
QY 2341 AAACCAATTAATGAATTTATTAAGTCAAGAAAAATTTATGCTGTAGTTATCA 2400
DB 2341 AAACCAATTAATGAATTTATTAAGTCAAGAAAAATTTATGCTGTAGTTATCA 2400
QY 2401 TTTGGGGAATTTCTTGTAAACCAAAAGGAAAAATTAATCTTGGCTTGGCTGACGAA 2460

DB 2401 TTTGGGGAATTTCTTGTAAACCAAAAGGAAAAATTAATCTTGGCTTGGCTGACGAA 2460
QY 2461 ACTCAGCTGGCTTGAAGTGAAGAAAGTACTCTCTCAAAATCTTAAGGCTCTAAATTAC 2520
DB 2461 ACTCAGCTGGCTTGAAGTGAAGAAAGTACTCTCTCAAAATCTTAAGGCTCTAAATTAC 2520
QY 2521 AGAGCTGAAACTTTAAAGGCAAGCTGAGTATTTAGTTGATGCTATGATTTGAAACTT 2580
DB 2521 AGAGCTGAAACTTTAAAGGCAAGCTGAGTATTTAGTTGATGCTATGATTTGAAACTT 2580
QY 2581 TAGTAAATTTGTCATATTAATTAAGCAATGCAATGATTTTCCCTCAAGCAATTAATTA 2640
DB 2581 TAGTAAATTTGTCATATTAATTAAGCAATGCAATGATTTTCCCTCAAGCAATTAATTA 2640
QY 2641 AGTGAACATGAATAAAAAAGCCAGACTTAAACAGAAAAAGTTGCAAAACATCATCA 2700
DB 2641 AGTGAACATGAATAAAAAAGCCAGACTTAAACAGAAAAAGTTGCAAAACATCATCA 2700
QY 2701 AGAGATTTAGTTTAACTGATGTTAAAGACACATTTTATGTTGAAGAAAGTATGTA 2760
DB 2701 AGAGATTTAGTTTAACTGATGTTAAAGACACATTTTATGTTGAAGAAAGTATGTA 2760
QY 2761 TTTTCAAGAGTTGATACATTTATGCTTTTTCAGGAGTCTTTCAGAAAAAGTCCCTTTG 2820
DB 2761 TTTTCAAGAGTTGATACATTTATGCTTTTTCAGGAGTCTTTCAGAAAAAGTCCCTTTG 2820
QY 2821 GGGGTACAGGAAGCTTGAAGAAACATTTGAAGAGTGAAGAAATGAGCAATTAAGAAAAAT 2880
DB 2821 GGGGTACAGGAAGCTTGAAGAAACATTTGAAGAGTGAAGAAATGAGCAATTAAGAAAAAT 2880
QY 2881 GGTTTTACAGGACCTGAATCTTTTACTTTGATTAATTTTATTTCTGCTTTCTTTT 2940
DB 2881 GGTTTTACAGGACCTGAATCTTTTACTTTGATTAATTTTATTTCTGCTTTCTTTT 2940
QY 2941 CTCTAGCTTAACAGACTTAAAGAGATGATGATGATGATGATGATGATGATGATGAT 3000
DB 2941 CTCTAGCTTAACAGACTTAAAGAGATGATGATGATGATGATGATGATGATGATGAT 3000
QY 3001 CTTCAAGCTGCCGCTGCCAGAAATCAAGAGTAAAGGCAAGAGTAAAGTGAATTTG 3060
DB 3001 CTTCAAGCTGCCGCTGCCAGAAATCAAGAGTAAAGGCAAGAGTAAAGTGAATTTG 3060
QY 3061 TTTTCAAGAGAGATCTGAGGAGAGGTTTCAAGTGGGTGATGAGCAGCTGATGATG 3120
DB 3061 TTTTCAAGAGAGATCTGAGGAGAGGTTTCAAGTGGGTGATGAGCAGCTGATGATG 3120
QY 3121 AAGAAATTTTAATGATGATCTGTCTAAGAGAGGCGGCTTGTCTTCCAGAGCAATTA 3180
DB 3121 AAGAAATTTTAATGATGATCTGTCTAAGAGAGGCGGCTTGTCTTCCAGAGCAATTA 3180
QY 3181 GAGCGAGCTTCCCAAGTCTGCTGAGCAATGCTGTCTAATTTTCCCTGGGGAATAAAGT 3240
DB 3181 GAGCGAGCTTCCCAAGTCTGCTGAGCAATGCTGTCTAATTTTCCCTGGGGAATAAAGT 3240
QY 3241 CAACTAATAAAAAAGTCTTTCTCTCTTCTTCCCTTCAACCGCTCTTTTCCCATTC 3300
DB 3241 CAACTAATAAAAAAGTCTTTCTCTCTTCTTCCCTTCAACCGCTCTTTTCCCATTC 3300
QY 3301 CCTAGAGAGAGAGAGAGCTCCCTTTTGGGAGAGCTATCTTAATTAAGCTGAGAA 3360
DB 3301 CCTAGAGAGAGAGAGAGCTCCCTTTTGGGAGAGCTATCTTAATTAAGCTGAGAA 3360
QY 3361 GCTGAGTGAAGCTCTTATGAGACAGTTTAAAGGAGATTAAGAGTGAAGTACATAG 3420
DB 3361 GCTGAGTGAAGCTCTTATGAGACAGTTTAAAGGAGATTAAGAGTGAAGTACATAG 3420
QY 3421 CTGGGAGAGACTTTAGATGAGAGTCCGCCCCCAATTTTATTAATTAAGCCAGT 3480
DB 3421 CTGGGAGAGACTTTAGATGAGAGTCCGCCCCCAATTTTATTAATTAAGCCAGT 3480
QY 3481 GAGACATCATTAAGATTTTACATCAGAGCTGTGCAAGACACATGAGCGAGAGGA 3540

Db 3481 GAGACATCATGAAAGTTCATAGCACTGAGAACCTGTGCAAGACCAATGGCCGACAGGGA 3540
QY 3541 GAGAGACATGATTAACCTTAAACAGCCTTGAAAGAAAAAACAACCTGCCCTGCTTAATTA 3600
Db 3541 GAGAGACATGATTAACCTTAAACAGCCTTGAAAGAAAAAACAACCTGCCCTGCTTAATTA 3600
QY 3601 AATGAGCCCACTTAAGTTTATATAGCCTTCCCTCTTGATTCATTCAGAGAAATTC 3660
Db 3601 AATGAGCCCACTTAAGTTTATATAGCCTTCCCTCTTGATTCATTCAGAGAAATTC 3660
QY 3661 AAGAAATAGACATTCCTACTACTAGCCCAAGAAAGAAATATACCTTCAGGCTGTG 3720
Db 3661 AAGAAATAGACATTCCTACTACTAGCCCAAGAAAGAAATATACCTTCAGGCTGTG 3720
QY 3721 GGAGGCACTGTTGGTAAAGGCTCTTAACAGGTTTTTATATATCCCTGCTTAATCACAAT 3780
Db 3721 GGAGGCACTGTTGGTAAAGGCTCTTAACAGGTTTTTATATATCCCTGCTTAATCACAAT 3780
QY 3781 GACAGAGTTTGTAAAGGCAACCTGAAATTTGCTGCTCAATCCGCACTGGCCTTAT 3840
Db 3781 GACAGAGTTTGTAAAGGCAACCTGAAATTTGCTGCTCAATCCGCACTGGCCTTAT 3840
QY 3841 AGAAGAACTGAAGTTGGTTTGCAGAAATTAAGTATGATGCAAGAAAGATGAATCCTAG 3900
Db 3841 AGAAGAACTGAAGTTGGTTTGCAGAAATTAAGTATGATGCAAGAAAGATGAATCCTAG 3900
QY 3901 AATTTTATATTTTGCAGAAATTAACCAAAATGTCTGAGAAATTAATCTGCTTAATCCAA 3960
Db 3901 AATTTTATATTTTGCAGAAATTAACCAAAATGTCTGAGAAATTAATCTGCTTAATCCAA 3960
QY 3961 AGCTAAGTAAATTTTGTAAACCAACCACTTTGTAATATATGTAAGAAATCCATGA 4020
Db 3961 AGCTAAGTAAATTTTGTAAACCAACCACTTTGTAATATATGTAAGAAATCCATGA 4020
QY 4021 AATCCCTTTTAACTCAAGGTGGGAAAGTTGATGCTTTTCTTTTATGTTATCCCA 4080
Db 4021 AATCCCTTTTAACTCAAGGTGGGAAAGTTGATGCTTTTCTTTTATGTTATCCCA 4080
QY 4081 ATGAGAGAAAGTAATAGGCTCAATAGTGGTAAATTTTAAATTTAAATATATAGCTGAT 4140
Db 4081 ATGAGAGAAAGTAATAGGCTCAATAGTGGTAAATTTTAAATTTAAATATATAGCTGAT 4140
QY 4141 CCGAGTGCAGTGGTGTATTAACACTACTGATCAACAACAGTTACAGATTTCTTTGTTCT 4200
Db 4141 CCGAGTGCAGTGGTGTATTAACACTACTGATCAACAACAGTTACAGATTTCTTTGTTCT 4200
QY 4201 TCTCCACTCCCACTGCTTCACTTAAGTGGCAAAAAAGAAAAATTTTATATTA 4260
Db 4201 TCTCCACTCCCACTGCTTCACTTAAGTGGCAAAAAAGAAAAATTTTATATTA 4260
QY 4261 CTACTCAAGACTAAATATTTATTTATCTAGTATTAAGCTGTATATTAATTTT 4320
Db 4261 CTACTCAAGACTAAATATTTATTTATTTATCTAGTATTAAGCTGTATATTTT 4320
QY 4321 ACTTGTAAACAGATGTAGGGAATACAGTTTATTTTATTTATTTATATATAT 4380
Db 4321 ACTTGTAAACAGATGTAGGGAATACAGTTTATTTTATTTATTTATATATAT 4380
QY 4381 TTAATTTATTTTGTGAATGAAATCTGTGCAACCAAGCTGAGAGTGGTGCATC 4440
Db 4381 TTAATTTATTTTGTGAATGAAATCTGTGCAACCAAGCTGAGAGTGGTGCATC 4440
QY 4441 TCAGATGACTGCAACCTGCTGCTGAGTTCAAGCAACCTGTCGCTGCTGCTT 4500
Db 4441 TCAGATGACTGCAACCTGCTGCTGAGTTCAAGCAACCTGTCGCTGCTGCTT 4500
QY 4501 TACTTTCTTAATCTGTTTATAGTATGATGATGATCCTTAACCTTTTCAATGCTGAACATC 4560
Db 4501 TACTTTCTTAATCTGTTTATAGTATGATGATGATCCTTAACCTTTTCAATGCTGAACATC 4560
QY 4561 TCGAATTAAGAGACCACTTTATTTATTTATGCTTCCCTCATATCAATTTGGCCATG 4620
Db 4561 TCGAATTAAGAGACCACTTTATTTATTTATGCTTCCCTCATATCAATTTGGCCATG 4620

QY 4621 AACTGTTTCAAGTGGCTCGGAACGGGGCAACCTTGAAATACCTTGATATCATGGGA 4680
Db 4621 AACTGTTTCAAGTGGCTCGGAACGGGGCAACCTTGAAATACCTTGATATCATGGGA 4680
QY 4681 CCATGACACTTGTATCTCTCTTCTGAGTTCTGACTTTGATTTGTTGACAGACCTT 4740
Db 4681 CCATGACACTTGTATCTCTCTCTGAGTTCTGACTTTGATTTGTTGACAGACCTT 4740
QY 4741 TCCAGCCCAAGTTTACAGAAATTCATTAATCTTTCTTCTAGTACTTAATGTTTCT 4800
Db 4741 TCCAGCCCAAGTTTACAGAAATTCATTAATCTTTCTTCTAGTACTTAATGTTTCT 4800
QY 4801 TTTTCAATTAATCTTTCATCTACTGGAATTAATATGTAATTAACAATCAACCCAC 4860
Db 4801 TTTTCAATTAATCTTTCATCTACTGGAATTAATATGTAATTAACAATCAACCCAC 4860
QY 4861 TCCATTTATTAAGTTTCTTCTCTCTGAGTTTGAAGCTGGCAATGATTAATTAAG 4920
Db 4861 TCCATTTATTAAGTTTCTTCTCTCTGAGTTTGAAGCTGGCAATGATTAATTAAG 4920
QY 4921 ATCTCAGAAATCTTGAAATCTTCTGTTCTTAATCTTTTAAATCATGTTCCCTAAT 4980
Db 4921 ATCTCAGAAATCTTGAAATCTTCTGTTCTTAATCTTTTAAATCATGTTCCCTAAT 4980
QY 4981 CTATCTTTCTTAATTTGT 5000
Db 4981 CTATCTTTCTTAATTTGT 5000

RESULT 3
US-10-027-632-132158
; Sequence 132158, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Mery, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108627.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132158
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-132158

Query Match 13.7%; Score 687.4; DB 13; Length 714;
Best Local Similarity 99.3%; Pred. No. 2,9e-128;
Matches 710; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 795 CTCAGAGGCTGAGGACAGAGATGTGTGAACCCGGAGGCGAGCTTGAGTGAACCG 854
Db 1 CTCAGAGGCTGAGGACAGAGATGTGTGAACCCGGAGGCGAGCTTGAGTGAACCG 60
QY 855 AGATTGGCCCACTGCACTCCAGCCTGGGCGACAGTGCAGAGACTGTCTCAAAAAA 914
Db 855 AGATTGGCCCACTGCACTCCAGCCTGGGCGACAGTGCAGAGACTGTCTCAAAAAA 914

```

RESULT 5
US-10-450-826-114
Sequence 114, Application US/10450826
Publication No. US2004010181A1
GENERAL INFORMATION:
APPLICANT: JI, Darren
APPLICANT: Axelrod, Douglas W.
APPLICANT: Cook, Jonathan S.
APPLICANT: Jaiswal, Neelam
APPLICANT: Eistein, Richard
APPLICANT: Houghton, Adam
APPLICANT: Mertz, Lawrence
TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
FILE REFERENCE: 044921-5039-WO
CURRENT APPLICATION NUMBER: US/10/450,826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255,882

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? PRIOR FILING DATE: 2000-12-18
? PRIOR APPLICATION NUMBER: US 60/285,691
? PRIOR FILING DATE: 2001-04-24
? NUMBER OF SEQ ID NOS: 149
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 114
? LENGTH: 172570
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: Genbank Accession No
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (1)..(172570)
? OTHER INFORMATION: n = a or c or g or t
US-10-450-826-114
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Query Match	7.4%;	Score 370.6;	DB 17;	Length 172570;
Best Local Similarity	68.2%;	Pred. No. 2.4e-63;		
Matches 639;	Conservative 0;	Mismatches 249;	Indels 49;	Gaps 7;

QY	11	TGCTGTGGCTCAGCGCTGTATTCGCCAGCACTTTGGGAAGC-----AGGAAGATCGCTTG	64
Db	136255	TGCGTGGCTCATGCTGTATTCGCCAGCACTTTGGGAAGCCAAAGTGGGTAGATCACTTG	136314
QY	65	AGCTCAGGAATTGGAGACAAGCGCTACGTAACTAGTGAACCTCTGTCTGTACAAATPAT	124
Db	136315	AGGTGAGGAGTTAGAAACCAGCGCTGGCCAACTGTGTGAACC-CTGTCTACTTAAAGT	136373
QY	125	AAAAGAAATTTTCCAGGCATGTGTGGGTGCACCCCAATGCCAGCTATTTGGGAAGCTGAG	184
Db	136374	ACAAAATTTAGCCAGCGCTGTGTGGTCACTCTGTATTCGACGACTATGGGAAGCCGAG	136433
QY	185	GTAGAGGAATGCTTGAAGCCAGAGATTGAAGACAAGGCTTAGGCAACTAGTGAAGCCT	244
Db	136434	ATGGGTGATCTCTTGAAGTCAAGAGTTCTATGACCAAGCGCTTGCCAACTGTGTGAACCC	136493
QY	245	GTGTCTATTAATA-----AATATTAAGCTGGTGTCTTGGCAAGGCGTGA--GCTAGCTA	298
Db	136494	ATCTCTACTTAATAATCAAAATTTAGCCGGCGGTGGTCGATGCTGTATTCGACGTA	136553
QY	299	CTCGGAAGCTGAGGTGGGAGGA-TCACTGAGCCGAGAGGCTGAGGCTGCATGTGAACAG	357
Db	136554	CTCAGAGGCTAGGCGAGAGAAATGTTGAACCCGAGAGGTGAGGTTGCAATGAGAACCA	136613
QY	358	TGATCACCAGCTGATTT-----CCAGCGTGGAAACAAGAGAGACCGCTGTTCCAAA	412
Db	136614	AGATCAACACACTGCATGCATGACATAGCGCTGGCGGACGAGCAAGATCTCAATCTCAAAA	136673
QY	413	AAAAAAAAAAAAAAAAATGCAAGAAAGACATCATTAACCTTGAGCTGGGACATPACTTTT	472
Db	136674	AAAAAAAAAACACACAAAAAAAACATTAAGCAAGCATGTGGCTACTCAGCAAGACTGA	136733
QY	473	ATGTGATGAATTCCACATCTTTTAGGAAGAAATTAGATTTCTGATPAATGTATTATA	532
Db	136734	GCGAGAGGATCACTTGAACCCAGAGGCGGAGGTGTCAGTGAACCAAGATCGGCCACT	136793
QY	533	ATTATATTATTAATTAATTCAATGGAATTAAATATTCGAGAAACTAGCTTCTCAGCTC	592
Db	136794	GCACTCGAGCGTGGGTGACAGATGAAGCTCCGCTCAAAAA-----136836	
QY	593	TCAGTTGTCAGTCAAAACCTTTAATGCTTTTGGCGGGTGGCGTGGCTCAGCGCTGTAA	652
Db	136837	-----AAAAAAAAAAAAAAAAATTTTGGCGAGCGTGTGGCTCAGCGCTGTAA	136893
QY	653	CCGAGACCTTTGGGAGGCCGAGCGGGGTGATCACAAGTTTGAAGATCGAGACATCTT	712
Db	136884	CCCCGACTTTGGGAGGCCAAAGCGGGGATCAAGAGTCAGAGGTGTGAAGACATCTT	136943
QY	713	GGCTAACACGATGAACCTGCTCTACTAATAAAATPACAAAATTTAGCGGGTGGCTGC	772
Db	136944	AGCTAACGATGAACCCCGTCTTCTACTAATAATPACAAAATTTAGCGGGCATGTGTG	137003

[illegible]

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RESULT 6
US-10-322-281-10/c
? Sequence 10, Application US/10322281
? Publication No. US20040126762A1
? GENERAL INFORMATION:
? APPLICANT: David W. Morris
? APPLICANT: Marc S. Malandro
? TITLE OF INVENTION: Novel Compositions and Methods in Cancer
? FILE REFERENCE: 529452001000
? CURRENT APPLICATION NUMBER: US/10/322,281
? CURRENT FILING DATE: 2002-12-17
? NUMBER OF SEQ ID NOS: 866
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 10
? LENGTH: 152759
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(152759)
? OTHER INFORMATION: n = A,T,C or G
? -S-10-322-281-10

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Query Match	7.0%;	Score 350.4;	DB 17;	Length 152759;
Best Local Similarity	68.3%;	Pred. No. 2.7e-59;		
Matches 572; Conservative	0;	Mismatches 241;	Indels 17;	Gaps 6;

QY	112	CTGTCAAAATTAATTAAGAAATTTTCACAGGCATGTGGCCTGCACCCCGCATGCAGCTAT	171
Dp	15973	CTTTTCATAAAGTTTATCAAAACCTGGCCAGTGCAGTGAACGATGCTGTATATCCAGC-AC	15915
QY	172	TTGGAGGCGTGAAGTGAAGGAATGCTTGAAGCCAGAGTTGAAGCAAGCCTTAGCAAC	231
Dp	15914	TTTGGAGGCGCAAGGTGGGTGATCACTGAGGCCACGAGGTTCAAGACCGACAGTGGCAAC	15855
QY	232	ATAGTAGAGCCCTGATGTCTATATAAAAT-----AATTAGCTGTTGTCTTGGCACAGGCC	286
Dp	15854	ATGGAGAAACCCCACTCTACAAAAAATTCAAAAATTTACCGGGCGGTGGTGGCACATGCC	15795
QY	287	TGCAG--CTAGTACTCCGGAAGCTGAGGTGGAGAGATCAC-TGAGCCCAAGAGGCTGAG	343
Dp	15794	TGTGGTCCAGCTACTCAGGAGGACTGAGGCAAGAAAGATCACTTGGAGCCAGAGGTTGAA	15735
QY	344	GCTGCAGGAACAGAGATCAACCCAGCTGATTTCCAGCCTGGAAGACAGAGGAAACCCCG	403
Dp	15734	GCTGAAGTAGCCATGATTTGTACCACTGCACCTCCAGCCTGAGTGAACAGATTAAGACCTTA	15675
QY	404	TTTCCAAAAAATAAAAAAAAAAAAAAAAAATGCAGAAAGAACATATATACTTGACTGGGAC	463
Dp	15674	TCTGGAAAAAATAAAAAAAAAAAAAA-----AAAAATTACAAAGTGTGCACACC	15622
QY	464	ATTAACCTTTATGTGATGAATTCACAACTCTTTAGAGAAAGAAATTGCAATTTCTGATAAAA	523
Dp	15621	AAAGAGCCTAGAACCTGGAGAGATCAATTAAGCACTAAGAGGTCTGTCTACTTTCT	15562
QY	524	TGTATTATATATATATTTATTAATTCAAAATGAGATTAATAATCTCTAGAGAAACATAGCTT	583
Dp	15561	CATTTTGCCTTTTATTTGTATATTTATTTATTTCTTAAGCAATCTCTAGTAAGTTTCTG	15502
QY	584	CTCACTCTCTCAGTTGTGATCAAAACTTTAA-TGATCTTTGGCCGGGTCCGGTGACTCA	642

Db 15501 ATGCTTCTTAGAAGATGTTTCAAGTAAAGTAGTTGAGCGCGGAGCGGTGGCTCA 15442
Qy 643 CGCCTGAATCCCGAGCATTTTGGAGGCCCGAGGGGGGTGATCAAGATTTAGAGATCG 702
Db 15441 CCCCTGAATCCCGAGCATTTTGGAGGCCCGAGGGGGGTGATCAAGATTTAGAGATCG 15382
Qy 703 AGACCATCTGTGCTTAACAGGCTGAACCTGCTCTAATAAATAAATAAATAAATAAATAA 762
Db 15381 AGACCTTCTGTGCTTAACAGGCTGAACCTGCTCTAATAAATAAATAAATAAATAA 15322
Qy 763 GGTGCGGTGCGAAGCGCTGTAGTCCAGCTGCTCAAGAGGCTGAGGCAAGAGATGCTG 822
Db 15321 GCGGTGCTGCGGCGCGCTGTAGTCCAGCTGCTCAAGAGGCTGAGGCAAGAGATGCG 15262
Qy 823 TGAACCCCGAGGCGGAGCTTTCAGTGAAGCCAGATTCGCCCACTGCTCAGCTCGG 882
Db 15261 TGAACCCAGAGGCGGAGCTTTCAGTGAAGCCAGATTCGCACTGCTCAGCTCGG 15202
Qy 883 CGACAGGCGAGACTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 932
Db 15201 TGACAGAGCAAGACTCGCTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAA 15152

RESULT 7

US-10-450-826-3/c
; Sequence 3, Application US/10450826
; Publication No. US20040101818A1
; GENERAL INFORMATION:
; APPLICANT: JI, Darren
; APPLICANT: Axelrod, Douglas W.
; APPLICANT: Cook, Jonathan S.
; APPLICANT: Jaiswal, Neelam
; APPLICANT: Elstein, Richard
; APPLICANT: Martz, Lawrence
; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
; FILE REFERENCE: 044921-5039-WO
; CURRENT APPLICATION NUMBER: US/10/450,826
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/255,882
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/285,691
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 92638
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Genbank Accession No. AC004596
US-10-450-826-3

Query Match 7.0%; Score 347.6; DB 17; Length 92638;
Best Local Similarity 65.9%; Pred. No. 7.8e-59;

Matches 618; Conservative 0; Mismatches 299; Indels 21; Gaps 7;

Qy 5 GGGCAATGCTGTGCTCAGCGCTGTATTTCCAGACATTTGGAGAGAG-----GAGGATC 59
Db 90650 GCGAAGTGGAGTGGCTCAACCTGTATCCAGACATTTGGAGAGAGAGAGAGAGAG 90591
Qy 60 GCTTGAAGCTCAGAAATTGAGACAGAGCTTGAACATAGTGAACCTTGTCTGTACAA 119
Db 90590 ACTAGAGGCGCAGAGATTGAGACAGAGCTTGAACATAGTGAACCTTGTCTGTACAA 90531
Qy 120 ATAAATAAAGAAATTTCCAGGAGATGAGTGGCTGCAACCCAGAGCCAGATTTGGAGAG 179
Db 90530 AAAATACAAAATTTGGCTGAGCATGAGTGGCTGCAACCTGTATCCAGACATTTGGAGAG 90471
Qy 180 CTGAGGTAGAGAGATGCTTGAAGCCAGAGATTTGAAGACAAAGCTTGAAGCAATAGTAG 239
Db 90470 CCGAGGCGAGGCTGATCACTGAGAGTCAAGAGATTGAGACCAAGCTTGTCCAACTGTGTA 90411

Qy 240 ACCCTGCTGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 292
Db 90410 ACCCATCTCTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 90351
Qy 293 TACCTAGTGAAGAGTGAAGTGAAGATCAAC-TGAGCCAGAGAGCTGAGGCTCAGT 351
Db 90350 CAGCCATCGGAGAGGCTGAGGAGAGAGATTCGCTTGAACCCAGAGAGAGAGGCTCTGT 90291
Qy 352 GAAAGTGAATCAACCAAGCTGATTCAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 411
Db 90290 GAGTGAAGATCGGCGCATTCATTCAGCTAGTGAACA-AGAGCAAACTGTGCAAAA 90232
Qy 412 AAAAAAAAAAAAAAAAAAAGCAAGAAAGACATCAATTAATCTGAGGAGATTAATCTT 471
Db 90231 AAAAAAAAAAACAACAACAACAACAACA-ACAACAACAACAACAACAACAACAACAACA 90173
Qy 472 TATGATGAATAATTCATATCTTTTGAAGAAATTAAGCATTTCTGATTAATAATGATTA 531
Db 90172 AATAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 90113
Qy 532 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 591
Db 90112 GGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 90053
Qy 592 CTCAGTTGTCAATCAAACTTTA--ATGCTCTTTGGCCGGGTGCGGTGCTCAGCTCTGT 649
Db 90052 CTCCTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 89993
Qy 650 AATCCAGCACTTTGGAGAGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 709
Db 89992 GGTCCAGCACTTTGGAGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 89933
Qy 710 CCTGGCTAACACGTTGAAACCTGCTCTCTAATAA-----AATACAAAATAATGCGGCT 765
Db 89932 CCTGGCTAATATGTTGAAACATCGCTCTAATAAATAAATAAATAAATAAATAAATA 89873
Qy 766 GGGGTGCGAGAGCGCTGTAGTCCAGCTGCTCAGAGAGGCTGAGGAGGAGGAGGAG 825
Db 89872 GGTGTATGAGGAGCGCTGTAAACCCAGCTTACCTTGGAGGCTGAGGAGGAGGAGG 89813
Qy 826 ACCCGGAGGCGGAGGCTTCAAGTGAAGCGAGATTTGGAGGAGGAGGAGGAGGAGGAG 885
Db 89812 ACCCGGAGGCGGAGGCTTCAAGTGAAGCGAGATTTCAACCACTGCACTCGGCTGG 89753
Qy 886 CAGTGGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAA 923
Db 89752 CAGAGTGAAGACTCAGTCTCAAAAAAAAAAATGATTAATAA 89715

RESULT 8

US-10-322-281-296/c
; Sequence 296, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 59748
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(59748)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-296

Query Match 6.9%; Score 347.2; DB 17; Length 59748;
Best Local Similarity 68.8%; Pred. No. 7.7e-59;
Matches 561; Conservative 0; Mismatches 228; Indels 27; Gaps 5;

126 AAGATATTTTCAGGAGTGTGGCGTGCACCCAGGCGCAAGCTATTTGGGAGGCTGAG 185
25609 ATGAAATGTCGGCGCGCGGTGCTCAGACCTGTAATCCAGACCTTTGGAGGCCAAG 25550
186 TAGAGGAAATGCTTGAAGCCAGAGATTGAAGACAAAGCTTGAAGCACTGAGACCTTG 245
25549 TGGGAGATCACTTGAAGTCAAGAGGTTCAAGACCAAGCTGGCCAAATGTTGAATCCCA 25490
246 TGTCTATAAAAAAT-----AATTAGCTGTGTCTTGGCAGAGCTCGAG--CTAGCTA 298
25489 TCTCTATAAAAAATCAAAAAATTAGCGGTGTGTGGCAATGCTCATAGTCCAGCTA 25430
299 CTGGAAAGCTGAGGTGGAGAGATCA-CTGAGCCAGAGAGCTGAGGCTCAGTGAACAG 357
25429 CTTGGAGGCTGAGCGGAGGAATCAGCTGAACTGGAGGCGAGAGTTGCACTGAGCCC 25370
358 TGATCAGCCAGCTGATTCAGCTGAGAGACAGAGAGAGACCTGTGTTCAAAAAAAA 417
25369 AGATGGCGCATTCAGCTCCAGCCTGGCAACAGAGTGAAGACTCCGCTCAAAAAACAA 25310
418 AAAAAAAAAAATGCAAGAAAGACATCAATACTGAGCTGGGACATACTTTATGTG 477
25309 AACAAAACATATGTTGAAGAAATTAATTAATCAATCTGATAGAGCTAGGGTTACTTA 25250
478 ATGAATTCACAACTTTTGAAGAAATTAAGCAATTCATTAATAATTAATTAAT 537
25249 TAGTCACAAAAATGCTTGTACTCAGGTAGTACT-----CTCCTAAGTACCTGAATTT 25194
538 ATATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 597
25193 ATCACTATACAT-----TATATACAGTAAACAAATTAATTAATTAATTAATTAAT 25149
598 TGTGAGCAAAACCTTAATGCTTTTGGCGGAGGCTGAGCTGATATCCAG 657
25148 CTTGAAATTAAGAAATTAAGAAATTAAGCCAGGACGCTCTCATGCTCTGTAATCCAG 25089
658 CACTTTGGAGGCGGAGCGGTGATCAAGAGTTAAGAGATGAGACCATCTGGCTA 717
25088 CACTTTGGAGGCGGAGCGGCGGATCAGAGGTGAGAGATGAGACCATCTGGCTA 25029
718 ACACGCTGAACCTGCTCTTACTTAATAATTAATAATTAATTAATTAATTAATTAAT 777
25028 ACACGCTGAACCTGCTCTTACTTAATAATTAATAATTAATTAATTAATTAATTAAT 24969
778 GCTGTGATGCTGCTGCTGCTGAGAGGCTGAGGAGAGAAATGCTGAACCCGGAGGCG 837
24968 GCTGTGATGCTGCTGCTGCTGAGGAGGCTGAGGAGAGAAATGCTGAACCCGGAGGCG 24909
838 GAGCTTGAAGTGAAGCCAGATTTGGCCACTGCACTGAGCTGGGCGACAGTGGAGACT 897
24908 GAGGTGCAAGTGAAGCTGAATTTGACCACTGCACTCCAGCTGGATGACAGAGGAGACT 24849
898 CTGCTCAAAAAAAGTGAATG 933
24848 CCAATCTCAAAAAAAGAGAGAGAGAGAGAGAG 24813

RESULT 9
US-10-017-161-2233/C
; Sequence 2233, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKISO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017.161

CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2233
LENGTH: 59588
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(59588)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(239)
FEATURE:
NAME/KEY: CDS
LOCATION: (19765)..(20013)
FEATURE:
NAME/KEY: CDS
LOCATION: (22071)..(22222)
FEATURE:
NAME/KEY: CDS
LOCATION: (25670)..(25814)
FEATURE:
NAME/KEY: CDS
LOCATION: (28077)..(28268)
FEATURE:
NAME/KEY: CDS
LOCATION: (30114)..(30265)
FEATURE:
NAME/KEY: CDS
LOCATION: (42934)..(43362)
FEATURE:
NAME/KEY: CDS
LOCATION: (46385)..(46558)
FEATURE:
NAME/KEY: CDS
LOCATION: (48143)..(48221)
FEATURE:
NAME/KEY: CDS
LOCATION: (50255)..(50359)
FEATURE:
NAME/KEY: CDS
LOCATION: (59242)..(59388)
US-10-017-161-2233

Query Match 6.9%; Score 345.2; DB 15; Length 59588;
Best Local Similarity 68.9%; Pred. No. 1.9e-58;
Matches 554; Conservative 0; Mismatches 203; Indels 47; Gaps 4;

136 CCAGGATGTCGCGCGTGCACCCCAAGTGCACGTAATTTGGAGGCTGAGGTGAGAGAA 195
46072 CCAGGATGTCGCGCGTGCACCCCAAGTGCACGTAATTTGGAGGCTGAGGTGAGAGAA 46013
196 GCTTGAAGCCAGAGTGAAGCAAGCTAGGCAATAGTGAACCTGTGTCTA-TAA 254
46012 GCTTGAAGCCAGAGTGAAGCAAGCTAGGCAATAGTGAACCTGTGTCTA-TAA 45953
255 AAAATTAATTAAGCTGTGTCTTGGCAAGGCTGAG--CTAGCTACTCGAAAGACTGAG 312
45952 AAAATTAATTAAGCTGTGTCTTGGCAAGGCTGAG--CTAGCTACTCGAAAGACTGAG 45893
313 GTGGAGATGAC-TGAGCCAGAGGCTGAGGCTGAGTGAACAGTATCAACCCAGCTG 371
45892 GTGGAGATGAC-TGAGCCAGAGGCTGAGGCTGAGTGAACAGTATGATGATCACACACTG 45833
372 GATTCAGCTGGAAGACAGAGGAGACCTGTTTCAAAAAAAGTGAATG 431
45832 TACTTACCTGCGGCAACAGAGAGACCTGCTGTAATAAAAAAAGAAATGAATTA 45773
432 CAAGAAAGACATCAATACTGACCTGGAGCATTAATTTATGTATGAATTCACAT 491

Accession	Sequence	Position
Db	45455 CTACTCAGAGAGCTGAGCGCAGAGAAAGCGCTGAACCTGGAGACCGGAGCTTGCAAGTGAG	45396
Qy	852 CCGAGATTGGCCCACTCAGACTCCAGCCTGGGCGCAGCTGCGAGACTCTGTCTTCAAAAAA	911
Db	45395 CCGGATTGGCCCACTCAGCTCCAGCCTGGATGACAGAGTGAGACACTCTGTCTCAAAAAA	45386
Qy	912 AAAAAAAAAAAGTTGATGTC	935
Db	45335 TAAAAAATAAAAAATAATTAGCC	45312

```

RESULT 11
US-10-271-416-1
Sequence 1, Application US/10271416
Publication No. US20040043021A1
GENERAL INFORMATION:
APPLICANT: Keith, Tim
APPLICANT: Little, Randall D.
APPLICANT: Van Eerdewegh, Paul
APPLICANT: Dupuis, Josee
APPLICANT: Del Maestro, Richard G.
APPLICANT: Allen, Kristina
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4045
CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/328,424
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 304905
TYPE: DNA
ORGANISM: Homo sapien
US-10-271-416-1

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Query Match	6.8%;	Score	341.2;	DB	16;	Length	304905;
Best Local Similarity	67.2%;	Pred. No.	2.6e-57;				
Matches	625;	Conservative	0;	Mismatches	253;	Indels	52;
						Gaps	8.

QY	10	ATGCTGAGCTCAAGCGTATATCCAGCACTTTGG-----GAGGCAAGGAGATGCTT	63
Db	24379	ATGCAAGTGCCTCATGCTCTGTAATCTAGCACTTTGGAGTCTAGGCAAGCAATATCACT	24433
QY	64	GAGCTCAGGAATTGGAGACAAGCCTTAGTAACATAGTGAACCTCTGTCTGTAACAATTA	123
Db	24439	GAAATTGGGAGTTTCGAGACTAGCCTTGCCAAATGTGAATCC-CCATCTCCACTTAAAA	24497
QY	124	TAAAGAAATTTTCCAGGCATGTGTGGGTGACCCCACTGTCGCACGTATTTTGGAGGCTTA	183
Db	24498	TACAAAAGT-----ATTGTGGCCCACTCTGTATCCCAAGCACTTTGGAGAGACA	24546
QY	184	GGTAGGAGGAATGCTTTGAAACCAGAGATTGAAGACAAGCCTTAGCAACATATGTGAACCC	243
Db	24549	GGCGGATGATCACTGAGGTCAAGGATTTCAAGCCAGCCTGGCCAAACATGGCAAAACC	24606
QY	244	TGTGTCATATAAAAT-----AATTAGCTGTGTCTTGGCCAGAGCTGCA--GCTAG	295
Db	24609	CGTCTCTAATAAAATTAACAAAAATTAAGCTGGGCATGTGTGTGGCACTCTGTATATCCAG	24666
QY	296	CTACTCGAAGACTGAGGTGGAGATCAC-TGAGCCCAAGAGAGCTGAGGCTCAGTGA	354
Db	24669	CTACCTGGGAGGCTGAGGCAAGAAATCGCTTGAACCCAGAGAGCGAGAGTTCAATGAG	24722
QY	355	CAGTGATCACCCAGCTGGATTCCAGCCTGGAAGACAGAGGAGAACCTGTGTTCAAAAA	414
Db	24729	CCGAAATCACACCATCGACTCCAGCCTGGGTGACAGAGGAAATTCCTGCTCAAAAAA	24788
QY	415	AAAAAAAAAAAAAATGACAGAAAAAGCATCTAATACTGACCTGGGACATACTTTAT	474
Db	24789	AAAAAAAAA-----ATTAGCTAGGGGTGTCAGCACTACTCTTAAT	24830

QY	475	GTGATGAAATTCACAACTCTTTTGGAGAAATTAGCATTTCTGATAAATATGTTTAAAT	534
Db	24831	CCGACGCTACTTTGGGAGCTGAGGCAAGACTCA-----CTTGAACCCAGAGAGG	24889
QY	535	TATATTAATTAATTCAAATGGAATTAATAATATCTGAGAACTAGCTTCTCACTCTC	594
Db	24882	GAGGTTGAAATGAGTCMAAGATTCCGTCACTTGCCGCTTCGGCTGGGAGACAGAGTAAGACT	24941
QY	595	AGTTGTAGTCAAAACCTTTATATGTCCTTTGGCCGGGTGGGTGGCTCAGCCCTGTAATCC	654
Db	24942	CTGCCTCAAAAATAATATTAATAATTAATAAAGCCGGGCGCAGTGGCTCAGCCCTGTAATCC	25001
QY	655	CAGCACTTTGGAGGCGCGAGCGGTGATCACAAGATTAGAGATCGAGACCATCTCGG	714
Db	25002	CAGCACTTTGGAGGCGCAAGGCAAGGACGATCAGAGGTGTCAGGAGATCGAGACCAACTCGG	25061
QY	715	CTAACAGGGTGAACCTCGTCTCTACTTAATAAATACAAAAATTAATGCGGGGTGCGGTGCCA	774
Db	25062	CTAACAGGGTGAACCCCGTCTCTACTTAATAAATACAAAAATTAATGCGGGGTGCGGTGCCG	25121
QY	775	GACGCTGTAGTCCGACGCTCTCAGGAGGCTGAGGACGAGAGATGGTGTGAACCCGGGAG	834
Db	25122	GGCCCTGTAGTCCGACGCTACTCGGAGGCTGAGGACGAGAGATGGCGTGAACCCGGGAG	25181
QY	835	GCGGAGCTTCAGGTGAGCGCGAGATTGCGGCACCTGCATCTCAGCCTTGGGCGACAGTGCAG	894
Db	25182	GCGGAGCTTCAGGTGAGCCGAGATGCGGCACCTGCATCTCAGCCTTGGGCGAGAGCAGAAC	25241
QY	895	ACTCTGCTCAAAAAAAAAAAAAAAAAAAAAA	924
Db	25242	TTCGCTCAAAAAAAAAAAAAAAAAAAAAA	25271

```

RESULT 12
US-10-087-192-112/C
, Sequence 112, Application US/10087192
, Publication No. US20020182586A1
, GENERAL INFORMATION:
, APPLICANT: Morris, David W.
, APPLICANT: Engelhard, Eric K.
, TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
, TITLE OF INVENTION: CANCER
, FILE REFERENCE: 529452000122
, CURRENT APPLICATION NUMBER: US/10/087,192
, CURRENT FILING DATE: 2002-03-01
, PRIOR APPLICATION NUMBER: US 09/747,377
, PRIOR FILING DATE: 2000-12-22
, PRIOR APPLICATION NUMBER: US 09/798,586
, PRIOR FILING DATE: 2001-03-02
, NUMBER OF SEQ ID NOS: 2059
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 112
, LENGTH: 45864
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (1)..(45864)
, OTHER INFORMATION: n = A,T,C or G
, US-10-087-192-112

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Query Match	6.8%	Score 340.8;	DB 13;	Length 45864;
Best Local Similarity	66.2%;	Pred. No. 1.3e-57;		
Matches 556;	Conservative 0;	Mismatches 272;	Indels 12;	Gaps 4;

QY 92 TAACATATAGGAACCCCTCTCTGTCAATTAATTAAGAATTTTCAGACGATGGGGGGT 151
Db 18139 TATCAGTATAAACCCAGGTATGATTTTAAACCTTACACGACCCGGGGGGGGCTC 18080
QY 152 GCAACCCCATGTGCACTTATTTGGGAGGCTGAGTATGAGAGGATCTTGAAACCGAGAGT 211
Db 18079 AACCCTGTATCCTTACCACTTTGGGAGGCTGAAAGTGGGGGAGTTCTTGAGGTCTAGAGAGT 18020

```

QY 212 TGAAGACAAAGCTTAGGCAACATAGTGAACCTGTGTCT-----ATATAAAATTAATTAC 266
DB 18019 TCGAAGACGCGGTGGCAACGTTGTAAACGCGATCTTACTGAATAATACAAAAATTAAT 17960
QY 267 TGGTGTCTTTGGCACAGGCTGTGAG--CTAGCTACTCGAAGAGCTAGGTTGGAGAGATCA 324
DB 17959 CAGGGGTGTGGCAAGTGTCTGTATGTCACAGCAGCTGGGAGGTTGAGGACAAAGATTA 17900
QY 335 CTGAGCCCAAGAGGCTGAGGCTGCAAGTGAACAGTATCAACGAGCTGAATTCAGGCTTG 384
DB 17899 CTGTAATATGAGAGGCGGAGAGCTGAGTGAAGTGAAGTCAACGACCTGCACTCAGCTTG 17840
QY 385 AAGACAGAGGAGACCTCTTTTCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 444
DB 17839 GCGACACAGCAAGTGTGTCTCAACCAACACACACACTTACATTCATTA 17780
QY 445 CATAAAGTGAACCTGGGAATTAATTTATGATGAATTAATTAATTAATTAATTAATTAATTA 504
DB 17779 TAAAGAAATTAATTTCTAAACCTGCTGAGCTGCTGACACCTAGATATCTCTATGTC 17720
QY 505 ATTACATTTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 563
DB 17719 ATTCTGTATCCAAATGCGCAGTTCTCTCTTTCTTCAAGAGCTGACCAAGATTTAG 17660
QY 564 ATATTCTGAGAACTAGCTTCTCACTCTCACTGCTCACTCAAACTTTAATGCTTT 623
DB 17659 GGAGCGACATGAACATCTTTTTCACATTCACATTTGAGCTTAATTAAGAAATAGACA 17600
QY 624 GCGCGGCTGCGGTGCTGACGCTGTATCCAGACCTTGGAGGCGGAGGCGGCTGA 683
DB 17599 GCGCGGCGCGGTGCTGCTCA---TGTATTCAGACCTTTGGAGGCGGAGGCGGAGG 17544
QY 684 TCACAAAGTTAGAGATGAGACATCTGCTGAACACGCTGAACCTGCTCTTAATTA 743
DB 17543 TCACAAAGTTAGAGATGAGACATCTGCTGAACATCTGCTGAACCTGCTCTTAATTA 17484
QY 744 AATTCAAAAAATTTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
DB 17483 AATTCAAAAAATTTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17424
QY 804 CTGAGGCGAGGAGATGATGTAACCGGAGGCGGAGCTTGGAGTGAAGCGGAGTTGGCG 863
DB 17423 CTGAGGCGAGGAGATGATGTAACCGGAGGCGGAGCTTGGAGTGAAGCGGAGTTGGCG 17364
QY 864 CACTGCACTCCAGCTGGGCGAGAGTGAAGTCTGTCTCAAAAAAATTAATTAATTAATTAAT 923
DB 17363 CACTGCACTCCAGCTGGGCGAGAGTGAAGTCTGTCTCAAAAAAATTAATTAATTAATTA 17304

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RESULT 13
US-10-087-192-286
; Sequence 286, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 87331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: misc_feature
; LOCATION: (1)...(87331)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-286
Query Match: 6.7%; Score 337.2; DB 13; Length 87331;
Best Local Similarity 66.0%; Pred. No. 9.4e-57;
Matches 622; Conservative 0; Mismatches 288; Indels 33; Gaps 8;
QY 11 TGGTGTGCTCAAGGCTGTATTCAGACCTTTGGAGGCT-----AGAGGATGCTTG 64
DB 5304 TCGAGTGGCTCATGCTGTATTCCTGCACTTTGGAGGCGCAAGGTGGGAGTCACTTG 5363
QY 65 AGCTCAGAAATTTGAGACCAAGCTTACCTAATAGTAA--CTCTGTCTGTACAAATA 122
DB 5364 AGCTCAGAAATTTGAGACCAAGCTTACCTAATAGTAA--CTCTGTCTGTACAAATA 5423
QY 123 ATAAAGAAATTTTCAGGAGTGGCGGCGACCCCGAGTGCAGCTATTTGGAGGCTG 182
DB 5424 CAAATTTGAAAGCGGCGGCTGTATTCAGCTGTATTCAGACCTTTGGAGGCTCA 5483
QY 183 AGTGAAGAAATGCTTGAAGCAGAGTGAAGCAAGCTTGAAGCAATAGTGAAGC 242
DB 5484 AGTGAAGAAATGCTTGAAGCAGAGTGAAGCAATAGTGAAGCAATAGTGAAGC 5541
QY 243 CTGTGTCTTAATAAAT-----AATTAGCTGTGTCTTGGCAGAGCTC 286
DB 5542 CCGTCTCTAATAAATCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5601
QY 287 TGCAG--CTAGCTACTCGGAAGCTGAGGTGGAGGATCAC--TGAAGCCAGAGGCTGAG 343
DB 5602 TTTAGTCCAGCTTACTCAGAGAGCTGAGGAGGAGAAATGCGTGAATCTGGAGGAGAG 5661
QY 344 GCTGAGTGAACATGATCAACCACTGATTCAGAGCTGGAAGACAGAGGAGACCTTG 403
DB 5662 GTTGAAGTGAAGCAGAGATGCGGCGCACTGCGCTGAGCTGAGTGAAGTGAAGTGAAG 5721
QY 404 TTTCAAAAAAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 461
DB 5722 CTTCAAAAAAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5781
QY 462 ACATTAATTTTATGATGAATTCACATCTTTTGAAGAAATTAATTAATTAATTAATTAAT 521
DB 5782 CAGGAGGCTGAGGAGAGAAATGCTTGGGCGGAGGCGGAGGTTACAGTGAACAGAG 5841
QY 522 AATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 581
DB 5842 ATGAGGCACTGAATCCAGCTGAGGCGGAGAGTGAAGTTCGCTCAAAATTAATTAAT 5901
QY 582 TTCTCACTCTCACT--TGTCACTCAAAATTTAATGCTCTTTGGCGGAGTCCGCTGCT 640
DB 5902 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5961
QY 641 CAGGCTGTAAATCCAGACCTTGGAGGCGGAGGCGGAGTGAATCAAGATTAGAGAT 700
DB 5962 CAGGCTGTAAATCCAGACCTTGGAGGCGGAGGCGGAGTGAATCAAGATTAGAGAT 7021
QY 701 CGAGACATCTGCTGTAACACGCTGAACCTGCTCTTAATTAATTAATTAATTAATTAATTA 760
DB 6022 CGAGACATCTGCTGTAACACGCTGAACCTGCTCTTAATTAATTAATTAATTAATTAATTA 6081
QY 761 CGGCTGCGGTGCGACAGCTGTATGCTCCAGCTGCTCAGAGGCTGAGGCGGAGATGAG 820
DB 6082 TGGGCGGTGCTGCGGTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6141
QY 821 TGTGAACCGGAGGCGGAGGCTTGAAGTGAAGCGGAGTGAAGCGGAGTGAAGCGGAGTGA 880
DB 6142 CGTGAACCGGAGGCGGAGGCTTGAAGTGAAGCGGAGTGAAGCGGAGTGAAGCGGAGTGA 6201
QY 881 GCGGACAGTGAAGCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 922
DB 6202 GCGGACAGTGAAGCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 6243

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RESULT 14
US-10-433-580-2/c
/ Sequence 2, Application US/10433580
/ Publication No. US20040091497A1
/ GENERAL INFORMATION:
/ APPLICANT: GENSET
/ TITLE OF INVENTION: SCHIZOPHRENIA RELATED VOLTAGE-GATED ION CHANNEL GENE AND PROTEIN
/ FILE REFERENCE: 93.WO1
/ CURRENT APPLICATION NUMBER: US/10/433,580
/ CURRENT FILING DATE: 2003-06-04
/ PRIOR APPLICATION NUMBER: US 60/251,317
/ PRIOR FILING DATE: 2000-12-05
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2
/ LENGTH: 237961
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 43726..43868
/ OTHER INFORMATION: exon 8
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 43998..44102
/ OTHER INFORMATION: exon 9
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 52093..52179
/ OTHER INFORMATION: exon 10
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 77568..77699
/ OTHER INFORMATION: exon 11
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 98226..98393
/ OTHER INFORMATION: exon 12
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 106567..106758
/ OTHER INFORMATION: exon 13
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 144109..144246
/ OTHER INFORMATION: exon 14
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 159794..159868
/ OTHER INFORMATION: exon 15
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 191292..191428
/ OTHER INFORMATION: exon 16
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 192967..193108
/ OTHER INFORMATION: exon 17
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 211540..211613
/ OTHER INFORMATION: exon 18
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 225006..225107
/ OTHER INFORMATION: exon 19
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 225544..225613
/ OTHER INFORMATION: exon 20
/ FEATURE:
/ NAME/KEY: exon
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/ LOCATION: 228450..228541
/ OTHER INFORMATION: exon 21
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 228630..228752
/ OTHER INFORMATION: exon 22
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 231289..231345
/ OTHER INFORMATION: exon 23
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 231589..231709
/ OTHER INFORMATION: exon 24
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 231813..231944
/ OTHER INFORMATION: exon 25
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 232900..233067
/ OTHER INFORMATION: exon 26
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 235355..235459
/ OTHER INFORMATION: exon 27
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 51090
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/ OTHER INFORMATION: 99-79335.pu
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/ NAME/KEY: primer_bind
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/ NAME/KEY: primer_bind
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OTHER INFORMATION: 99-79338.pu
FEATURE:
NAME/KEY: primer_bind
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OTHER INFORMATION: 99-79338.tp complement
FEATURE:
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OTHER INFORMATION: 99-79339.pu
FEATURE:
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NAME/KEY: primer_bind
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OTHER INFORMATION: 99-79316.pu
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Query Match 6.7%; Score 336.8; DB 16; Length 237961;
Best Local Similarity 66.3%; Pred. No. 1.8e-56;
Matches 556; Conservative 0; Mismatches 257; Indels 25; Gaps 4;

QY 117 CAATATATAAAGATTTTCAGAGCATGTGCGTGCACCCCAAGTCCAGCTATTGGG 176
DB 82061 CAAAACAGAGTGACGCGCAGAGTAGTGTCTCAGCTGTAATTCAGACACTCTGGG 82002

QY 177 AGGCTAGGTAGAGAGAAATGCTTGAAGCCAGAGTTGAACAAAGCTAGGCAACAATGT 236
DB 82001 AGGTCAAGATGATGATGCTGAGCCAGAGTTGAGACCGCTGCTTAACATGCG 81942

QY 237 GAGACCTGTGTATATAAATAATTAAGTGTGTCTTGGACAGAGGCTGAGAGTAC 296
DB 81941 GAAACCCCATCTCTACTAGAAATACAA---AATTAGCTGGGTGTGCTGTATCCAGC 81885
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QY 297 TACTCGAAGACTGAGGTGGAGATCACT-GAGCCAGAGGCTAGAGCTGAGTGAAC 355
DB 81884 TTCTTGGATGCTTAAGGCAAGGAACCACTGGAATCTTGGAGGCAAGGTTGAGGAGC 81825

QY 356 AGTATCACCACGCTGATTCAGGCTGGAAGCAGAGGAGGACCGCTGTTCCAAAAA 415
DB 81824 CGAGATGTGCCACTCACTTGAAGCTTGAAGCAACAGAGTGGAGCTGTCTCAAAAAA 81765

QY 416 AAAAAAAAAAAAAATGCAAGAAAAGACATCA-----TAACTTGACCTG 459
DB 81764 AAAAAAAAAAAAAAGGAGACAAAAAACAACAAACCAAAACCCCAAGCTGAGTGAACAA 81705

QY 460 GACATTAATCTTTATGTATGAATTCACAATCTTTAGGAAGAAATTCATTTGTGAT 519
DB 81704 ATTCAGAAATGCTTAAGTATGTTCAAGTACACTGAAGGGGTCTATGTGTTTAAATG 81645

QY 520 AAAATGATATATATATATATATATATATATATATATATATATATATATATATAT 574
DB 81644 AACAAATACACCTACCTAGTTTATTTATTTATTTTTCAGAGATTTCAAGTTAGT 81585

QY 575 AACTAGCTTCTCACTCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 634
DB 81584 TTTTACCTGTTAATGATTTTGGCGCTTGTTAAGAAATGAATGACATGTGGCGGCGG 81525

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; Sequence 1546, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1546
; LENGTH: 26444
; TYPE: DNA
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: n = A, T, C or G
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Db	19497	TGAGAGGCCAGAGGGGGGTGATCACTGAAGTCAGAGGTTCCAGACCAAGCCTGGCCACA	19556
QY	233	TAGTGAACCCCTGTGTCTATAAAAAAT-----AATTAGCTGTGTCTTGGCACAGCCT	287
Db	19557	TGGGAAAACCCCACTCTCTACTAAAAAATAATTAATTAATTAAGCTGGAGGTGGCAGGCACCT	19616
QY	288	GCA--GCTAGCTACTCGGAAGACTGAGTGGGAGAGATCACTGAGCCAGAGGCTTAGAGC	345
Db	19617	GTATCCCACTACTTGGAGGCTTAAGCAGAGAAATGTCTTGACCCAGAGAGTGAAGT	19676
QY	346	TGCAGTGAACAAGTATCAACCAGCTGATTCCAGCCTGGAAGCAGAGGAGAACCTGTT	405
Db	19677	TGCAGTAGGTGAGATTGACCACTTGCATCCAGCCTGGGTGATGAGTGAAGACTGTCTC	19736
QY	406	TCCAAAAAATAAAAAAAAAAAAAAATGCAAGAAAGACATCATTAACCTTGAACCTGGGACAT	465
Db	19737	AAAAAAAAAAAAAAAAAAGTAATTTTAAAGCTTGAATGACATATGTCTTCCNNNNNNNN	19796
QY	466	AACCTTT-----ATGTGATGAATTCACAATCTTTTGGAGAAATTA-----	508
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QY	509	-GCATTTCTGATPAAAAATGTATTTATTTATTTATTTATTAATTCAAATGAAATTAATAT	567
Db	19857	TACATATTTTACATTTTACTATTTACTTAAATTTGTATGTAATTTGAGTACAGACTACCTCT	19916
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Db	19917	TTATCTGTGAAAACCTTCAGACTCTCCCTATTACTTTAATTTCAGTGAACATTTATTA	19976
QY	622	-----TTGGCCGGGTGGGTGTGGCTCAGCGCTGTATATCCAGACACTTTGGAGGCCGA	673
Db	19977	TTAAAAAAATGGCCAGGCGCTGTGGGTCAAGCGCTGTAAATCCAGACTTTGGAGGCCGA	20036
QY	674	GGCGGTGATTCACAAGGTTAGAGATTCAGACCATCTGGCTAAACGGGTAAACTTCG	733
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Db	20097	TCTCTACTAAAAATACAAAAAATTAGCCGGGTGTGGGTGCAGACCGCTGTATCCAGCT	20156
QY	794	GCTCAGAGGCTAGAGCAGGAGAAATGTGTGAACCCGGAGGCGAGACTTGAAGTGAAC	853
Db	20157	ACTCAGAGGCTAGAGCAGGAGATGTGTGAACCTGGGAGGCAAGATTTCAGAGTGAAC	20216
QY	854	GAGATTGCGCACTGCATCTCAGCCTGGGCGACAGTGCAGAGACTGTCTCAAAAAAAA	913
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Job time : 1623.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 17:41:01 ; Search time 318.254 Seconds
(without alignments)
13849.312 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	402.6	6.5	1930	5	PCT-US95-07874-1
5	327.6	5.3	128779	4	US-09-497-855A-38
6	306	4.9	22481	3	US-08-367-841A-43
7	306	4.9	22481	5	PCT-US95-07201-43
8	306	4.9	22484	3	US-09-875-223-2
9	306	4.9	22484	4	US-09-875-114-2
10	305	4.9	87350	3	US-08-781-891-79
11	305	4.9	87350	4	US-09-618-166-79
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28	279.2	4.5	62804	3	US-09-800-960-3	Sequence 3, Appl
29	279.2	4.5	62804	4	US-10-096-960-3	Sequence 3, Appl
30	277.2	4.5	55827	4	US-09-813-133A-3	Sequence 3, Appl
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32	275.4	4.4	162450	3	US-09-345-882-1	Sequence 1, Appl
33	275	4.4	39982	4	US-09-820-924-3	Sequence 3, Appl
34	275	4.4	39982	4	US-10-369-628-3	Sequence 3, Appl
35	274.4	4.4	14796	3	US-08-975-080-35	Sequence 35, Appl
36	274.4	4.4	14796	3	US-09-630-706-10	Sequence 10, Appl
37	274.4	4.4	14796	3	US-09-496-694B-3	Sequence 3, Appl
38	273.4	4.4	90541	4	US-09-759-359A-3	Sequence 3, Appl
39	273.4	4.4	90541	4	US-10-207-973-3	Sequence 3, Appl
40	273.2	4.4	26928	4	US-09-544-398B-6	Sequence 6, Appl
41	273.2	4.4	26928	4	US-09-543-771-6	Sequence 6, Appl
42	271.2	4.4	62804	3	US-09-800-960-3	Sequence 3, Appl
43	271.2	4.4	62804	4	US-10-096-960-3	Sequence 3, Appl
44	271	4.4	114793	4	US-10-148-806-3	Sequence 3, Appl
45	270.8	4.4	162450	3	US-09-345-882-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1									
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Sequence 3, Application US/09801861									
Patent No. 6492154									
GENERAL INFORMATION:									
APPLICANT: YAN, Chunhua et al.									
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC									
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES									
FILE REFERENCE: CLO01098									
CURRENT APPLICATION NUMBER: US/09/801,861									
CURRENT FILING DATE: 2001-03-09									
NUMBER OF SEQ ID NOS: 10									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 53332									
TYPE: DNA									
ORGANISM: Human									
US-09-801-861-3									
Query Match									
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Matches 6201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	CTAATATCCCAAGAACTCCCTTTGTAAAGTTTGTACAAATAATTAATATGATAGAG	120						
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QY	121	TTAATAGTTTATGATGATGTGAACCCAGAGCCATATCAGCCTTACCAAAATGGCACA	180						
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QY	181	ATTGATATATCATCAAGTTATCTTCAAGAGCTTCAGGCGCTTAATGATGTCAAGAAA	240						
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QY	241	ATGTGAAGCCCTCAGCCATCTGAAGACAGTGTATACAGCAATGATCAAAAGAAAA	300						
DB	20240	ATGTGAAGCCCTCAGCCATCTGAAGACAGTGTATACAGCAATGATCAAAAGAAAA	20299						
QY	301	CCACAGGCGCTTCCCTTCCCAATCTTGAAGTGAAGCAGTCTTCAATTTCCATAGTAGT	360						
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QY	361	AAATTTTCAGATACAGCTTGTAGAGCTCAAGTCTGGAAGAAAGCTCCCATCAAG	420						

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QY 421 GAAATTTATCTTAAGATCTGTAATGATATCTAATTTTTGTACATTTGGAAATATATAGT 480
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QY 481 TGTTAACCTGGGCGGGGTGCTCAAGCTGTAAATCCAGAGCCCTTTGGAGGCGAGAGTGGG 540
Db 20480 TGTTAACCTGGGCGGGGTGCTCAAGCTGTAAATCCAGAGCCCTTTGGAGGCGAGAGTGGG 20539
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Db 20540 CAGATCATGAGTCAAGAGATTGAGACACAGCTAGCCACATGATGAAAACCCGCTCTTA 20599
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QY 1141 GAGAAATGTAGACAGTTGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1200
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QY 1381 GAGAAAGAAATTAATGAGAGATGAGATTTTCAAGGCTTGAAGACCTCAATACAG 1440
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Db 21860 AGATCGGCGCACTGGGCTCCAGCTGGGCGACAGATGATGATGATGATGATGATGATGATG 21919
QY 1921 AAAAAAATTAATAATGTTTCAAGCTTAAACAACATGATTTCAACAGCTTAAAGTGAAG 1980
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Db 22280 TTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 22339
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Db 22340 AATCTTTAAAGCACTGGCTGTGATCTTATTTTTCAGAGAGAAATCCAAAGATC 22399
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Db 22400 TGAAGAGCAAAACATTTTGCCTGAGGTTTAAAGCAAGCTTATGCAATGCTTAAAGTGA 22459
QY 2461 TTCTTAGTTAAATTTCTTCCACTAGGCAATGCTTCTAGTCTGTTGCTGCTG 2520
Db 22460 TTCTTAGTTAAATTTCTTCCACTAGGCAATGCTTCTAGTCTGTTGCTGCTGCTG 22519
QY 2521 AATACGAATATATATGAGAAACAGCATACACAAGCTTGGGAGAAATATATTTGGGTG 2580
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QY 2581 GCTGAGAGCTCTATTTCTAAGAATGTGACCTTAGCGAGGGTATGTGGCTCACACCT 2640
DB 22580 GCTGAGAGCTCTATTTCTAAGAATGTGACCTTAGCGAGGGTATGTGGCTCACACCT 22639
QY 2641 ATTAATCCAGACATTTGGAGGCGCAAGTCAAGAAATCGCTTGAACCAAGATTCAAG 2700
DB 22640 ATTAATCCAGACATTTGGAGGCGCAAGTCAAGAAATCGCTTGAACCAAGATTCAAG 22699
QY 2701 CTAGCATGGGCAACATAGCAAGACCTCATCTCAAAAAATTTAAATCAGCTGACA 2760
DB 22700 CTAGCATGGGCAACATAGCAAGACCTCATCTCAAAAAATTTAAATCAGCTGACA 22759
QY 2761 TGGTGCAATACGCTTATGCTTCACTACCTGGGAAGCTAGTGGGTGATCGCTTGACA 2820
DB 22760 TGGTGCAATACGCTTATGCTTCACTACCTGGGAAGCTAGTGGGTGATCGCTTGACA 22819
QY 2821 CAGGATTTGAGGCTAAGGTGAGGCAATGATCACACAATGCACTCCAGCTTGAAGTACAG 2880
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QY 2881 AGGAGACCCCTGCTCCCTAAAAAGAAAGAAATGTGATTTTATCTTAGACAGTACAGT 2940
DB 22880 AGGAGACCCCTGCTCCCTAAAAAGAAAGAAATGTGATTTTATCTTAGACAGTACAGT 22939
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DB 23000 GTGGCTGTAGATATATGAAAGAAATAGAGACTAGAGTCAAGGATTCACCTTAAGTG 23059
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DB 23060 TTTGTTGTTGTTTGTGAGACAGAGTCTCTTTTGTGACCCAGGCTAAGTGAATGATG 23119
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QY 3181 CCCAAGCTGTGAATTAAGGTGAGGCAAGGTTTATGATGAGTCTGGCTAGT 3240
DB 23180 CCCAAGCTGTGAATTAAGGTGAGGCAAGGTTTATGATGAGTCTGGCTAGT 23239
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DB 23240 GCCTCTCAAACTTCAAGTGAAGCAAGTGAACCGGAACTGACTGAACAGTCTGGT 23299
QY 3301 TAAAGCTGAGCTCTGATTTCTAATGATGATGATGATGATGATGATGATGATGATG 3360
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QY 3361 GCCAAGCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3420
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QY 3421 AGTGAATTAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3480
DB 23420 AGTGAATTAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 23479
QY 3481 GTTAATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3540
DB 23480 GTTAATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 23539
QY 3541 GACGAGAGAAATGTAGCTCTATTTAACAAGAAATAGAGAAAGTGTGTTGAGAGAAA 3600
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QY 3601 GAGGAGTCTGTTTCAAGAGTGTGAGGTTCCAGGTGAAGCAGGATCTCCAAAGGGAAT 3660
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DB 23660 GAGCAGTAGGCAACTAAAAAGAAATCTGTGCTCAAGAGGAGCTGTGAGCTGACGTGT 23719
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QY 3961 GTATTACAAAGATCAGGAATACAGCTTAAAGTCAATCTTGACTGCAATTTGACTGTG 4020
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QY 4021 ATTTGAGGGGACACCTAATTAATTAAGGAATTTATGTTGGGTATATGAGGCACAAG 4080
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QY 4081 GAAGAGTTATCCAAATCAAGCAGGTGAGGATGAGGATGATTTCTCAAGGTGAGGCA 4140
DB 24080 GAAGAGTTATCCAAATCAAGCAGGTGAGGATGAGGATGATTTCTCAAGGTGAGGCA 24139
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DB 24140 TCAATGAATGTGGGAAGGGGCAACAGATCCATGCTCCATCCAGGCAAGCCACTTCCA 24199
QY 4201 GAAAGCTCAATAGAGTTCAAGTATCCAGAGTCTGATCCCTAATCTTTCTGGGTTT 4260
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DB 24620 ATTGGATGAGGCAATCTTTTATTTTGAAGTGTATATTTCCCTGACCTTACTTCTC 24679
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DB 24680 CTGTTTCTTCTACTCTCTCCCTACTCAACAGAAATCTTCTCTCTACTCAT 24739
QY 4741 TCCCTGAATGCTGTGCTGTTAAGTTCCAGCTTGAAGTGAAGGCTAATGAGAACGAC 4800

Db	24740	TTCCGTGAATGCTGTGTCTGTCTTTAAAGTTTCACAGCTTGAACAGTGAAGGCTAATCAGAAACAC	24719
Qy	4801	AGTGTATCAGATGTGATGTGATGTGTGGAGAAAGTGTGACATATATGACCAATTACTTA	4860
Db	24800	AGTGTATCAGATGTGATGTGATGTGTGTGGAGAAAGTGTGACAGATATATGACCAATTACTTA	24859
Qy	4861	GCCGGAACTGACGGGAAAAACAAGATGTGACGCATATTTTTCTGTGATCTGTAGTATTAA	4920
Db	24860	GCCGGAACTGACGGGAAAAACAAGATGTGACGCATATTTTTCTGTGATCTGTAGTATTAA	24919
Qy	4921	ATGATGATGTGTCCATTCACTGTGTATGAGAATCAGAAAGAAAAATTTATTTTGGAGAG	4980
Db	24920	ATGATGATGTGTCCATTCACTGTGTATGAGAATCAGAAAGAAAAATTTATTTTGGAGAG	24979
Qy	4981	ATTACCAAGATTTGTGTTTTGACATCCTAAAGTTTGAGGTGATTATGGGATGTGACAGGGGA	5040
Db	24980	ATTACCAAGATTTGTGTTTTGACATCCTAAAGTTTGAGGTGATTATGGGATGTGACAGGGGA	25039
Qy	5041	GCTCCAGACTGTGTGGCCCTAAAGTATGAAAGCAATCTGATGTGAGATATTAAGATTTTGA	5100
Db	25040	GCTCCAGACTGTGTGGCCCTAAAGTATGAAAGCAATCTGATGTGAGATATTAAGATTTTGA	25099
Qy	5101	AATATATCAGAATACGGTGTTCATTATAGACACTGTCAGTGGGTAAAGATATGCTTAAGGAGC	5160
Db	25100	AATATATCAGAATACGGTGTTCATTATAGACACTGTCAGTGGGTAAAGATATGCTTAAGGAGC	25159
Qy	5161	ATGTGTAGATGTATTAACAGAAAGATCAAAAGCGAACCCTTAAGAAATTAACAATATGTATTTA	5220
Db	25160	ATGTGTAGATGTATTAACAGAAAGATCAAAAGCGAACCCTTAAGAAATTAACAATATGTATTTA	25219
Qy	5221	TTTATATATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT	5280
Db	25220	TTTATATATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT	25279
Qy	5281	ACGGGAATCTGCCTCTGTGCTGCCAGAGCTGGAAGTGCAGTGGCGGAAACTCAGCTCACTGA	5340
Db	25280	ACGGGAATCTGCCTCTGTGCTGCCAGAGCTGGAAGTGCAGTGGCGGAAACTCAGCTCACTGA	25339
Qy	5341	ACCTCCGCTTCTGTGGTTCAAGGAGAGCTCTGCTCAAGCTCTCAAGTATGCTGGGACTA	5400
Db	25340	ACCTCCGCTTCTGTGGTTCAAGGAGAGCTCTGCTCAAGCTCTCAAGTATGCTGGGACTA	25399
Qy	5401	CAGGCACCCACCAACCTCACTGACCTAATTTTTGTATTTTTATAGAGAGAGGGGTTTCAAC	5460
Db	25400	CAGGCACCCACCAACCTCACTGACCTAATTTTTGTATTTTTATAGAGAGAGGGGTTTCAAC	25459
Qy	5461	ATGTGTGCACAGGCTGTGCTTGAACCTTGTGACTTGTAGATTCACCTGCTTGGGCTTCC	5520
Db	25460	ATGTGTGCACAGGCTGTGCTTGAACCTTGTGACTTGTAGATTCACCTGCTTGGGCTTCC	25519
Qy	5521	AAAGTGTGGGATTAACAGTATGAGCCACTGTGTCTGTGGCCATTTTTGTTTTTATATAGAG	5580
Db	25520	AAAGTGTGGGATTAACAGTATGAGCCACTGTGTCTGTGGCCATTTTTGTTTTTATATAGAG	25579
Qy	5581	ATGGGATCTTGCTATGTTGGCCACAGGCTGCTGAACTCCTGGACTCAAGCAATCCTCT	5640
Db	25580	ATGGGATCTTGCTATGTTGGCCACAGGCTGCTGAACTCCTGGACTCAAGCAATCCTCT	25639
Qy	5641	GCTTTGGCTTCTCAAAAGTTCTGGGATTTACATGTAGTCCCTGGGCTGGCCAGAAATAT	5700
Db	25640	GCTTTGGCTTCTCAAAAGTTCTGGGATTTACATGTAGTCCCTGGGCTGGCCAGAAATAT	25699
Qy	5701	CAATATATTAATTTTGTATGAAGTAAACCTTAAGAAAGAAACAGCCAGAGGGGACGAAG	5760
Db	25700	CAATATATTAATTTTGTATGAAGTAAACCTTAAGAAAGAAACAGCCAGAGGGGACGAAG	25759
Qy	5761	AAAAATTAGAGATTTGTGAAACCAAAAGAAAGAGTCCCTCAGAAAGAAAGCATGTCT	5820
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Db	25820	ATGATGCCAATATGCTGCCAAGATTAAGAAATTAAGAAAGTATCATATGGGTTTCATAGAAAA	25879

Qy	5881	GTGATGGGAAACCAATGCTAAATAAAACATTGGTAATGACACAAATGCTGGCAAAAGCATTTT	5940
Db	25880	GTATGAGAAACCAATGCTAAATAAAACATTGGTAATGACACAAATGCTGGCAAAAGCATTTT	25939
Qy	5941	TATAGGGGAGATGAATTTTGTATTTTCAGAGGACAAACAGTTCATPACAAATGGCAAGATCTA	6000
Db	25940	TATAGGGGAGATGAATTTTGTATTTTCAGAGGACAAACAGTTCATPACAAATGGCAAGATCTA	25999
Qy	6001	GTGTGTGACCAAGGAGATTAGTGTCTGAAGTGGATTTGAAGAGAGATCATTTGGAGCTGA	6060
Db	26000	GTGTGTGACCAAGGAGATTAGTGTCTGAAGTGGATTTGAAGAGAGATCATTTGGAGCTGA	26059
Qy	6061	GGTTGGCTAGAGCTGTCTCATGACACATTAATGTCATGAGTCAACAGCTGTGATCCAG	6120
Db	26060	GGTTGGCTAGAGCTGTCTCATGACACATTAATGTCATGAGTCAACAGCTGTGATCCAG	26119
Qy	6121	TGCCCAATCTTCAGTGAATGAACAGAGAGGATTGAGATTCAATGTAATGACCGCTTAAA	6180
Db	26120	TGCCCAATCTTCAGTGAATGAACAGAGAGGATTGAGATTCAATGTAATGACCGCTTAAA	26179
Qy	6181	GAAAGATTAATGAAAGATGTGG 6201	
Db	26180	GAAAGATTAATGAAAGATGTGG 26200	
RESULT 2			
US-10-224-562-3			
; Sequence 3, Application US/10224562			
; Patent No. 6730506			
; GENERAL INFORMATION:			
; APPLICANT: YAN, Chunhua et al.			
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: CL001098DIV			
; CURRENT APPLICATION NUMBER: US/10/224,562			
; CURRENT FILING DATE: 2002-08-21			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 53332			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US-10-224-562-3			
Query Match 100.0%; Score 6201; DB 4; Length 53332;			
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 6201; Conservative 0;			
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Qy	61	CTAAATACCGAAGAACTCCCTTTGTAAATTTGTAACAAAAATTAATATGATAGAG	120
Db	20060	CTAAATACCGAAGAACTCCCTTTGTAAATTTGTAACAAAAATTAATATGATAGAG	20119
Qy	121	TTAATACCTTATAGAAATGTGAACCAAGAGCCATATCAGCGCTAGCAAAAATGGCAGA	180
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Qy	181	ATTCAATATCATCAAAAGTTATCTTCAAGAGCTTCAGCGCTTAATGATGTCTAAAGAA	240
Db	20180	ATTCAATATCATCAAAAGTTATCTTCAAGAGCTTCAGCGCTTAATGATGTCTAAAGAA	20239
Qy	241	ATGTGAAGAGCCTCAGGCATCTGAAGGACAGTGTTAACAGCAATTGATCAAAAAGAAAA	300
Db	20240	ATGTGAAGAGCCTCAGGCATCTGAAGGACAGTGTTAACAGCAATTGATCAAAAAGAAAA	20299
Qy	301	CCACAGGCGCTTCCCTCCCTCCCACTTGAATGATAGCAGTCTTCATTTTCCATGTAGT	360
Db	20300	CCACAGGCGCTTCCCTCCCTCCCACTTGAATGATAGCAGTCTTCATTTTCCATGTAGT	20359

QY 361 AAATTTCTAGATACAGCTTTGAGCTCAAACTCTGAAAGAAAGCTCCATTCAG 420
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QY 421 GAAATTTCTAGATACAGCTTTGAGCTCAAACTCTGAAAGAAAGCTCCATTCAG 480
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QY 481 TGTAGCCCTGAGCGGCTGCTCAAGCTGTAATCCAGCCCTTTGGAGGCCAGATGG 540
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QY 541 CAGATCATAGAGTCAAGAGATTGAGACCAAGCTTACCAATGCTGAAACCCGCTCTA 600
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DB 21020 CAAATAGAAATGTTTCAATGTAATGTTAAAGAACCTGTGAAGGTTGAAGCAATTAATTA 21079
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DB 21200 AAGACAGTGAAGAGAGTTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 21259
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QY 1561 AATATGATCTAGTCTGATGATGTCAGAGGATGTCAGAGATGTCAGAGATGTCAGAGATGTCAGAG 1620
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DB 21800 ACTCAGAGGCTGAGCAGAGAGAAATGCGTGAACCCGAGAGTGAAGTGTGCTGAGCCG 21859
QY 1861 AGATCGCGCATCGGCTCCAGCTGTGGGAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1920
DB 21860 AGATCGCGCATCGGCTCCAGCTGTGGGAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 21919
QY 1921 AAAAAAATAAAAAAGTTTCAGATCTTAAACAATGATTTCAACAGTGTAGATAGAG 1980
DB 21920 AAAAAAATAAAAAAGTTTCAGATCTTAAACAATGATTTCAACAGTGTAGATAGAG 21979
QY 1981 AGATGTTTCAAGGAGAGAAATGTTTTCAGCAAGAGTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2040
DB 21980 AGATGTTTCAAGGAGAGAAATGTTTTCAGCAAGAGTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 22039
QY 2041 ATGTTCAAG 2100
DB 22040 ATGTTCAAG 22099
QY 2101 TTGCAATCTCAAGTTCATTAATGCTGATTAAGTAATCAATGATGATGATGATGATGATGATGATGATGAT 2160
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DB 22160 TTTTAAAAATGAATTAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 22219
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DB 22280 TTATGAT 22339
QY 2341 AATCTTTAAAGCATGCGCTGCTGTAATCTTATTTTGGAGAGAAATCCAAAGATC 2400
DB 22340 AATCTTTAAAGCATGCGCTGCTGTAATCTTATTTTGGAGAGAAATCCAAAGATC 22399
QY 2401 TGAGAGAGCAAAATTTTGGCTGAGGTTTGAAGCAAGCTTATGCAATGCTTAAAGTGA 2460
DB 22400 TGAGAGAGCAAAATTTTGGCTGAGGTTTGAAGCAAGCTTATGCAATGCTTAAAGTGA 22459
QY 2461 TTCTTAGTTAAATTTCTTCCAGTGAAGTCAATGCTGATGCTTCTAGTTCTGTTGGCTGA 2520
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Db 22520 AATACGAAATATATATGTGAACAAGCATACACAAGCTGGGGAAATATATATGGTGGTG 22579
Qy 2581 GCTGAGAGCCTCATTTTCTAAGAAATGTGACCTTAGGACGGGTATGTGGCTCACACCT 2640
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Qy 2641 ATTAATTCAGACATTTTGGGAGGCGCAAGTCAAGAAATCGTTTAACCCAAAGATTCAAGA 2700
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Qy 2761 TGGTGGCATACGCTGTAGTCCCACTACCTGGAAAGTAGTGGGTGATCGCTTGACA 2820
Db 22760 TGGTGGCATACGCTGTAGTCCCACTACCTGGAAAGTAGTGGGTGATCGCTTGACA 22819
Qy 2821 CAGGATTTGAGGCTAAGGTGAGCCATGATCACACAATGCACTCCAGCTTGATGACAG 2880
Db 22820 CAGGATTTGAGGCTAAGGTGAGCCATGATCACACAATGCACTCCAGCTTGATGACAG 22879
Qy 2881 AGGAAGACCCTGCTCCCTAAAAAAGAAATGTGATTTTATTCCTTAGACAGTACAGT 2940
Db 22880 AGGAAGACCCTGCTCCCTAAAAAAGAAATGTGATTTTATTCCTTAGACAGTACAGT 22939
Qy 2941 CATTAAGTCAATTAAGTTGAGTTGAGAGAAATATATATGATCAGAGAAATTTATTAATCACT 3000
Db 22940 CATTAAGTCAATTAAGTTGAGTTGAGAGAAATATATATGATCAGAGAAATTTATTAATCACT 22999
Qy 3001 GGGGTGTAGAGATATATGAAGAATAAGACATAGAGTCAGGATTCATTTAAGT 3060
Db 23000 GGGGTGTAGAGATATATGAAGAATAAGACATAGAGTCAGGATTCATTTAAGT 23059
Qy 3061 TTTGTTGTTTGTGTTGAGCAGAGTCTCTTTTGTGTTACCAGGCTAGAGTCAATGTGTG 3120
Db 23060 TTTGTTGTTTGTGTTGAGCAGAGTCTCTTTTGTGTTACCAGGCTAGAGTCAATGTGTG 23119
Qy 3121 CAGTCATGGCTACCGCAGCTCAAACTCCAGCCTCAAAATTAATCTTCCAGCTGGGCTT 3180
Db 23120 CAGTCATGGCTACCGCAGCTCAAACTCCAGCCTCAAAATTAATCTTCCAGCTGGGCTT 23179
Qy 3181 CCCAAGGTCTGGAATTAAGAGTGTAGAGCCAAAGGTTTATGATGTGGTCTGGCTAAT 3240
Db 23180 CCCAAGGTCTGGAATTAAGAGTGTAGAGCCAAAGGTTTATGATGTGGTCTGGCTAAT 23239
Qy 3241 GCCTCTCAAACTTCAGTGTGAGCAGACAAAGTACCGGAACTGTCAACAAGCTGGGTT 3300
Db 23240 GCCTCTCAAACTTCAGTGTGAGCAGACAAAGTACCGGAACTGTCAACAAGCTGGGTT 23299
Qy 3301 TAAAGCTGTAGCCTCTGCATTTCTAACATGTAGTCAAGCTGATGCAATGTGTGTCAAGA 3360
Db 23300 TAAAGCTGTAGCCTCTGCATTTCTAACATGTAGTCAAGCTGATGCAATGTGTGTGTCAAGA 23359
Qy 3361 GCCAAGCAGCTGTAGCAGCAAGATCTAGTTAGCAATTAAGATCAAGTGTGATTAATGTGT 3420
Db 23360 GCCAAGCAGCTGTAGCAGCAAGATCTAGTTAGCAATTAAGATCAAGTGTGATTAATGTGT 23419
Qy 3421 AGTGAACAATTAAGATGTGAGAAATGTGAATACTAGTAAACAAGAAGTTCACTCTTG 3480
Db 23420 AGTGAACAATTAAGATGTGAGAAATGTGAATACTAGTAAACAAGAAGTTCACTCTTG 23479
Qy 3481 GTTAATCTGTAGCATGTAGAGAGGAAAGATGTGGGCAAACTAACTAGTTTGTGTGACT 3540
Db 23480 GTTAATCTGTAGCATGTAGAGAGGAAAGATGTGGGCAAACTAACTAGTTTGTGTGACT 23539
Qy 3541 GACGAGAGAAATTTGTAGCTCTATTAACAGAAATAGAGAGAAAGTTGGTTGGAGGAAA 3600
Db 23540 GACGAGAGAAATTTGTAGCTCTATTAACAGAAATAGAGAGAAAGTTGGTTGGAGGAAA 23599
Qy 3601 GAGAGTCTGTGTTTCAAGCTGTGTGAGGTCCAGGTGAGACAGATCTCCAAAGGGAAT 3660
Db 23600 GAGAGTCTGTGTTTCAAGCTGTGTGAGGTCCAGGTGAGACAGATCTCCAAAGGGAAT 23659
Qy 3661 GAGCAGTAGCAACCTAAAGAAATCTGTGCTCAGAAAGGAGCTGTGACTGCAGTGT 3720
Db 23660 GAGCAGTAGCAACCTAAAGAAATCTGTGCTCAGAAAGGAGCTGTGACTGCAGTGT 23719
Qy 3721 AGATCTGAGGCTCATCAGACATAGAGTTTAAAGACAAAGAGTAGGCAACCAAGAGAC 3780
Db 23720 AGATCTGAGGCTCATCAGACATAGAGTTTAAAGACAAAGAGTAGGCAACCAAGAGAC 23779
Qy 3781 AAATACACAAAGAGAGAGAGCTGATGATGAGACTTTTCTCTTTTATAGATGAGAGAGGA 3840
Db 23780 AAATACACAAAGAGAGAGAGCTGATGATGAGACTTTTCTCTTTTATAGATGAGAGAGGA 23839
Qy 3841 ACAGGAAATGAAGAGATGAAGGAAAGCAGCTTGTAGAAATGTAGACATCTGAAAAAAA 3900
Db 23840 ACAGGAAATGAAGAGATGAAGGAAAGCAGCTTGTAGAAATGTAGACATCTGAAAAAAA 23899
Qy 3901 ATACACACTGTATGGAATCAAGGAAAGAAATTTTCAAGAAAGAGGTATGTGTGACA 3960
Db 23900 ATACACACTGTATGGAATCAAGGAAAGAAATTTTCAAGAAAGAGGTATGTGTGACA 23959
Qy 3961 GTATTACAAGCATCAGAAATACAGCTTAAAGTCACTCTTGTGACTTGACTTGTGTGG 4020
Db 23960 GTATTACAAGCATCAGAAATACAGCTTAAAGTCACTCTTGTGACTTGACTTGTGTGG 24019
Qy 4021 ATTTGTAGGGACACACTAATTAATTAAGAAATTAATGTGGGTATGTAGAGCAAAAG 4080
Db 24020 ATTTGTAGGGACACACTAATTAATTAAGAAATTAATGTGGGTATGTAGAGCAAAAG 24079
Qy 4081 GAAAGGTTATCAANTCAAAACAGAGTGGAGATGAGATGATCTCCAAAGGTGAGAGCA 4140
Db 24080 GAAAGGTTATCAANTCAAAACAGAGTGGAGATGAGATGATCTCCAAAGGTGAGAGCA 24139
Qy 4141 TCAGTGAATGTGGGAAGGGGACAGAGCATCCATGCCATCCAGGCAAGCCACCTCCA 4200
Db 24140 TCAGTGAATGTGGGAAGGGGACAGAGCATCCATGCCATCCAGGCAAGCCACCTCCA 24199
Qy 4201 GAAAGCTCATGAGAGTTGAGTATTCAGAGAGTCTGTATCCTTAATCTTTCTGGGTTT 4260
Db 24200 GAAAGCTCATGAGAGTTGAGTATTCAGAGAGTCTGTATCCTTAATCTTTCTGGGTTT 24259
Qy 4261 TGCATAGGCTTCAATGTGTAGGAGCATGATTTAATTAACATATGGCCACATGGTATCAACT 4320
Db 24260 TGCATAGGCTTCAATGTGTGTAGGAGCATGATTTAATTAACATATGGCCACATGGTATCAACT 24319
Qy 4321 AACCTTCAACCCCTCTCCCTCCCTAATCATGCTTGTGCTTTCCAGTGAACCATGCCCTA 4380
Db 24320 AACCTTCAACCCCTCTCCCTCCCTAATCATGCTTGTGCTTTCCAGTGAACCATGCCCTA 24379
Qy 4381 TCTTAAGCTAACCAATGTGTCTGCCAGCTATCATGTCACTTACAAAAAGACATCACTTTG 4440
Db 24380 TCTTAAGCTAACCAATGTGTCTGCCAGCTATCATGTCACTTACAAAAAGACATCACTTTG 24439
Qy 4441 GAGATTTCAAGGATTTTGAAGTGTGGCTGTGAGAAATTAAGTGAAGATCAAAATTAATAT 4500
Db 24440 GAGATTTCAAGGATTTTGAAGTGTGGCTGTGAGAAATTAAGTGAAGATCAAAATTAATAT 24499
Qy 4501 TTCAACAATATCAAGTGTGTATTTTATATCAGGCGCCATTAATGTTTTTAAACAAAG 4560
Db 24500 TTCAACAATATCAAGTGTGTATTTTATATCAGGCGCCATTAATGTTTTTAAACAAAG 24559
Qy 4561 AGGTATTAATTTCAATTTTCTTTTATTAAGCTTACATGATGACATGTGTGTGAATAG 4620
Db 24560 AGGTATTAATTTCAATTTTCTTTTATTAAGCTTACATGATGACATGTGTGTGAATAG 24619
Qy 4621 ATTGGAGTAGGGCAATATCTTTTGTGAAATGTATTAATTCCTGAGCCTTACTTCTC 4680
Db 24620 ATTGGAGTAGGGCAATATCTTTTGTGAAATGTATTAATTCCTGAGCCTTACTTCTC 24679
Qy 4681 CTGTGTTTCTTCTACCTCTCTCCCTTACTCAACAGAAAACTTCTCTCTTACTCAT 4740
Db 24680 CTGTGTTTCTTCTACCTCTCTCCCTTACTCAACAGAAAACTTCTCTCTTACTCAT 24739
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Qy	4741	TCCTCGAATGCTGGTGTCTGTATTAAGTTTCCAGCCTTGCACGTAGAGGCTATATCGAACCAAC	4800
Db	24740	TCCTCGAATGCTGGTGTCTGTATTAAGTTTCCAGCCTTGCACGTAGAGGCTATATCGAACCAAC	24799
Qy	4801	AGTGTACAGATGTGAGATGATGGTGGAGAAAAGTGACAGATATGAGACCAATTACTTA	4860
Db	24800	AGTGTACAGATGTGAGATGATGGTGGAGAAAAGTGACAGATATGAGACCAATTACTTA	24855
Qy	4861	GCCGGAACTGACGGGGAAAAACAGAGTCACCGATATTTTTTCTGGATCTGAGTATTA	4920
Db	24860	GCCGGAACTGACGGGGAAAAACAGAGTCACCGATATTTTTTCTGGATCTGAGTATTA	24919
Qy	4921	ATGATGATGATGGTGCATTCACTGTGATAGAGAAATCAGAAAGAAAATTATTTTGGAGAG	4980
Db	24920	ATGATGATGATGGTGCATTCACTGTGATAGAGAAATCAGAAAGAAAATTATTTTGGAGAG	24979
Qy	4981	ATACCATGAATTTGTTTTGAACAACATGCTAAAGTTTGAAGTATATGAGATGACAGGCA	5040
Db	24980	ATACCATGAATTTGTTTTGAACAACATGCTAAAGTATATGAGATGACAGGCA	25039
Qy	5041	GCTCCAACTGTGTGGGCTTAAAGTAAAGGCACTGTAGTTGGAGATTAATAATTGA	5100
Db	25040	GCTCCAACTGTGTGGGCTTAAAGTAAAGGCACTGTAGTTGGAGATTAATAATTGA	25099
Qy	5101	AATCATCAGATACGGTGTGTTCAATTAGAGCACTGCAGTGGGTAGATGCTAAGGAGAC	5160
Db	25100	AATCATCAGATACGGTGTGTTCAATTAGAGCACTGCAGTGGGTAGATGCTAAGGAGAC	25155
Qy	5161	ATGTGTAGAGTGAATACAGAAAGATCAAAAGCCGAAACCTTAAGAAATTAACATATGTATT	5220
Db	25160	ATGTGTAGAGTGAATACAGAAAGATCAAAAGCCGAAACCTTAAGAAATTAACATATGTATT	25219
Qy	5221	TTTATTTATTTATATGTTTATTTTAAATTTTATTTTATTTATTTATTTATTTTATTTAG	5280
Db	25220	TTTATTTATTTATATGTTTATTTTAAATTTTATTTTATTTTATTTATTTATTTATTTTATTTAG	25279
Qy	5281	ACGGGAAGTCTGCTCTGCTGCCACAGGCTGAGATGACAGTGGCGCAAACTCAGCTCACTGCA	5340
Db	25280	ACGGGAAGTCTGCTCTGCTGCCACAGGCTGAGATGACAGTGGCGCAAACTCAGCTCACTGCA	25339
Qy	5341	ACCTCCGCTTCCTGGGTTCAGAGGAGCTCCTGCTCAGCTCAGCTCAAGTAGCTGGGACAT	5400
Db	25340	ACCTCCGCTTCCTGGGTTCAGAGGAGCTCCTGCTCAGCTCAGCTCAAGTAGCTGGGACAT	25399
Qy	5401	CAGGACCAACCACTCACTGACTAATTTTGTATTTTATGATAGAGACGGGGTTTCACC	5460
Db	25400	CAGGACCAACCACTCACTGACTAATTTTGTATTTTATGATAGAGACGGGGTTTCACC	25455
Qy	5461	ATGTTGGCCAGGCTGCTTGAACCTTGTACCTTGAATTTCACTGCTTGGCTTCC	5520
Db	25460	ATGTTGGCCAGGCTGCTTGAACCTTGTACCTTGAATTTCACTGCTTGGCTTCC	25519
Qy	5521	AAAGTGTGGGATTAACAGATGATGAGCACACTGTGCTGGCTATTTTTTGTTTTATATAGAG	5580
Db	25520	AAAGTGTGGGATTAACAGATGATGAGCACACTGTGCTGGCTATTTTTTGTTTTATATAGAG	25579
Qy	5581	ATGGGGTCTTGTCTATGTGTCCCAAGGCTGTGTGAACTCTGTGACTTCAGACAAATCCTCCT	5640
Db	25580	ATGGGGTCTTGTCTATGTGTCCCAAGGCTGTGTGAACTCTGTGACTTCAGACAAATCCTCCT	25639
Qy	5641	GCCTTGGCCTCTCAAAAGTTCTGGGATTAACAATGTAGTCCCTGAGGCTGGGCCAGAAAT	5700
Db	25640	GCCTTGGCCTCTCAAAAGTTCTGGGATTAACAATGTAGTCCCTGAGGCTGGGCCAGAAAT	25699
Qy	5701	CAATATATTGATTTTATGATAGAAATAGAACCTATGAAAAGACCAAGCCAGAGGGGCAAG	5760
Db	25700	CAATATATTGATTTTATGATAGAAATAGAACCTATGAAAAGACCAAGCCAGAGGGGCAAG	25759
Qy	5761	AAAAATTATGAGATTTGTGGAACCAAAAGAGAGTGGCTCAGAGAAAGAAAGGATGCTCT	5820
Db	25760	AAAAATTATGAGATTTGTGGAACCAAAAGAGAGTGGCTCAGAGAAAGAAAGGATGCTCT	25819

Oy	5821	ATGATGCCAAATCTGTCAAAGATTAAGAAATTAAGAATATCATTTGGGTTTCATAGAAAA	5880
Db	25820	ATGATGCCAAATGCTCGMAAGATTAAGAAATTAAGAATATCATTTGGGTTTCATAGAAAA	25877
Oy	5881	GTCAATGGGAAACCATGTGTAAAAAACAATTTGTGAATGACACAAATCGTTGCAAAAGCATTTT	5940
Db	25880	GTCAATGGGAAACCATGTGTAAAAAACAATTTGTGAATGACACAAATCGTTGCAAAAGCATTTT	25933
Oy	5941	TATATGGGGGATGAAATTTTGTATTTTCAGAGACAAACAGTTTCCATACAAATGGCAAGATCTA	6000
Db	25940	TATATGGGGGATGAAATTTTGTATTTTCAGAGACAAACAGTTTCCATACAAATGGCAAGATCTA	25999
Oy	6001	GTGTGTGACCAACGGGAGTTAGTGTCTGGAAGTGAATTGGGAAGACAGATCATTTGSAAGCTGA	6060
Db	26000	GTGTGTGACCAACGGGAGTTAGTGTCTGGAAGTGAATTGGGAAGACAGATCATTTGSAAGCTGA	26055
Oy	6061	GGTTGGCTAGAGCTGTTTCTTCATGSGACCTAATATGTCATGAGTGTCAACAGCTGTGTATCCAA	6120
Db	26060	GGTTGGCTAGAGCTGTTTCTTCATGSGACCTAATATGTCATGAGTGTCAACAGCTGTGTATCCAA	26113
Oy	6121	TGCCACATCTTTCAGTGAATGACAGAGAGGGATTGAGAGTTTCAGTGAATGACCGCTAAAA	6180
Db	26120	TGCCACATCTTTCAGTGAATGACAGAGAGGGATTGAGAGTTTCAGTGAATGACCGCTAAAA	26173
Oy	6181	GAAGAGTAATGGAAGATGTGG 6201	
Db	26180	GAAGAGTAATGGAAGATGTGG 26200	

```

1      RESULT 3
2      US-08-544-900-1
3      Sequence 1, Application US/08544900
4      Patent No. 5736331
5      GENERAL INFORMATION:
6      APPLICANT: Lin, Stanley Li
7      APPLICANT: Rothofsky, Marlie Lynn
8      TITLE OF INVENTION: Method for Identifying Nucleia
9      TITLE OF INVENTION: Acid Encoding c-fos Promoter
10     TITLE OF INVENTION: Activating Proteins
11     NUMBER OF SEQUENCES: 3
12     CORRESPONDENCE ADDRESS:
13     ADDRESSSEE: Schering-Plough Corporation
14     ADDRESSSEE: Patent Department K-6-1 (1990)
15     STREET: 2000 Galloping Hill Road
16     CITY: Kenilworth
17     STATE: New Jersey
18     COUNTRY: USA
19     ZIP: 07033-0530
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: Apple Macintosh
23     OPERATING SYSTEM: Macintosh 7.1
24     SOFTWARE: Microsoft Word 5.1a
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/544, 900
27     FILING DATE:
28     CLASSIFICATION: 435
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US 08/272,412
31     FILING DATE: 8-JUL-1994
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Thompson, Paul A.
34     REGISTRATION NUMBER: 35,385
35     REFERENCE/POCKET NUMBER: OC0439K
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 908 298 5150
38     TELEFAX: 908 298 5388
39     TELEX:
40     INFORMATION FOR SEQ ID NO: 1:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 1930 base pairs
43     TYPE: nucleic acid
44     STRANDEDNESS: double

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QY 699 GAG-GTGCAGCGCAAAATCAACCAATGCACTGTAGCTGTGATGACAGGCAAGCT 757
DB 3660 GAGCTTGCAGTGGCGGAGATGGCTCCACGACCTAGAGCTGGAGACAGATGAACT 36601
QY 758 CCAACTCAAAAAAAAAAAAAAAAAAATATGTAAGTTGTGCTATTAACAAATTAATAG 817
DB 3660 CTATCTCAAAAAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 36541
QY 818 CAGTGAGAAACAAGTCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 877
DB 36540 TATTTACATGTGATCTGTATCAAAAGATCTCATGTATCTTAATTAATTAATTAAT 36481
QY 878 ATTAATTAAGGAACCTTAACCAAGCTCTGGAAGTAAAGTTTGAAGAATGTTGAGAC 937
DB 36480 CAGGTATCTCAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 36423
QY 938 AAAGGTTAAAGAGTGAATAAAAAAAAAAATTAATAATAATAATAATAATAATAATAATA 997
DB 36422 ACACTTGAAGTAACTTCAAGAGGCTTCTATCTGTGTGCTGAGCTGATCTCAAACTC 36363
QY 998 GATAGGAGCTTAAGTAAGAAATCAATAGAAATGTTTCAATGTAATGTAAGACCTG 1057
DB 36362 TGGCTCAAACTATCAACCCATTTTGGCTTCCAAAAATGCTGGG-ATTACAGCATGAG 36305
QY 1058 TAAGGTGAAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1117
DB 36304 CACTGACCTGCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 36245
QY 1118 TTGGCAATTTAAATAGAGGACAGAAATGTAAGATGTAAGTGAATGTAAGTGAATG 1177
DB 36244 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 36185
QY 1178 TCTGCAGACATGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1237
DB 36184 CACTAGTAAGAAATTTCTGTAATGATCTAGTAATTAATTAATTAATTAATTAAT 36125
QY 1238 CAGAATTAATGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1297
DB 36124 TATTCCTCAGTCTAGATTTTGAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36065
QY 1298 AAGATTAAGAGAGCTGTGATAGTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1357
DB 36064 GAGATTAAG 36005
QY 1358 TTGATTAATTAAG 1417
DB 36004 CTAAAG 35945
QY 1418 TTGAGTGAATCTCAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1475
DB 35944 TGAAGTGTCAAG 35885
QY 1476 CCTCAAG 1535
DB 35884 AAAATTAATTAAG 35825
QY 1536 ACACTTGTAG 1595
DB 35824 TCCCAAGTCAATGTTCTTTCCTAGATGTCATGAGCTTCAATATCAGAGAGAGAG 35765
QY 1596 CAAAGATATCTTCTAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1655
DB 35764 TTAAGATGATCTGCTCTATGTAATCTTATCTTATCTTATCTTATCTTATCTT 35705
QY 1656 TAATCCAG 1715
DB 35704 TAATCCAG 35645
QY 1716 TCTGTGTTAAG 1774
DB 35644 TCC---CTAAACAG 35588
QY 1775 GGTGGGGGGGCGCTGTAGTCCAGCTAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1834

DB 35587 GGTGGAGCGGCTGTAGTCCAGCTATTCGAGAGCTGGGAGAGAGAGAGAGAGAGAG 35528
QY 1835 CCGGAG 1893
DB 35527 CCGGAG 35468
QY 1894 GAGTGAAGTGTCTCAAAAAAAAAAATTAATAATAATAATAATAATAATAATAATA 1937
DB 35467 GAGCGAG 35424

RESULT 6
US-08-367-841A-43
Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tomblin-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367, 841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/257, 963
FILING DATE: 07-JUN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/952, 796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: p1-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
US-08-367-841A-43
sequence for PBDf plus flanking sequences.

Query Match 4.9%; Score 306; DB 3; Length 22481;
Best Local Similarity 55.8%; Pred. No. 36-62;
Matches 756; Conservative 0; Mismatches 575; Indels 25; Gaps 8;
1614 TCAGAGAGTTTCAAGATCGGCGCGGCGGCTGAGCTACGCTTAATCCAGACATTTGGG 1673

Db 12803 TTAAAGCTGAGTGAAGGCGCGGCGGCTGCTGCTGATTCAGACCTTTG93 12862
QY 1674 AGGCCAGAGCGGTGATCA CAAGTCAAGATCAAGACCATCTGTTTAAACGGTGA 1733
Db 12863 AGGTGGAGGTGGGTGATCAAGAGTCAAGATCCAGACCATCTGTTTAAACGGTGA 12922
QY 1734 AACCCGCTCTCAAAAATATATTAAGTCAAGCGGTGCTGGGGCGGCTGTAAT 1793
Db 12923 AACCCGCTCTCAAAAATATATTAAGTCAAGCGGTGCTGGGGCGGCTGTAAT 12982
QY 1794 CCCAGCTACTCAGAGGCTGAGCGAGAGATGCGCTGAACCCGGAGGTAGATTTC- 1852
Db 12983 CCCAGCTACTCAGAGGCTGAGCGAGAGATGCGCTGAACCCGGAGGTAGATTTC 13042
QY 1853 GTGAGCGAGATGCGCGCATCTGCGCTCAGCTGGCGGACAGATGAGCTGCTCAA 1912
Db 13043 GTGAGCTGAGCTGCGACCATCTGCACTCGGCGGACAGATGAGCTCGCTCAA 13102
QY 1913 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCAATTCAAGCTAG 1972
Db 13103 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCTTTTAACTTTCTTTT 13162
QY 1973 AATAGAGAGCATGTTTACAGGAGAGAAAAATGTTTTCAGAAAGTACAGATAGGAAA 2032
Db 13163 TTAGAGACAGAGCTCATCTCATCACTCATCACTCATCACTCATCACTCATCTGCTCA 13222
QY 2033 TAAAGATATGTTTCAAGAAAGAGACCCAGAGCTATGTTTGT-----TAGGTTAG 2085
Db 13223 CTCGAATCTTGGGCTCTGAGTTCAACCAATCTCATGCTTCCCAATACCTGG 13282
QY 2086 AGGAAACACAGTGTGTTTCAATCTCAAGTTCATAGTGCATTAAGTAAATCAATATGG 2145
Db 13283 GACCAAGGACAGTGCACACCGCCAGCTAATTTTGGGTATTTTATAGAGATGG 13342
QY 2146 GGTTCACAACTGTCATTTTAAAAATGAAATTAATGATGAGAGAGAAATGAAATATT 2205
Db 13343 GCCTACCAATGTTGCTCAGGTGTGTCGAAACCTCGAGCTCAAGATGATCATCTTCCTC 13402
QY 2206 AGCATGATTAACATTTTGAAGAGCAATTTATTTCTGCAACTTTTGTCCAAATTTGA 2265
Db 13403 GGCCTGC-CAAAGTGTGGGATTAAGGCAATTAAGCCATGCACTGCCCAATTTTGA 13461
QY 2266 ACTGATTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2325
Db 13462 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 13521
QY 2326 AGATGCAAGTCAAAAAATCTTTAAGCACTGCGCTGCTTAACTTCTTATTTTGCAGAG 2385
Db 13522 CAGGCTGAGATACAGTGGCACTATCTCAGCTCACTGCAACCTTGCCTCGGTTCAAG 13581
QY 2386 GAGAAATCCAAAGTCTGAGAGAGCAAAATTTTGTGCTGAGTTATGAACACAGCTTATGC 2445
Db 13582 CGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13641
QY 2446 CATTCCTAAAGATGTTTCTAGTTAAATTTCTTCCCACTAGTGCATGCACTTTCTA 2505
Db 13642 GTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 13694
QY 2506 GTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2565
Db 13695 GGTCTGCAACTCTGCACTCAAGTGAATCAACCACTGCAAGCTCCCAAGTGTGAG--- 13751
QY 2566 TATATTGGGTAGTGTGCTGAGAGCTCATTTTCTAAAGAAATGAGACTTTAGGACGGTGA 2625
Db 13752 -ATTATATGGGTAGGCACTCGCTGATGTTTATTAAGGTGGGTCTATGGGGCTGGGG 13810
QY 2626 TGGTGGCTCAACCTTAATTTCAAGACTTTGGGAGGCAAGTCAAGATGCTTTGAA 2685
Db 13811 CGGTGGCTCATGCTGCTTAATCCAGACCTTTGGTAAACGAGGCGGGGTGATCAAGGT 13870
QY 2686 CCCAAGATTCAAGACTAGAGTGGGCAATAGCAAGACTCATCTCAAAAAAT-TT 2744

Db 13871 --CAGAGATCGAGACCATCTGCTTAAACACGGTGAACCCGCTCTCTATAAAATACA 13928
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Db 13929 AAAATTAATCCAGAGCTGTTGTTGAGGCGCTTGTAGTCCAGCTACTCGGAGGCTGAGGC 13988
QY 2805 GGTGATGCTC--TTGCAAGAGTTTGAAGCTTAAGGTGAGCATGATCAACAATGCA 2862
Db 13989 AGAGATATGCTGTAATCTGGAGGCGAGCTTTCAGATGAGCGAGATCAACGCTGA 14048
QY 2863 CTCAGCTTGAATGACAGAGAGAACCTGCTCCTTAAAGAAAGAAATGATGATTTTA 2922
Db 14049 CTCAGCTTGAATGACAGAGAGAACCTGCTCCTTAAAGAAAGAAATGATGATTTTA 14108
QY 2923 TTCTTGAACAGTACATGATTTATTTAAGTTTG 2958
Db 14109 AGGTTCGCTTATAGTTCACAAGTGTAAACCTG 14144

RESULT 7
PCT-US95-07201-43
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki;
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22481 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: P1-147
; LOCATION:
; IDENTIFICATION METHOD:

OTHER INFORMATION: full length genomic
OTHER INFORMATION: Sequence for PDR plus flanking sequences.
PCT-US95-07201-43

Query Match 4.9%; Score 306; DB 5; Length 22481;
Best Local Similarity 55.8%; Pred. No. 3e-62;
Matches 756; Conservative 0; Mismatches 575; Indels 25; Gaps 8;

1614 TCAGAGAGTTTCAGATCGCCGCGCGCTGCTCAGCCTGTATATCCAGCATTTGGG 1673
12803 TTAAAGCTCAGAGAGGCGCGCGCGCTGCTCAGCCTGTATATCCAGCATTTGGG 12862
1674 AGCCCGAGCGGCTGATCAGAGTCAAGATCAAGATCAAGATCAAGATCAAGATCA 1733
12863 AGGTGAGGTGGGTGATCAGAGTCAAGATCAAGATCAAGATCAAGATCAAGATCA 12922
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12923 AACCCGCTCTCAAAAAATATATAATTTAGTGTGTGTGTGTGTGTGTGTGTGTGT 12982
1794 CCCAGCTACTCAGAGAGCTGAGGCGAGAGATGGCGTGAACCCGAGAGTGAAGTTGC- 1852
12983 CCCAGCTACTCAGAGAGCTGAGGCGAGAGATGGCGTGAACCCGAGAGTGAAGTTGCA 13042
1853 GTGAGCGAGATCGCCGCTGCGGCTCCAGCTGCGGCGAGAGATGAGATGAGTGTCTCA 1912
13043 GTGAGCTGAGCTGCGACACTGCACTCCAGCTGCGGCGAGAGATGAGATGAGTGTCTCA 13102
1913 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCAATTCACAGTCTAG 1972
13103 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCAATTCACAGTCTAG 13162
1973 AATGAGAGAGCATGTTTACAGGAGAGAGAAATGTTTTCAGCAAAAGTACAGAGTGA 2032
13163 TTAGAGACAGAGCTCAGTCCATCCAGTGTGAGTACAGTGTGCGATCTTGTCTCA 13222
2033 TAGAGATATGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2085
13223 CTGCAATCTTGGGCTCTGAGTTCAACCAATCTCAGCTCCCAATTAAGTCTG 13282
2086 AGGAAACAGAGTGTGTTGCAATCTCCAGGTTCCATTAAGTGTGTTGAATCAATATG 2145
13283 GACCAACAGGAGCTGCGACCAAGCTAATTTTGTGTGTGTGTGTGTGTGTGTGTGT 13342
2146 GGTTCAGCACTGCAATTTTAAAAATGAATTAAGATGAGAGAGAGAGAGAGAGAG 2205
13343 GCTTCACATGTTGCTCAGGTTGTGAAATCTCAGAGTCAAGATCAATCTTCTC 13402
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2266 ACTGACTATATATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2325
13462 TATTTATATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 13521
2326 AGATGCAATTAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2385
13522 CAGGCTGAGTACAGGAGCTATCTCAGTCACTCAACCTGCTGCTGCTGCTGCTGCT 13581
2386 GAGAAATCCAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2445
13582 CGAATCTGTGCTCAGCTCCTGAGTACCTGAGATTAAGGATCAACCAATCTCC 13641
2446 CATGCTAAAGAGATTTAGTTTAAATTTCTTCCCACTAGTGCATCTGCACTTTTA 2505
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2506 GTTCTGTGCGCTGAATAACAGATATATTAAGTGAACAGATATCAAGTCTGGGAAA 2565
13695 GGTCTGCACTCTGAGCTCAAGTATTAACCACTCAGCTCCCAAGTGTGGG--- 13751
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13752 -ATTATGATGAGAGCACTCGCTGATGCTTTTAAAAAGGGGCTATGCGGCTGGCG 13810
2626 TGTGCTCAGACCTATTAATTCAGACATTTGAGAGGCCAAGTCAAGAGATCGTTGA 2685
13811 CGGTGCTATGCTGTATATCCAGACATTTGTGTAGACCGAGCGGTGTGTATCAAGGT 13870
2686 CCCAGAGTTCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGAT 2744
13871 --CAGAGATCAAGACATCTGCTTACACAGGTGAACCCGCTCTTCAAAAAATACA 13928
2745 AAAATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2804
13929 AAAATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13988
2805 GGTGATCGC--TTGACACAGAGATTTTGAAGGCTGAAGTGAAGCATGATACACATGCA 2862
13989 AGGAGATGCGGTGAACCTGGAGCGAGCTTGAAGTGAAGCATGATACACATGCA 14048
2863 CTCAGCTTGAAGTGAAG 2922
14049 CTCAGCTTGAAGTGAAG 14108
2923 TTCCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2958
14109 AGGTTTGGCTTATAGTCAAGATGTTTAACTG 14144

RESULT 8

US-09-875-223-2
Sequence 2, Application US/09875223
Patent No. 6391850
GENERAL INFORMATION:
APPLICANT: No. 6391850, Western University
APPLICANT: No. 6391850, Bouck
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-2303
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US 08/899,304
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2
LENGTH: 22484
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: 1...22484
OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2

Query Match 4.9%; Score 306; DB 3; Length 22484;

Best Local Similarity 55.8%; Pred. No. 3e-62;
Matches 756; Conservative 0; Mismatches 575; Indels 25; Gaps 8;

1614 TCAGAGAGTTTCAGATCGCCGCGCGCTGCTCAGCCTGTATATCCAGCATTTGGG 1673
12803 TTAAAGCTCAGAGAGGCGCGCGCGCTGCTCAGCCTGTATATCCAGCATTTGGG 12862
1674 AGCCCGAGCGGCTGATCAGAGTCAAGATCAAGATCAAGATCAAGATCAAGATCA 1733
12863 AGGTGAGGTGGGTGATCAGAGTCAAGATCAAGATCAAGATCAAGATCAAGATCA 12922
1734 AACCCGCTCTCAAAAAATATATAATTTAGCAGGCGTGTGCGCGCGCTGTAGT 1793

Db 12923 AACCCGCTCTCTAATAAATAATTAAGTGGGTGTGTGGGGGGCGCTGTAGT 12982
QY 1794 CCCAGCTACTCAGAGAGGCTGAGGAGAGAAATGGCTGAAACCCGGAGGTAGAGTTGC- 1852
Db 12983 CCCAGCTACTCAGAGAGGCTGAGGAGAGAAATGGCTGAAACCCGGAGGTAGAGTTGC 13042
QY 1853 GTGAGCCGGAATGCGCGCACTGCGCTCCAGCTGGGGAGACAGAGTGAAGATCTGGCTCMA 1912
Db 13043 GTGAGCTGAGCTGCACTGCACTCCAGCTGGGGAGACAGAGTGAAGATCTGGCTCMA 13102
QY 1913 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCACTTTTCAACAGTCTAG 1972
Db 13103 AAAAAAAAAAAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 13162
QY 1973 AATAGAGAGCATGTTACAGAGAGAGAAATGTTTTCAGAAAAGTACAGAGTAGGAAA 2032
Db 13163 TTGAGAGCAGAGTCTCCTCATCACCAGTGTGAGTACAGAGTGTGCGATCTTGGCTCA 13222
QY 2033 TAGAGGATATGTTCAAGAGAGAGGAGCCCAAGTCAATGTTGT- - - - -TAGGTTAG 2085
Db 13223 CTGCAATCTTGGCTCTGAGTTCACCAATTTCTCATGCTCCAGCTCCCAATAGCTGG 13282
QY 2086 AGGAAACACAGTGTTCATCTCCAGTTCATAGTCCGTTATGAATCAATATGT 2145
Db 13283 GACCAAGGACGTCACACCGCCAGTAAATTTTGGGTATTTTGTAGTAAAGATGG 13342
QY 2146 GGTTAGCACTGATTTTAAAAATGAATTAATGATGAGAAAGAAATATAT 2205
Db 13343 GCCTCACAGTGTGCTCAGGTGTGTGAAATCTCGAGTCAAGATCATCTTCCTC 13402
QY 2206 AGCATGATTAATTTTGAAGAAGCAAGTATATTTTCTGCACTTTTGTCTCAATTTGT 2265
Db 13403 GGCCTGC-CAATGCTGGGATTAATAGCATTAAGCACTGCACTGCTCCCAATTTT 13461
QY 2266 ACTGTAATTAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2325
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QY 2326 AGACTCAGTCAGAAAAATCTTTAAGACATGCGCTGTCTAATCTTCTTAATTTTGCAG 2385
Db 13522 CAGGCTGAGTACAGTGCATCTCAGTCACTGCACTGCACTGCACTGCACTGCACT 13581
QY 2386 GAGAAATCCAAAGCTGAGAGAGCAAAATTTTGGCTGAGTATGAACACAGCTATAG 2445
Db 13582 CGAATCTGCTGCTCAGCTCCTGAGTGTGAGTATGAGGATGACGATCACCATGCTCC 13641
QY 2446 CATGCTAAAGATGATTTCTAGTAAATTTCTTCCCATAGTGCATATGCACTTCTA 2505
Db 13642 GTTAATTTTATTTTATTTTATTTAGTAAAGCGGTTTC- - - - -ACGTTGTGCCAGAT 13694
QY 2506 GTTCTGTGGCTCGAAATACAGAAATATATAGTAAACAGATACACAAATCTGGGAAA 2565
Db 13695 GGTCTGAACTCTGACCTCAAGTATGACCACTCAGCTCCCAAAATGTGTGG- - - 13751
QY 2566 TATATTTGGTGTGCTGAGAGCTCATTTTCTAAGAAATGTGACCTTAGGAGAGTA 2625
Db 13752 -ATTATAGGTGTAGGACATCGGCTGATGTTTAAAAAGGTGTGATGGGCTGGCG 13810
QY 2626 TGTGTGCTACACTTAATTAATTCAGCACTTTGGAGGCCAATGAAGATGCTTGA 2685
Db 13811 CGGTGTCTATGTCTGTAAATCCAGACATTTGGTAAACGAGCGGGGTGATCAAGGT 13870
QY 2686 CCCAAGGTTCAAGATGAGAGTGGGACATAGCAAGACCTCATCTCTCAAAAAT-TT 2744
Db 13871 --CAGAGATCGAGACATCTCTCAACCGGTGAACCCCGTCTCTCAAAAATACA 13928
QY 2745 AAAAAATCAGCTGAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 2804
Db 13929 AAAAAATTAACAGGATGTTGTTGGGCGCTGTAGTCCAGCTACCTCGGAGGCTAGGCG 13988
QY 2805 GGTGATCGC--TTGACACAGAGTTTGAAGGCTAAGGTGAGCCATGATCAACAATGCA 2862
Db 13989 AGGAGATGCGGTGAACCTGGAGGCGGAGCTTGACAGTAGCCGAGATCAACGCACTGTA 14048

QY 2863 CTCAGCTTGAGTACAGAGAGACCTGTCTCTAATAAAGAAAGAAATGTGATTTA 2922
Db 14049 CTCAGCTTGAGTACAGAGAGACCTGTCTCTAATAAAGAAAGAAATGTGATTTA 14108
QY 2923 TTCCTTAGACAGTACAGTATGATCATTAAGTTTG 2958
Db 14109 AGGTTTGGCTTATAGTCAAGGTGTTAACTTG 14144

RESULT 9
US-09-875-114-2
; Sequence 2, Application US/09875114
; Patent No. 6670333
; GENERAL INFORMATION:
; APPLICANT: No. 6670333chwestern University
; APPLICANT: No. 66703331 Bouck
; APPLICANT: David Dawson
; APPLICANT: Paul Gilis
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
; FILE REFERENCE: 0290-2302
; CURRENT APPLICATION NUMBER: US/09/875,114
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 08/899,304
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 22484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1...22484
; OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-114-2

Query Match 4.9%; Score 306; DB 4; Length 22484;
Best Local Similarity 55.8%; Pred. No. 3e-62;
Matches 756; Conservative 0; Mismatches 575; Indels 25; Gaps 8;

QY 1614 TCAAGAGTTTCAGATCGGCGCGCGGTGCTCAACGCTGTAAATCCAGACATTTGGG 1673
Db 12803 TTAAGACTGACAGTGAAGGCGCGGCGGTGCTCAACGCTGTAAATCCAGACATTTGGG 12862
QY 1674 AGCCGAGGCGGCGGTGATCAACAAGGTCAAGAGATCAACCACTCTGTTAAACAGGTGA 1733
Db 12863 AGGTGAGGTGGGTGATCAACAAGGTCAAGAGATCAACCACTCTGTTAAACAGGTGA 12922
QY 1734 AACCCGCTCTCACAAAAAATTAATAATTAAGCAGGCGTGTGGCGGCTGTAGT 1793
Db 12923 AACCCGCTCTCACAAAAAATTAATAATTAAGCAGGCGTGTGGCGGCTGTAGT 12982
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Db 12983 CCCAGCTACTCAGAGAGGCTGAGGACAGAGATGCGGTGAACCCGGAGGTAGAGTTGC 13042
QY 1853 GTGAGCCGAGATGCGCGCACTGCGCTCCAGCTGGGGAGACAGAGTGAAGATCTGGCTCMA 1912
Db 13043 GTGAGCTGAGCTGCACTGCACTCCAGCTGGGGAGACAGAGTGAAGATCTGGCTCMA 13102
QY 1913 AAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACATGCACTTTTCAACAGTCTAG 1972
Db 13103 AAAAAAAAAAAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 13162
QY 1973 AATAGAGAGCATGTTACAGAGAGAGAAATGTTTTCAGAAAAGTACAGAGTAGGAAA 2032
Db 13163 TTGAGAGCAGAGTCTCCTCATCACCAGTGTGAGTACAGAGTGTGCGATCTTGGCTCA 13222

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QY 2033 TAGAGATATGTTCAAGAAAGAGACCCAGAGTACGTGTTGT-----TAGGGTAA 2085
DB 13223 CTGCAATCTTGGCTCTCTGAGTTCAACCAATCTCAGCTCCCAATACCTG 13282
QY 2086 AGGAAACACAGTGTGTTGCAATCTCAAGGTTCCATTAGTGCCTTAATATATG 2145
DB 13283 GACACAGGACGTGACCAACCCCAAGCTAATTTTGGGTATTTTGTAGATG 13342
QY 2146 GGTAAAGCACTGATTTTAAATAATGAATGAAGAAAGAAATAGAAATAT 2205
DB 13343 GCCTCAACATGTTGTCAGGTTGTGTAACCTCAGAGTCAAGATCAATCTTC 13402
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QY 2266 ACTGATATATATTTTATGATGATGATGAATACAGATATATATATTTCTA 2325
DB 13462 TATTTATATTTTATTTTATTTTACTTATTTTATTTTGAAGAGGTTCTA 13521
QY 2326 AGACTGCACTCAAAAATCTTTAAAGCACTGCTGCTTAACTCTTATTTTGA 2385
DB 13522 CAGGCTGAGTACAGTGGCACTATCTCAGGTACCTGCAACCTGCTCTG 13581
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DB 13582 CGAATCTGCTGCTCAGCTCTCAGTATGAGTATTAAGGATCACCACCAT 13641
QY 2446 CATTTGCTAAAGATTTCTTAAATTTCTTTCCCACTAGTGCATCTGCACT 2505
DB 13642 GTTAATTTTGTATTTTATTTTATTTAGAGAGGGTTTC-----AC 13694
QY 2506 GTTCTGTTGGCTGAAATACAGATATATTTATGAAACAGCATACAAAG 2565
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DB 13989 AGAGAGATGCGTGAACCTGTGGAGGAGGCTTGCAGTGAAGCAATC 14048
QY 2863 CTCACGCTGAGTGAAGAGAGAACTGCTCTTAAAGAAAGAAATGTGAT 2922
DB 14049 CTCACGCTGAGGAGAGAGAGCAATCTCGCTCTCAAAAAAAGTGG 14108
QY 2923 TTCCTTGAACAGTACATCTTATGATTAAGTTTG 2958
DB 14109 AGGTTTCGGCTTATAGTCACAAGTGTTTAAACCTG 14144

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RESULT 10
US-08-781-891-79
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Ohshima, Junko

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; APPLICANT: Mulligan, John T.
; APPLICANT: Schellender, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620cemburg Ph. D., Carol
; REGISTRATION NUMBER: 39,317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-781-891-79

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Query Match 4.9%; Score 305; DB 3; Length 87350;
Best Local Similarity 52.6%; Pred. No. 9,9e-62;
Matches 777; Conservative 0; Mismatches 695; Indels 5; Gaps 5;

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QY 458 TTGTACATTTGGAATATATATATGTTTATGTTGAGGCGGCTGCTCAACGCTTAATCCCA 517
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DB 8994 GCACCTTTGGAGCCAGAGCGGGTGGATCCGAGGTCAAGAGATGAGACCATCTGCT 9053
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DB 9114 TGCCTGTATCTCCAGTACTCTGGAGGCTGAGGAGAGAAATGTGTGAACCCAGAGGC 9173
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Db 9413 AGTGTATGATCATAGCTCACTGTAACCTCAAATTCCTGGGCTCAAGCAATTCCTTCC 9472
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Db 9473 TCACCTCAGCTTCCCAAGTACTACAGCATGCACTACAGACCAGATTATTAACAA 9532
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QY 1178 TCGCCGACATGTGAAAGAGAGACAGTAGGCAAGAGATTGAAGATTATCAAGA 1237
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QY 1478 TCAAGGACTTACAGCCAAAACAAGATAGAAATACACACAAATCTATTTATAGAGC 1537
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Db 10132 ATCCGACACTTTGGAGGCGGAGCGGTGATCAAGGTCAAGAGATTAAGAAATC 10191
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QY 1897 TGAGACTGCGTCAAAAAAAAAAAAAAAAAAAAAA 1933
Db 10370 CGACACTCTTGTCTCAAAAAAAAAAAAAA 10406

RESULT 11
US-09-618-166-79
; Sequence 79, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui
Yu, Chang-Bn
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McNameister, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79
Query Match 4.9%; Score 305; DB 4; Length 87350;
Best Local Similarity 52.6%; Pred. No. 9.9e-62;
Matches 777; Conservative 0; Mismatches 695; Indels 5; Gaps 5;
QY 458 TTGTACATTTGGAATATATTAATTTAGTTGTAGCTGCGCGGCTGCTACGCTGTATCCCA 517
Db 8934 TGGAAATATTTCTTAAATACTATGATATTTGGCCGGGTCAGTGGCTCATCCTGTATCCCA 8993
QY 518 GCCCTTTGGAGGCGCAGAGTGGGAGATCATGAGGTCAAGATTGAGCCAGCCTAGCC 577
Db 8994 GCACCTTTGGAGGCGCAGAGCGGAGGTGATCCGAGGTCAAGAGATCAAGACCATCTGGCT 9053
QY 578 AACATGTGAACCCCGTCTCTACTTAAAGATACAAAAATTAAGCCAGGTGTGTGGCCGA 637
Db 9054 AACATGATGAACCGCGTCTCTACTTAAATAATTAAGCCAGGTGTGTGGCCGAG 9113
QY 638 CACCTGTAAACCCAGCTCTCTGAGAGATGAGGAGAGGAATTTGTTAAACCCAGAGGC 697
Db 9114 TGCCTGTATCCCACTACTCTGGAGGCTGAGGAGGAGGAATGTGTAAACCCAGAGGC 9173
QY 698 AAGAGTGCAGAGAGCAAGATCAACCAATGCACTGTAGCTGTGATGACAGGCAAGACT 757
Db 9174 GGAAGTTGCAAGTGAAGCCAGATCTGTGCCACTGCACTCCAGCTTGAGCAACAGCAGACT 9233
QY 758 CCAACTCAAAAAAAAAAAAAAAAAAAATATATTAAGTTGTCTATTAACAATTAATAGG 817
Db 9234 CTGTCTCAAAAAAAAAACCAACCACTGAACCAAAAAAAAACTAATAAAAAA 9293
QY 818 CAGTGAGAGCAAGTGTATAAGCTATGACCAATGATTAAGTAATTAATTAATTAATTAATTA 877
Db 9294 AACTATGTATTAAGCATGGTGTGGCAACTATAGGCTGTAGAGCAAAATCTGATGCTGTT 9353
QY 878 ATAAATTAAGGAACCTAACCCAGTCTTGGAGTAAGTTTGGAAAGAAATGTTTGAAGAC 937

[illegible]

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US-08-520-373D-4
: Sequence 4, Application US/08520373D
: Patent No. 6451763;
: GENERAL INFORMATION:
: APPLICANT: Tombran-Tink, Joyce
: APPLICANT: Steele, Fintan R
: APPLICANT: Chader, Gerald J
: APPLICANT: Beeceira, Sofia P
: APPLICANT: Johnson, Lincoln V
: APPLICANT: Rodriguez, Ignacio R
: TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
: FILE REFERENCE: 2026-4203U51
: CURRENT APPLICATION NUMBER: US/08/520,373D
: PRIOR FILING DATE: 1995-08-29
: PRIOR APPLICATION NUMBER: 08/377,710
: PRIOR FILING DATE: 1995-01-25
: PRIOR APPLICATION NUMBER: 08/279,979
: PRIOR FILING DATE: 1994-07-25
: PRIOR APPLICATION NUMBER: 07/894,215
: PRIOR FILING DATE: 1992-06-04
: PRIOR APPLICATION NUMBER: 07/952,796
: PRIOR FILING DATE: 1992-09-24
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 14581
: TYPE: DNA
: ORGANISM: HUMAN
: FEATURE:
: OTHER INFORMATION: mRNA: 6683; EXON: 6683-6790; EXON 11584-11675;
: OTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON:
: OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
: US-08-520-373D-4

Query Match          4.9%; Score 304.4; DB 4; Length 14581;
Best Local Similarity 55.7%; Pred. No. 5,8e-62;
Matches 755; Conservative 0; Mismatches 576; Indels 25; Gaps 8;

OY 1614 TCAGAAAGTTTCAGANTGCGCGGCGGGGCTCTACAGCGCTGTAATCCACAGCACTTTGGG 1673
DB 12814 TTAAGACTGCAAGTAGAGGGGCGCGGGCGGTGCTCACGCTGTAAATCCACAGCACTTTGGG 12872

OY 1674 AGCGCGAGGGGGGTGATCTCAAGGTTCAGGAGATCAAGACCAATCCGTGTTAAACAGGGTGA 1733
DB 12874 AGGTGGAGGGGGGTGATCTCAAGGTTCAGGAGATCAAGACCAATCCGTGTTAAACAGGGTGA 12933

OY 1734 AACCCGCTCTCTACAAATAATTAATAAAATTAAGCCAGGCGGTGGCGGGCGCTGTAGT 1793
DB 12934 AACCCGCTCTCTACTAATAAATTAATAAAATTAAGCTGGGTGTGTGGGGGGCGCTGTAGT 12999

OY 1794 CCAGCTACTCAGAGGGCTGAGGCGAGGAGAGATGGCGGTGAACCCGGAGGTGAGTTGGC- 1852
DB 12994 CCAGCTACTCAGGAGGGCTGAGGCGAGGAGAGATGGCGGTGAACCCGGAGGTGAGTTGCA 13055

OY 1853 GTGAGCGGAGATGGCGGCACTGGCGCTTCAGGCTGGGGCGACAGAGTGAAGTGGCTTCAA 1912
DB 13054 GTGAGCTGAAGCTGGCGACCACTGCACTTCAGGCTGGGGCGACAGAGTGAAGTCCGCTTCAA 13111

OY 1913 AAAAAAAAAAAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACACTGCAGATTTCACACGCTGAG 1972
DB 13114 AAAAAAAAAAAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 13177

OY 1973 AATAGAGAGCATGTTATCAGAGGAGAGAAATGTTTTCAGCAAAAGTATCAGAGTAGGGA 2032
DB 13174 TTAGAGACAGAGTCTCATCTCCATCAACCAAGCTGAGATACAGAGGTGCGATCTTTGGCTCA 13233

OY 2033 TAGAGATATGTTTCAGAGAAAGAGACCCCAAGATCATGTTTTGT-----TAGGGTTAG 2085
DB 13234 CTGCAATCTTGGGCTCTCTGAGTTCAACCAATTCATGCTCAGCCTCCCAATTAAGCTGG 13299

OY 2086 AGGAAACACAGTGTTTTGCATATCCAGAGTTTCATTAGTGTGCTTATGAATCAATCAATGGT 2145
DB 13294 GACCAACAGGACATGTCACCAAGCCCAAGCTAATTTTTTTGGGTATTTTTTATGTAAGATGGG 13355

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QY	2146	GGTTAGGCAACCTGCATTTTAAAAATGAAATTAATGATGAGAGAGAAATTAATTT	2205
Db	13354	GCCTCACCATTTGCTCAGGTGGCTGMAACTCTGAGCTCAAGTATCATCTTCTC	13411
QY	2206	AGCATGCATTAATTTTGAAGAGCAAGTATTTATTTCTGCAACTTTTGGCTCAATTGTA	2265
Db	13414	GGCCTGCG - CAAAGTCTGGGGATTATAGGCATTAACCACTGCACCTTCCCAATTTT	13472
QY	2266	ACGTGACTTAATTTTATGATAGATGTGAATACAGATATACATATATTTCTACTGT	2325
Db	13473	TATTTATATTTATTTTATTTTACTTATTTATTTTGAACAAGGCTCTCATCTGTACCC	13531
QY	2326	AGACTGCAGTCAAAAAATCTTTAAAGCACTGGCTGTAACTTCTTATTTTGGCAGAG	2385
Db	13533	CAGGCTGGAGTACAGTGGCACTATCTAGCTCACTGCAACCTCTGCTCTGGGTTCAAG	13592
QY	2386	GAGAAATTCAGAGATCTGAGAGACAAATTTTGGCTGAGGTATATGAACCAAGCTTAATGC	2445
Db	13593	CGAATCTCGTGGCTCAGGCTCTGAGTGTGGGATTACAGGATGCAACCATGCCCC	13655
QY	2446	CATTCGTAAGATGATCTTAGTAAATTTCTTCCACTAGTGCCATCTGCACTTTCTA	2505
Db	13653	GTTAATTTTTTTTGTATTTTATAGAAACGGGTTTCT-----ACGCTGTGGCCAGGAT	13708
QY	2506	GTTCCTGTGGCCTCAAAATATACGAATATATTATAGTAAACAGCATATACAAGTCTGGGAAA	2565
Db	13706	GGTCTCGAATCTCGACCTCAAGATTTCAACCACTCAGCTCTCCAAAGTGTCTGG--	13766
QY	2566	TATATGGGTATGCTGCTGAGAGCTCATTTTCTAAGAAATGTGAACCTTAGGCAAGGTA	2625
Db	13763	-ATTATAGTGTGAGCACACTCGCTGATGGTTTTTAAAAAGTGGGTATGGGCTGGCG	13822
QY	2626	TGTTGGCTCACACCTATATTTCCAGCATTTTGGAGGCCAAGTCAAGAAATGCTTTGAA	2685
Db	13822	CGGTGGCTCATGCTGTATATCCAGCATTTTGTGTAGTCCAGAGCGGGTGTATCAAAAGT	13881
QY	2686	CCCAAGATTCAGACATGAGATGGGCAACATAGCAAGACCTCATCTCTACAAAAAAT-TT	2744
Db	13882	--CAGGAGATCGAACAACATCCTGCTTAACAAGGTGAACCCCGCTCTACTTAAAAATACA	13933
QY	2745	AAAAATCAGCTGAGCATGTGTGGCATACGCTGTATGTCCACTTACTCGGAGACTTAGTG	2804
Db	13940	AAAAATTAACCAAGGCATGTGTGTGGCGCTGTATGTCCAGCTACTCGGAGGCTGAGGC	13993
QY	2805	GGTGGATCGC--TTGACACAGAGATTTGAAGCTTAAGGTGAGCATATATCAACAATGCA	2862
Db	14000	AGGAGATATGCGGTATACCTTGGAGGCGGAGCTTGCACTGAGCCGAGATCATCGCACCGTA	14055
QY	2863	CTTCAGGCTTAGTGTACAGAGAGAAAGACCTGTCTCTTAAAAAAGAAATGTGATTTT	2922
Db	14060	CTTCAGGCTTAGGCGACAGAGGAGAGATCTCGCTCAAAAAAAGGAGGATCTCAT	14119
QY	2923	TTCTTTAGACATGATCACTATTAGTCAATTAAAGTTTG	2958
Db	14120	AGGTTTGGCTTATAGGTCACAAGTGTTTAAACCTG	14155
RESULT 13			
US-09-544-398B-8			
Sequence 8, Application US/09544398B			
Patent No. 6770461			
GENERAL INFORMATION:			
APPLICANT: Carulli, John P.			
APPLICANT: Little, Randall D.			
APPLICANT: Recker, Robert R.			
APPLICANT: Johnson, Mark L.			
TITLE OF INVENTION: High bone mass gene of 11q13.3			
FILE REFERENCE: 032796-013			
CURRENT APPLICATION NUMBER: US/09/544,398B			
CURRENT FILING DATE: 2002-06-10			
PRIOR APPLICATION NUMBER: US 09/229,319			
PRIOR FILING DATE: 1999-01-13			

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; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739), (33749), (33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-544-398B-8

Query Match      4.8%; Score 296.8; DB 4; Length 33769;
Best Local Similarity 55.3%; Pred. No. 5,6e-60;
Matches 823; Conservative 0; Mismatches 622; Indels 43; Gaps 11;

QY 486 GCCTGGCCCGGTGCTCAAGCCTGTATATCCAGCCCTTTGAGAGGCGAGAGTGGCGAGAT 545
Db 20381 GCCGGGTGCGGTGGCTCAAGCCTGTATATCCAGCATCTGGAGGCCGAGGGGAAGATCC 20440

QY 546 CATGAGGTTCAGGAGTTTGGAGCCAGCTTAGCCAACTGTGTAAACCCCGTCTTACTTAAA 605
Db 20441 CTTGAGCTTAGGAGTTTGAAGCAGACCTGAGCAACAT-GTGAAACCCCGTCTTACCAA 20499

QY 606 GATACAAATAATTACCGAGTGTGGGCGACACCTGTAAACCCGAGTCTCGAGAGAG 665
Db 20500 AATAC-AAAAATTAGCCAGGTGTGGTGGCGACTCTGTATGTCCAGACTCTGGAGGC 20558

QY 666 TGAGCGAGAGAAATTGCTTGAACCCAGAGGCAAGG-TGACGCGACAAAGATCACACC 724
Db 20559 TGAGCGCGAGAGATGCTTGAAGCTGGAGGTGGGGGCTGCAGTGAGTGAATTAATGAC 20618

QY 725 AATGACGTGTAGCCCTGGATGACAGGGCAAGACTCCAACTCAAAAAAAAAAAAA--AAAAA 782
Db 20619 AATGACATTCAGCCTGGGTGAAGAGTGAGACTCTGTCTCAAAAAAAAACAAGTTTAAAAA 20678

QY 783 GAAATATGTAAATTGTGTCTATTAACAATAATATAGGCAGTGAAGAGCAAAAGTGTAAAGC 842
Db 20679 AAAAAAATGTGATGATGGGTGTGGCTACAGATAGTCTTTTGCCCTTACTTAGAATGAAC 20738

QY 843 TATGACCATGTGTAAGTACTGTGTGGAACATATATAGGGAACCTTAACCCAGTCC 902
Db 20739 GTGCCACATTTGTCTATTAAGAAATTTCAAGGGCTGTGTGGCAAAATGCCACAGACCTGAC 20798

QY 903 TGGAAGTAGGTTTGGAAAGGAATGTTT-----GAGCAAAAGGGTTTAAAGAGA----- 952
Db 20799 GCTGTCCAAATTTCTGAAGAAGTCTCGCATTCCTCAGGGGCCAGAAATTTTCAGAGAAGAT 20858

QY 953 -----GTGAAAAAAAAAATTTAAATATCCAGTTTAGCTGTGTGAGAAATGGGATAGGAG 1006
Db 20859 CTGTAGGCTGTAGTTAAGAGGAAGCAGCTTCAAAAGCCCTGGGGGCAAAAGGGGAAAGGGG 20918

QY 1007 CTAATCTAGAGAAATCAATATAGGAATGTTTCATGATATGTTAAGGACCCCTGTGTAAGGGTGA 1066
Db 20919 TGCCCAAG--GACTGCGGTGGTACTTACCGGAAGAGCGCTTCAGATGGGACAGGTGGA 20975

QY 1067 AGACCATTTACATTAATCTGACCATCGCGGAGCTTTTATTTTATATGTTATGCTTGGCAAT 1126
Db 20976 TGAAGCTGAGCTTGCGCTCAGGCCAGTAGAGCTTCTGCTCTCCAGATGATGTCAATC 21035

QY 1127 TAAATAGAGGACAGAGAAATGTAGCACTTGTGATGTGATCAAGTTGAAATTTGTGCCAGA 1186
Db 21036 CATTGGGCGAATTAATGTCCAGTCCACAAATGATCTTCCGAGTGTCCATCATCATCTTG 21095

QY 1187 CATGTGAAAGAAAGAGACAGGTAGGCAAGAGAGTTGAAGAGATTATCAAGACAGAAAGTTA 1246
Db 21096 CCGCTCAATCCGGGGCGCTCTCACCCAGTCTGTCCAGTACATGTACTGTGACGGGGGC 21155

QY 1247 ATGTGCTGGCCAGTGGCATCTA-----GTCTGAGTCTAATCTGAGGAAAGAAATG 1297

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Db 21156 AGGCGAAGAGAGAGGCTAACACAGATCTGTTTCTTTTGTCTGATATGACGAC 21215
Qy 1298 AAGTAAAGCAGCTTCTGATATGTTATGAGAAGAGTGAAGGCTTCAAGACCTACAGGTG 1357
Db 21216 ATGAAACAAAGACAGTGAACCTTCGCCCTAAATCTCAACCCATCGGAAATACCAACAGGT 21275
Qy 1358 TTGATTAATATGAAGAAATGATTTGGAGAAAGATTAATCTGTGAGAGAGTGAAGTTTTCAGGC 1417
Db 21276 ATGGTTTCAGGATATCTCGCTTAAGCTGGCAATCAAAATATATCTATTTTCCACTTGT 21335
Qy 1418 TTGAGTACTCTCATATACAGACACTGTGTGTAATGCTTCAAGACATGATCCCTGCC 1477
Db 21336 CTCAGTTAAACAGTAAATTTCTGGGACCTTCCTCTTGTGATGAGAAAGATTTCTTGTTC 21395
Qy 1478 TCAAGGACCTTACAGCCAAAACAAAGATTAAGAAATACACACCAATAC---TATTTATA 1533
Db 21396 TTTTGTGATGATTCCTAGTGTACTCTGCTGTMAAGTTTAAAGAACTTCAGGTATTTCT 21455
Qy 1534 GGCACCTGTGTAGAAATATCAAGAAAGAAATACATCTAGTATCTGATCTGAC--- 1590
Db 21456 GATTTTGTGCTACATGAAGAAATGCTGTAAATGAACCTTAAAGGCAATTCAAAACACT 21515
Qy 1591 --GGCATCAAGATATCTTCTAGTTTCAAGAAAGTTTCAGATCGGCGGGCGGTGGCTC 1648
Db 21516 CAGGATGGAATATTTATTTAGTGTATTAAGAAATGAGCTATCGCTGGGCCAGTGGCTC 21575
Qy 1649 ACCGCTGTAAATCCAGACATTTGGAGAGCCGAGCGGGTGTATCAAGAGTCAGAGATC 1708
Db 21576 ACACCTCTAATCCAGACATTTGGAGAGCCAGCGGGTGTATCAAGAGGTGGGAGATC 21635
Qy 1709 AAGACCATCTGTGTTAAACGCTGTAACCCCTGTCTTACAAAATATTAATAATTTAGCC 1768
Db 21636 AAGCCATCTCTGTGTTAAACAGTGAACCCCTGTCTTAAATAATCAAAACATTAGCC 21695
Qy 1769 AGGAGTGTGGCGGGCGCTGTAGTCCAGCTACTCAGGAGGCTGAGGCGAGAGAAATGCG 1828
Db 21696 AGGGTGTGTGTGACACCTGTAGTCCAGCTACTTGAAGAGCTGAGGCGAGAGAAATCAT 21755
Qy 1829 GTGAAACCGGAGAGTGAAGTTTGC-GTGAGCCGAGATCGCGCACTCGCTCCAGCTGG 1887
Db 21756 TTGAACCCGGGAGGGGAGAGTGTGACGTGAGAGAAATCGACCATTTGCACTCTCTGG 21815
Qy 1888 GCGACAGAGTGAAGCTGCTCTCAAAAAAAAAAAAAAAAAAAAAAG 1935
Db 21816 GCGACAGAGGAGACTCCATCTCAAAAAAAAAAAAAAAAAAGAAAG 21863

RESULT 14
US-09-543-771-8
Sequence 8, Application US/09543771
Patent No. 6780609
GENERAL INFORMATION:
APPLICANT: John P. Canulli et al.
TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
FILE REFERENCE: 032796-013
CURRENT APPLICATION NUMBER: US/09/543, 771
CURRENT FILING DATE: 2000-04-05
EARLIER APPLICATION NUMBER: US 09/229, 319
EARLIER FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: US 60/071, 449
EARLIER FILING DATE: 1998-01-13
EARLIER APPLICATION NUMBER: US 60/105, 511
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 8
LENGTH: 33769
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unaurc
LOCATION: (33739), (33749), (33758)
OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown

Query Match	Best Local Similarity	Score	DR	Length
Matches 823; Conservative	55.3%	296.8	4	33769
		Prid. No. 5,6e-60		
		Mismatches 622; Indels 43; Gaps 11		
Qy	486	GCCCTGGCGCGGTGGCTCAAGCCTGTAAATCCCAAGCCTTTGGAGGCGAGAGTGGCAGAT	545	
Db	20381	GCCGGGTGGGTGGCTCAAGCCTGTAAATCCCAAGCCTTTGGAGGCGAGAGTGGCAGAT	20440	
Qy	546	CATGAGCTGAGAGTTTGAGACCAGCCTAAGCCAACTGGTGAACCCCGTCTTACTAA	605	
Db	20441	CTTGAGCTTGAAGTTTGAGACCAGCCTGAGCAACAT-GTGAAGCCCGCTCTTACCAA	20499	
Qy	606	GATTCACAAAATTAAGCAGGTGTGTGGGCGACACTGTAAACCCAGCTCTCGAGAGG	665	
Db	20500	AATATC-AAAAATTAGCAGGTGTGTGGGCGACACTCTGTATGTCCTCAGCTAATCCGAGGCG	20558	
Qy	666	TGAGGCGAGAGATTGCTTGAACCCAGAGGCGAGAGG-TGACGCGAGCAAGATCAACC	724	
Db	20559	TGAGGCGAGAGATTGCTTGAACCCAGAGGCGAGAGG-TGACGCGAGCTGAGATTATGAC	20618	
Qy	725	AATGCACTGTAGCCTGATGACAGGCGCAAGACTCAACTCAAAAAA-AAAAA	782	
Db	20619	ATTGCACTCCAGCTGGGTGAAGAATGAGACTGTGTCTCAAAAAAAGATTAAGAA	20678	
Qy	783	GAATATGTAAAGTTGTGCTATTAACAAATTAATAGGAGTGAAGCAAAAGTCTAAAGC	842	
Db	20679	AAAAAAATGTGATGGGTGTGGGCTACAGATAGTCTTTTCTGCTTAAATGAAC	20738	
Qy	843	TATGACATGTGTAACTAGAAATCTGTGGGAACACATATTAAGGAACCTAACCCAGTGC	902	
Db	20739	GTGCCACATTTGCTATTAAGAAATTTAAAGGCGCTGTGGCAAAATGCGACACAGCCTGAC	20798	
Qy	903	TGAAAGTAAGTTTGGAAAGAAATGTTT-----GAGACAAAGGTTTAAAGG-----	952	
Db	20799	GCTGTTCCAAAGTTCTGAAGAGTCTGTGATTTCTCAGAGGCCCAAGATTTCAAGAAAGAT	20855	
Qy	953	-----GTGAAAAAATAAATAATACAGTTTACGTGTGTGAGAAATGGGATAGGAG	1006	
Db	20859	CTGAGAGCCTGAATTAAGAAAGAACGCTTCAAAAGCCCTGGGGGAACAAAGGGAAAGGGG	20918	
Qy	1007	CTAACTAGAGAAATCAAATAGGAATTTTTCATGTGTATTTAAAGAACCTTGTAAAGGTGA	1066	
Db	20919	TGCCCCAG---GACTCGTGTGTGTACTTAACCGAACAGGCCCTGCAGTTGGCAGCGTGA	20979	
Qy	1067	AGACATTTACATTAATGTGACCAATGGCGGGAATTTTTTTTAAATGTAAATGCTTGGCAAT	1126	
Db	20976	TGAAGCTGAGCTTGGGTGACGCCCAATGAAGCTTTCTGCTCTTCAGAGTGTATGATGTC	21033	
Qy	1127	TAAATAGAGAGCAGAGAAATGTAGACAGTTGATTTGAGTCAAGATTTGAAGTTCTGCACA	1186	
Db	21036	CATTTGGGCCAGTAATATGTCAGATCCACATATATCTTCCGGGGTGGCGCATCATCTCGT	21099	
Qy	1187	CATGTGAAGAAAGAGACAGATAGGCAAGAGATTGAAGATTTCAAGACAAAGTTTA	1246	
Db	21096	CCCGCTCAATCCCGGGCGTCTCACCCCACTGTCCAGATCAATGTACTCTGTACCGGGCG	21155	
Qy	1247	ATGTGCTGCGCAATGGCATCTA-----GTCTGAGTCTAATCTGAGGAGGAAGT	1297	
Db	21156	AGGCAAGAGAACACATCAACAGATCTGTTTTTGTGTTTGTCTGCAATGATGAGAC	21215	
Qy	1298	AAGATTAAGCAGCTTGTGATAGTTATGAAGAGATGGAAGGCTTCAAGACCTACAGTGC	1357	
Db	21216	ATGAAACACACAGCAGTGAATTTGCCCTTAAATCTCACCCATCGGAAATACCAACAGT	21279	
Qy	1358	TTGATTTAAATGAAGATATTTGAGAAAGAAATTAATCTGTGAGAGATGATTTTCAAGC	1417	
Db	21276	ATGTGTTTCAAGTATTTCTGCTTAAGCTGGGCAATCAAAATATTAATTTTCAACTGTT	21339	
Qy	1418	TTTGAAGTCTCTCACTACACACCTGTGTCTAAATGCTTCAAAAGACATGATCCCTGCCC	1477	
Db	21336	CTCAGTTAACAGTAATTTCTGGGCACTTTCCTTCTTGTGATATGAAGAAATTTCTTGTTC	21399	


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: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 59235
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 59242
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 63290
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 66614
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 68660
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 68697
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 68718
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 68733
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 68739
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 69785
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 79134
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 79198
:
: OTHER INFORMATION: unknown
: NAME/KEY: unsure
: LOCATION: 86336
:
: OTHER INFORMATION: unknown
:
:
: JS-09-791-211-3

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Query Match	4.7%	Score 291.6	DB 4	Length 87543
Best Local Similarity	52.0%	Pred. No. 1.5e-58		
Matches 769	Conservative	0	Mismatches 704	Indels 5
Gaps				
QY	458	TTGTACATTTGGAAATATATTAAGTTGTTAGCTGTGGCCGCGGTGACTACCGCTGTATCCCA	517	
Db	9124	TGGAATATTTCTAAAAAATAATATATATATGGCCGGGGTGCAGTGGCTATATGCTGTATATCCCA	9185	
QY	518	GCCCTTTGGAGGCCAGAGTGGGCGAGATCATAGGTGAGAGTTTGAGACCAAGCTTAACC	577	
Db	9184	GCACCTTTGGAGGCCAGAGCGGGGTGTGATCCGAGGTGAGAGATGAGACCATCTCTGCT	9243	
QY	578	AACATGTGTAAACCCCGTCTCTACTATAAAGATACAAAAATTBAGCCAGTGTGTGGCGCA	637	
Db	9244	AACATGTGTAAACCGCGTCTCTACTATAAATAACAAAAATTBAGCCGAGTGTGTGGCGAG	9303	
QY	638	CACCTGTATCCCGACGTGCTGAGAGATGAGAGCGAGAAATTGCTTAAACCCAGAGAGC	697	
Db	9304	TGCTGTATGTCCTCCAGCTACTCGGGAGGCTGAGGCGAGAAATGTGTAAACCCAGAGAGC	9365	
QY	698	AGAG-GTGCAGCGAGCAAGATTCACACCAATGCACTTGAGCTTGATGACAGGGCAAGC	756	
Db	9364	GGAAGTTCAGATGAGCCGAGATCTGGCACTGTCACTCCAGCTTGGGCAACGAGGCGAGC	9422	
QY	757	TCCAACCTCAAAAAAAAAAAAAAAAAAGAAATATGTATGTTGTCTATTAACAAATTAATAG	816	
Db	9424	TCTGTCTCAAAAAAAAAAACCAACCACTGAAACAAACAAAAAACTAAAAAAAAACAAAAACAAA	9483	
QY	817	GCAGTGAGAGCAAGTCTTAAGCTTATGACCATGTGTAACTAGAAATCTGTGGAAACA	876	

Dh	9484	AAACTATGATATAGACATGGGTTGGCAAACTATAGGCTGTGAGGCCAAATCTGCATGCTG	9543
Oy	877	CATATATAGGGAACCTTAAACCAGTCTCTGGAAAGTAAAGTTTGGAAAGAAATGTTTGAGA	936
Dh	9544	TTTTATATTTTTTATATTTTTTGAACATAGGGGTCACTACAGGCTGTCAACAGGGCTGGAGAG	9603
Oy	937	CAAAAGGGTTAAAGAGATGAAAAAAAATTTAAATTAACAGTTTAAAGCTGTGTGGAGAATG	996
Dh	9604	CAGTGGTATATGATCTATAGCTCACTGTAACTTCAAAATTCCTGGGCTCAAGCAATTTCTTTC	9663
Oy	997	GGATAGGAGATAACTAGAGAAATCAATATGAAATGTTTCATGGTATGTTAAGAACCTG	1056
Dh	9664	CTCACTCAGTTCCTCCAAAGTATGCTACAGGATGCACTACCAAGACCAGTTAATTAATAACA	9723
Oy	1057	GTAAGGGTGAAGACCATTTACATTATCTGCACCATCGGGGACTTTTTTTTATGCTAATG	1116
Dh	9724	AATTTTTTTTTTGGTAGAGACAGTCTCAGTATGTTTCCAGGCTGGTTTTTCAATCTCTTG	9783
Oy	1117	CTTGGCAATTTAAATTAAGAGACAGAAATGTAACAGTTGGATGATGTCAGATTTGAAG	1176
Dh	9784	CCTCAATCAAGTCTCTCACTTCAAGCTCTTAAGATGCTGGATATATAGGCTTGAGCATC	9843
Oy	1177	TTCTGCAGACATGTGAAAGGAAGAGAACAAGTAAAGAGATGTAAGATTTATCAAG	1236
Dh	9844	ACGCTTGACATATGTTTTTTGTAAATAAAGTTTTCTCAGAACACAGCCATGCTTTGT	9903
Oy	1237	ACAGAACTTAATGTGCTGGCCAGTGGCATCTAGTCTGAGTCTAATCTGAGGGAAGAACT	1296
Dh	9904	ATGTTTATGATAGGGCT-GCCTGAGTTAAGATGTGGCTCAAAAGCTATCATGCGCTAT	9962
Oy	1297	GAAGATTAAGCAGCTTGCTGATAGTTATGAAAGATGTAAGGCTTCAAGAACCTACACGT	1356
Dh	9963	AAAGCCTGAATACTTATCTATCTGAGTCTTTATTAAGAAAGTGTTCGACCTGTACTAG	1002
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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	334.4	5.4	31474	10	US-09-764-891-8149	Sequence 8149, App
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17	333.4	5.4	104245	16	US-10-655-847-4	Sequence 4, Appl1
18	333.4	5.4	170245	17	US-10-717-597-322	Sequence 322, App
19	331	5.3	506	14	US-10-066-543-1709	Sequence 1709, App
20	331	5.3	549	14	US-10-066-543-194	Sequence 194, App
21	330.6	5.3	164875	15	US-10-085-117-322	Sequence 322, App
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45	313.4	5.1	32191	15	US-10-074-024-446	Sequence 446, App

ALIGNMENTS

RESULT 1	
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; Sequence 3, Application US/09801861	
; Patent No. US02002119544A1	
; GENERAL INFORMATION:	
; APPLICANT: YAN, Chunhua et al.	
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC	
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES	
; FILE REFERENCE: C1001098	
; CURRENT APPLICATION NUMBER: US/09/801,861	
; CURRENT FILING DATE: 2001-03-09	
; NUMBER OF SEQ ID NOS: 10	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 3	
; LENGTH: 53332	
; TYPE: DNA	
; ORGANISM: Human	
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Matches 6201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db 24140 TCAGTAATGTGGGAAGGGGCAAGAGCATCCATGCGCATCCAGGCAAGCCCTCA 24199
Qy 4201 GAAAGCTCCATGAGATTCAGATTCAGAAAGTCTGTACCTTAATCTTTCTGGGTTT 4260
Db 24200 GAAAGCTCCATGAGATTCAGATTCAGAAAGTCTGTACCTTAATCTTTCTGGGTTT 24259
Qy 4261 TGCATAGGCTCATATGTGTAGGCAATATTTAAACTATGTGGCCATGTGATCAACTT 4320
Db 24260 TGCATAGGCTCATATGTGTAGGCAATATTTAAACTATGTGGCCATGTGATCAACTT 24319
Qy 4321 AACCTTCAACCCCTCTCCCTCCCTTAATCATGCTGTGTGCTTTCAGTGAACAGTCCCTA 4380
Db 24320 AACCTTCAACCCCTCTCCCTCCCTTAATCATGCTGTGTGCTTTCAGTGAACAGTCCCTA 24379
Qy 4381 TCCTAAGCTAACCAATGTCTGCAAGCTATCAGTCAACTCTACAAAAGACATCACTTTG 4440
Db 24380 TCCTAAGCTAACCAATGTCTGCAAGCTATCAGTCAACTCTACAAAAGACATCACTTTG 24439
Qy 4441 GAGATTTCAAGATTTTAGAGTGTGCTGTCAGAAATTTAGTTGAAGATCAATATATAT 4500
Db 24440 GAGATTTCAAGATTTTAGAGTGTGCTGTCAGAAATTTAGTTGAAGATCAATATATAT 24499
Qy 4501 TTCACAATATCAAGTGTGTATTTATATAGGCGCATTAATATGTTTAAACAAAG 4560
Db 24500 TTCACAATATCAAGTGTGTATTTATATAGGCGCATTAATATGTTTAAACAAAG 24559
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QY 4561 AGGTGATTAATTCAGATTTCTTTTAAAGCTTACAGTATGACAGTGTGTGAATAG 4620
Db 24560 AGGTGATTAATTCAGATTTCTTTTAAAGCTTACAGTATGACAGTGTGTGAATAG 24619
QY 4621 ATTGGATGAGGGGCAATCTTTTGTAAATGTTATATCCCTGACCTTCTC 4680
Db 24620 ATTGGATGAGGGGCAATCTTTTGTAAATGTTATATCCCTGACCTTCTC 24679
QY 4681 CTTGTTTCTTCACTCTCTCCCTACTCAACAAGAAAATCTCTCTCTACTCAT 4740
Db 24680 CTTGTTTCTTCACTCTCTCCCTACTCAACAAGAAAATCTCTCTCTACTCAT 24739
QY 4741 TCCCTGAATGCTGTCTGTAAAGTTCCAGCTTGAAGTGAAGCTTAATCAAGAAC 4800
Db 24740 TCCCTGAATGCTGTGTGTAAAGTTCCAGCTTGAAGTGAAGCTTAATCAAGAAC 24799
QY 4801 AGTGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4860
Db 24800 AGTGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24859
QY 4861 GCCGGAATCTGACGGGAAAAACAAGATCAGCATATTTTCTGTGATCTGATATTTAA 4920
Db 24860 GCCGGAATCTGACGGGAAAAACAAGATCAGCATATTTTCTGTGATCTGATATTTAA 24919
QY 4921 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4980
Db 24920 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24979
QY 4981 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040
Db 24980 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25039
QY 5041 GCTCCAGACTGTGTGGGCTTAAAGTAAAGCAATCTGATGATGATGATGATGATGAT 5100
Db 25040 GCTCCAGACTGTGTGGGCTTAAAGTAAAGCAATCTGATGATGATGATGATGATGAT 25099
QY 5101 AATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160
Db 25100 AATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25159
QY 5161 ATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5220
Db 25160 ATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25219
QY 5221 TTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 5280
Db 25220 TTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 25279
QY 5281 ACCGGAGTCTGCTGCTGCCAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5340
Db 25280 ACCGGAGTCTGCTGCTGCCAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 25339
QY 5341 ACCTCCGCTTCTGCTGCTCAAGGAGCTTCTGCTCAAGCTTCAAGTGAAGTGAAGTGAAG 5400
Db 25340 ACCTCCGCTTCTGCTGCTCAAGGAGCTTCTGCTCAAGCTTCAAGTGAAGTGAAGTGAAG 25399
QY 5401 CAGGCAACCACTCACTGATCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 5460
Db 25400 CAGGCAACCACTCACTGATCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 25459
QY 5461 ATGTGGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5520
Db 25460 ATGTGGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25519
QY 5521 AAAAGTCTGGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5580
Db 25520 AAAAGTCTGGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25579
QY 5581 ATGGGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5640
Db 25580 ATGGGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25639

QY 5641 GCCTGGCTCTCAAAAGTTCTGGATTACATGTGATGCTCCCTGGCCAGAAATAT 5700
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QY 5821 ATGATGCCAAATGCTGCAAAAGATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 5880
Db 25820 ATGATGCCAAATGCTGCAAAAGATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 25879
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Db 25880 GTCATGGGAAACCATGCTTAAACCAATGATGATGATGATGATGATGATGATGATGAT 25939
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QY 6001 GTGTGTGACCAAGGAGTTAGTCTGAAAGTGAATTTGAGAGCAATCATTTGAGCTGA 6060
Db 26000 GTGTGTGACCAAGGAGTTAGTCTGAAAGTGAATTTGAGAGCAATCATTTGAGCTGA 26059
QY 6061 GGTGTGCTGAGCTGTCTCATGACACATGATGATGATGATGATGATGATGATGATGAT 6120
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Db 26180 GAAAGTATGAGAGATGTGG 26200

RESULT 2
US-10-224-562-3
; Sequence 3, Application US/10224562
; Publication No. US20030022229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-562-3

Query Match 100.0%; Score 6201; DB 14; Length 53332;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20000 CACCATGGGCTCAGGCAATTTATGAAAGCAAAATATACAGCTTAAATAGATGTGAC 20059
QY 61 CTAATATCCCAAGAAATCTCCCTTTGTAAGATTTGTAACAAATTAATATGATGAG 120
Db 20060 CTAATATCCCAAGAAATCTCCCTTTGTAAGATTTGTAACAAATTAATATGATGAG 20119

Qy	121	TTAATAGTCTTAATGGAATGCTGAACCCAAAGACATATACAGGCTGTGCAAAATGGCAG	180
Dp	20120	TTTAATAGTTCTTAATGGAATGCTGAACCCAAAGACATATACAGGCTGTGCAAAATGGCAG	2017
Qy	181	ATTCAATATATCATCAAGATTATCCCTTCAGAGCTTCAGCCCTATATGATGCTTAAAGAA	240
Dp	20180	ATTCAATATATCATCAAGATTATCCCTTCAGAGCTTCAGCCCTATATGATGCTTAAAGAA	2023
Qy	241	ATGTGAAACGCGCTCAGCCATCTGAAGACAGTGTTCAGCAATTGATCAAAAAGAAAA	300
Dp	20240	ATGTGAAACGCGCTCAGCCATCTGAAGACAGTGTTCAGCAATTGATCAAAAAGAAAA	2029
Qy	301	CCACAGGCGCTCCCTCCCTCCCACTATCTGATGTAACAGTCTCATTTTCCATAGAGT	360
Dp	20300	CCACAGGCGCTCCCTCCCTCCCACTATCTGATGTAACAGTCTCATTTTCCATAGAGT	2035
Qy	361	AAATTTTCTAGATACAGCTGTAGAGCTCAAAAGTACTGAAAGAAAGAGCTCCCATTCGAA	420
Dp	20360	AAATTTTCTAGATACAGCTGTAGAGCTCAAAAGTACTGAAAGAAAGAGCTCCCATTCGAA	2041
Qy	421	GAAATTTATCTTAAAGATACGTGAATATGATCTAAATTTTGTACATTTGGAAATATATAGT	480
Dp	20420	GAAATTTATCTTAAAGATACGTGAATATGATCTAAATTTTGTACATTTGGAAATATATAGT	2047
Qy	481	TGTAGGCTGGCGGGGGTGGCTCAGCGCTGTATATCCGAGCCCTTTGGAGGCGCAGAGTGG	540
Dp	20480	TGTAGGCTGGCGGGGGTGGCTCAGCGCTGTATATCCGAGCCCTTTGGAGGCGCAGAGTGG	2053
Qy	541	CAGATCATAGAGTACAGAGTTTGAGACAGCTTACGCAATGATGTAACCCCGTCTCTA	600
Dp	20540	CAGATCATAGAGTACAGAGTTTGAGACAGCTTACGCAATGATGTAACCCCGTCTCTA	2059
Qy	601	CTAAAGATACAAAATAATTAAGCAGGTGTGTGGCGCACCTGTATACCCGAGCTGTCTGA	660
Dp	20600	CTAAAGATACAAAATAATTAAGCAGGTGTGTGGCGCACCTGTATACCCGAGCTGTCTGA	2065
Qy	661	GAGGTGAGGCGAGAGAAATGTCTTGAACCCAGAGGCGAGAGGTGCACGACAAAGATCA	720
Dp	20660	GAGGTGAGGCGAGAGAAATGTCTTGAACCCAGAGGCGAGAGGTGCACGACAAAGATCA	2071
Qy	721	CACCAATGCACTGTAGCTGGATGACAGGGCGAGAATCTCCAATCTCAAAAAAAAAAAAAA	780
Dp	20720	CACCAATGCACTGTAGCTGGATGACAGGGCGAGAATCTCCAATCTCAAAAAAAAAAAAAA	2077
Qy	781	AAGAAATATGTAAAGTTGTGCTATTAACAATTAATAGGCACTGAGAAACAAAGTCTTAAG	840
Dp	20780	AAGAAATATGTAAAGTTGTGCTATTAACAATTAATAGGCACTGAGAAACAAAGTCTTAAG	2083
Qy	841	CCTATGACCATGGTAACTAGGAATATCTGTGGAAACATATAAGGGAACCTTAACCACT	900
Dp	20840	CCTATGACCATGGTAACTAGGAATATCTGTGGAAACATATAAGGGAACCTTAACCACT	2089
Qy	901	CTGTGAAGTAAAGTTTGGAAAAGGAATGTTTGAGGACAAAGGGGTTAAAGAGTGAAGAAA	960
Dp	20900	CTGTGAAGTAAAGTTTGGAAAAGGAATGTTTGAGGACAAAGGGGTTAAAGAGTGAAGAAA	2095
Qy	961	AAAAATTTAAATAACAGTTTAACTGTGTGTGAGAAATGGATAGGAGCTTAACAGAGAAAT	1020
Dp	20960	AAAAATTTAAATAACAGTTTAACTGTGTGTGAGAAATGGATAGGAGCTTAACAGAGAAAT	2101
Qy	1021	CAAAATAGGAATGTTTCACTGTGATTTAAAGACCTGTGTAAGGTTGAAGACCATTAACATTA	1080
Dp	21020	CAAAATAGGAATGTTTCACTGTGATTTAAAGACCTGTGTAAGGTTGAAGACCATTAACATTA	2107
Qy	1081	TTCTGCACATGCGGGGACTTTTTTTATGTGTAATGCTTGCCAAATTAATTAAGAGGCA	1140
Dp	21080	TTCTGCACATGCGGGGACTTTTTTTATGTGTAATGCTTGCCAAATTAATTAAGAGGCA	2113
Qy	1141	GAGAAATGTAACAGATTGGAATTAAGTCAAGTTGAAGTTCTGCAGACATGTGAAGAGAG	1200
Dp	21140	GAGAAATGTAACAGATTGGAATTAAGTCAAGTTGAAGTTCTGCAGACATGTGAAGAGAG	2119
Qy	1201	AGACAGGTAGGCAAGAGTTTGAAGAGATTATCAAGACAGAGTTAATGTGCTGGCCAGT	1260

Db	21200	AGACAGGTAAAGCAAGAGTTGAAGAGATTATACAGACAGAAAGTTAATGTGCTGGCCAGT	2125
OY	1261	GGCATTCTAGTCTGAGCTTAATCTGAGGGAAGAAAGTAGAGATTAAGCAGCTTGCTGATAGT	1320
Db	21260	GGCATTCTAGTCTGAGCTTAATCTGAGGGAAGAAAGTAGAGATTAAGCAGCTTGCTGATAGT	2131
OY	1321	TATCAAGAAGTGAAGAGCTTCAAGGACCTACAGAGTGTGAATTAAATAGAAAGATGATTG	1380
Db	21320	TATCAAGAAGTGAAGAGCTTCAAGGACCTACAGAGTGTGAATTAAATAGAAAGATGATTG	2137
OY	1381	GAGAAAGAAATTAACGTGAGAGAGTGAATTTTACAGCTTGAGTGACTCTCACATACCAGA	1440
Db	21380	GAGAAAGAAATTAACGTGAGAGAGTGAATTTTACAGCTTGAGTGACTCTCACATACCAGA	2143
OY	1441	CAGTGTCTAAATGCTTCAAAAGACATGATCCCTGACCCTCAAGGACCTTACAGCCAAAAC	1500
Db	21440	CAGTGTCTAAATGCTTCAAAAGACATGATCCCTGACCCTCAAGGACCTTACAGCCAAAAC	2149
OY	1501	AAGAGATTAAGAAATACACACCAATACATTAATATGAGACACTTGTTGTAGAAATATCAAGAAAG	1560
Db	21500	AAGAGATTAAGAAATACACACCAATACATTAATATGAGACACTTGTTGTAGAAATATCAAGAAAG	2155
OY	1561	AAATACAGATCTAGTACTGTATGATGTGTGCAAGGACATCAAGATATATCTTCTAGTTTCAAGAA	1620
Db	21560	AAATACAGATCTAGTACTGTATGATGTGTGCAAGGACATCAAGATATATCTTCTAGTTTCAAGAA	2161
OY	1621	GTATTCAAGATCGGCGGGCGGGGTGAGCTCAGCGCTGTATCCAGACCTTTGGAGGCGGA	1680
Db	21620	GTATTCAAGATCGGCGGGCGGGGTGAGCTCAGCGCTGTATCCAGACCTTTGGAGGCGGA	2167
OY	1681	GGCGGGTGGATCACAGAGTCAGAGAGATCAAGACATCTCTGTTTAAACCGTGAACCCCG	1740
Db	21680	GGCGGGTGGATCACAGAGTCAGAGAGATCAAGACATCTCTGTTTAAACCGTGAACCCCG	2173
OY	1741	TCTCTACAAAAAATATTAATAAAATTAAGCAGCGCGGTGGGGGCGCTGTATGATCCCACT	1800
Db	21740	TCTCTACAAAAAATATTAATAAAATTAAGCAGCGCGGTGGGGGCGCTGTATGATCCCACT	2179
OY	1801	ACTCAGAGAGCGCTGAGCAGAGAGATGGCTGTAACCCGGAGGTATGAGTTTGCCTGAGCCG	1860
Db	21800	ACTCAGAGAGCGCTGAGCAGAGAGATGGCTGTAACCCGGAGGTATGAGTTTGCCTGAGCCG	2185
OY	1861	AGATCGCGCACTGCGCTCAGCGCTGGGCGACAGAGTGAGACTGCGTCTTCAAAAAA	1920
Db	21860	AGATCGCGCACTGCGCTCAGCGCTGGGCGACAGAGTGAGACTGCGTCTTCAAAAAA	2191
OY	1921	AAAAAAAAAAAAAGTTTCAGATCTTAAACAACCTGATTTTCAACGCTACAGAAATGGAG	1980
Db	21920	AAAAAAAAAAAAAGTTTCAGATCTTAAACAACCTGATTTTCAACGCTACAGAAATGGAG	2197
OY	1981	AGCATGTTTACAGGAGAGAAAATGTTTTACAGAAAGGTACAGAGTAGGAGAAATAGAGAT	2040
Db	21980	AGCATGTTTACAGGAGAGAAAATGTTTTACAGAAAGGTACAGAGTAGGAGAAATAGAGAT	2203
OY	2041	ATGTTTCAAGGAAGAGACCCCAAGTCAATGTTTGTAGGAGTTAGAGAAAACAAGTGT	2100
Db	22040	ATGTTTCAAGGAAGAGACCCCAAGTCAATGTTTGTAGGAGTTAGAGAAAACAAGTGT	2209
OY	2101	TTTGCAATCTCAGGTTCCATTAGTGCGCTTATGAAAATCAATATGTGTGTTAGCAACCTGCA	2160
Db	22100	TTTGCAATCTCAGGTTCCATTAGTGCGCTTATGAAAATCAATATGTGTGTTAGCAACCTGCA	2215
OY	2161	TTTTTAAAAAATGAATAATAGATGAGAGAAGAAATGAAAATATTAAGCATGATTAACATT	2220
Db	22160	TTTTTAAAAAATGAATAATAGATGAGAGAAGAAATGAAAATATTAAGCATGATTAACATT	2221
OY	2221	TTGAAAGAGCAAGTATTAATTTTCTGCAACTTTTGCTCCAAATGTGAACTGTACTTAATATTT	2280
Db	22220	TTGAAAGAGCAAGTATTAATTTTCTGCAACTTTTGCTCCAAATGTGAACTGTACTTAATATTT	2227
OY	2281	TTATGTATGATGTGAATTACCAATACATATATATTTCTTACTGTGACTGCACTGCAATAA	2340

Db 22280 TTATGTATGATGTGATACAGATACATATATTTCTTACTGTAGACTGCAGTCAAAA 22339
QY 2341 AATCTTTAAAGCACTGGCTGTGTCTAACTTCTTATTTTGCAGAGGAAATCCAGATC 2400
Db 22340 AATCTTTAAAGCACTGGCTGTGTCTAACTTCTTATTTTGCAGAGGAAATCCAGATC 22339
QY 2401 TGAAGAGCAAACTTTTGCCTGAGTTATAGAACCGACTTATGCGCTTATGCTTAAAGTGA 2460
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QY 2461 TTTCTTAAATTAATTTCTTCCCACTAGTGCATATGCACTTCTTATTTCTGTTGGCTGA 2520
Db 22460 TTTCTTAAATTAATTTCTTCCCACTAGTGCATATGCACTTCTTATTTCTGTTGGCTGA 22519
QY 2521 AATACGAAATATATATATAGTAAACAGCATACACAAAGTTGGGAAATATATTTGGTATGTTG 2580
Db 22520 AATACGAAATATATATATAGTAAACAGCATACACAAAGTTGGGAAATATATTTGGTATGTTG 22579
QY 2581 GCTGAGAGCTCTATTTTCTAAGAAATGTGACCTTAGGCGAGGGTATGTTGGCTCACACCT 2640
Db 22580 GCTGAGAGCTCTATTTTCTAAGAAATGTGACCTTAGGCGAGGGTATGTTGGCTCACACCT 22639
QY 2641 ATAATTCAGACACTTTTGGAGGCCAAGTCAAGAAATCGCTTGAACCCAGAGTTCAAGA 2700
Db 22640 ATAATTCAGACACTTTTGGAGGCCAAGTCAAGAAATCGCTTGAACCCAGAGTTCAAGA 22699
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Db 22700 CTATGCAATGGGCAACATACGAAAGCTCATCTCTACAAAAATTTTAAATTAATCACTGACGA 22759
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QY 2821 CAGAGTTTGAAGCTTAAGTGAAGCATGATACACAACTGCACTCCAGCTTGAAGTACAG 2880
Db 22820 CAGAGTTTGAAGCTTAAGTGAAGCATGATACACAACTGCACTCCAGCTTGAAGTACAG 22879
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Db 22880 AGGAGAGCCCTGTCCTTAAAGAAAGAAATGTGATTTTATCTTGAACAGTACAGT 22939
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QY 3001 GTGTGCTGTAGATATATGAAAGAAATTAAGACATAGAGTCAAGATTCACCTTAAGTGA 3060
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QY 3061 TTTGTTGTTTGTGTTTGAAGACAGAGTCTCTTTTGTTAACCCAGGCTAGAGTCAATGAGTG 3120
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Db 23300 TAAAGCTGAGCTCTGCAATTTCAACATGATCAAGCTGATGCAAGTGTGCTGTCAAGA 23359
QY 3361 GCCAAGCACTGAGCAGCAAGGATCTGATTAGCAATTAATGATCAAGTGTGATTAATGAT 3420
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QY 3421 AGTGACATTAAGATGAGAGGAATGTGAAATCAGTAAACAAAGAAAGTCACTCTTG 3480
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QY 3721 AGATCTGAGGGTCAATCAGCAATAGATTTTAGAGAACAAAGATGAGCAACCAAAAGAGC 3780
Db 23720 AGATCTGAGGGTCAATCAGCAATAGATTTTAGAGAACAAAGATGAGCAACCAAAAGAGC 23779
QY 3781 AATATACAAAGAGAGAGAGACTGATGATGAGACTTTTCCCTTTTATGATGAGAGAGA 3840
Db 23780 AATATACAAAGAGAGAGAGACTGATGATGAGACTTTTCCCTTTTATGATGAGAGAGA 23839
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QY 3901 ATACACACTGTATGAGAAAGTCAAGGAAAGAAATTTCAAGAGAGGGTATGTGACGA 3960
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QY 3961 GTATTACAAAGCATCAAGAAATTAAGCTTAAAGTCAATCTTGAATGACCTTGTGAG 4020
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QY 4681 CTTGTTTTCTTCACTCTCTCTCCCTTACTCACAAGAAAATTTCTCTCTCTACTCAT 4740
DB 24680 CTTGTTTTCTTCACTCTCTCTCCCTTACTCACAAGAAAATTTCTCTCTCTACTCAT 24739
QY 4741 TCCCTGAATGCTGTGTCTGTTAAAGTTCCAGGCTTGAAGATGAGGCTAATCAGAACAC 4800
DB 24740 TCCCTGAATGCTGTGTCTGTTAAAGTTCCAGGCTTGAAGATGAGGCTAATCAGAACAC 24799
QY 4801 AGTGTACAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4860
DB 24800 AGTGTACAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24859
QY 4861 GCGGGAACCTGACCGGGAACCAAGAGTCAAGCTATTTTCTGTGATCTGATATTTAA 4920
DB 24860 GCGGGAACCTGACCGGGAACCAAGAGTCAAGCTATTTTCTGTGATCTGATATTTAA 24919
QY 4921 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4980
DB 24920 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 24979
QY 4981 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040
DB 24980 ATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25039
QY 5041 GCTCCAGACTGTGTGGGCTTAAGTAAAGGCAATCTGATGATGATGATGATGATGATGATGAT 5100
DB 25040 GCTCCAGACTGTGTGGGCTTAAGTAAAGGCAATCTGATGATGATGATGATGATGATGATGAT 25099
QY 5101 AATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160
DB 25100 AATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25159
QY 5161 ATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5220
DB 25160 ATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25219
QY 5221 TTTATTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 5280
DB 25220 TTTATTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 25279
QY 5281 ACGGAGTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5340
DB 25280 ACGGAGTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25339
QY 5341 ACCTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5400
DB 25340 ACCTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25399
QY 5401 CAGGACCCACCACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5460
DB 25400 CAGGACCCACCACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25459
QY 5461 ATGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5520
DB 25460 ATGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25519
QY 5521 AAAGTCTGGGATTTACAGTATGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5580
DB 25520 AAAGTCTGGGATTTACAGTATGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25579
QY 5581 ATGGGGTCTTGTCTATGTTGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5640

DB 25580 ATGGGGTCTTGTCTATGTTGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25639
QY 5641 GCCTTGCCCTCTCAAGTTCTGGGATTTACATGATGATGATGATGATGATGATGATGATGATGAT 5700
DB 25640 GCCTTGCCCTCTCAAGTTCTGGGATTTACATGATGATGATGATGATGATGATGATGATGATGAT 25699
QY 5701 CAATATTTATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5760
DB 25700 CAATATTTATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 25759
QY 5761 AAAAATTAGAGATTTGGAACCAAAAGAGAGGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 5820
DB 25760 AAAAATTAGAGATTTGGAACCAAAAGAGAGGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 25819
QY 5821 ATGATGCCAAATGCTGCAAGATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTA 5880
DB 25820 ATGATGCCAAATGCTGCAAGATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTA 25879
QY 5881 GTCATGGGAACCATGCTGTAATAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5940
DB 25880 GTCATGGGAACCATGCTGTAATAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 25939
QY 5941 TATAGGGGATGATTTTGTATTTTCAAGAGCAAAACAGTTCCATATGATGCAAGATCTA 6000
DB 25940 TATAGGGGATGATTTTGTATTTTCAAGAGCAAAACAGTTCCATATGATGCAAGATCTA 25999
QY 6001 GTGTGTACCAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6060
DB 26000 GTGTGTACCAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 26059
QY 6061 GGTGTGTAGCTGTGCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6120
DB 26060 GGTGTGTAGCTGTGCTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 26119
QY 6121 TGCCCAATCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6180
DB 26120 TGCCCAATCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 26179
QY 6181 GAAGAGTATGAGAGATGTGG 6201
DB 26180 GAAGAGTATGAGAGATGTGG 26200

RESULT 3
US-10-027-632-4668
; Sequence 4668, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4668
; LENGTH: 454

QY 196 AAGTATCCCTCAAGAGCTTCAGCGCTATGATGCTTAAGAAATGTAAGCCCTC 255
DB 645 AAGTGTCCCTGCAAGAGCTTCGCGCTTAATGATGCTTAAGAAATGTAAGCCCTC 704
QY 256 AGCCATCTGAGAGCAGTGTGTACAGCAATTCATCAAAAAAGAAACACAGGCCCTTCCC 315
DB 705 AGCCGCCCAAGAGCAGTGTGTACAGCAATTCATCAAAAAAGAAACACAGGCCCTTCCC 754
QY 316 CTTCCCCCATCTGATGATGAGAGCTTCCTTCATTCANAGTAAATTTCTAGATAC 375
DB 765 CTTCCCCCATCTGATGATGAGAGCTTCCTTCATTCANAGTAAATTTCTAGATAC 824
QY 376 AGCTGTAGAGCTCAAGTACTGAGAAAGCTCCATTCAGAAAGAAATTTATCTTAAG 435
DB 825 GTCTTGTAGAGCTCAAGTACTGAGAAAGCTCCATTCAGAAAGAAATTTATCTTAAG 884
QY 436 ATACTGTAATGATGATCTAA-TTTTGTGACATTTGGAATATATAGTTGT 483
DB 885 ATACTGTAATGATGATCTAA-TTTTGTGACATTTGGAATATATAGTTGT 933

RESULT 6

US-09-814-353-20512
; Sequence 20512, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20512
; LENGTH: 3802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-20512

Query Match 6.5%; Score 402.6; DB 10; Length 3802;
Best Local Similarity 92.5%; Pred. No. 1.4e-82;
Matches 434; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 16 CAATTATGAAGCCAAATATACAGCTTAATAATAGATCTGACCTTAATACCGCAAG 75
DB 438 CAATTATGAAGCCAAATATACAGCTTAATAATAGATCTGACCTTAATACCGCAAG 497
QY 76 AACTCCCTTTGTAAGATTGTGAACAAAATTAATATGATGATGATTAAGTTCTAATG 135
DB 498 CACCCCTTTGTAAGATTGTGAACAAAATTAATATGATGATGATTAAGTTCTAATG 557
QY 136 GAATGTGAACCAAGACCATATCAAGCGCTAGCAAAATGCGCAATTCATATATCA 195
DB 558 GAGTGTGACCAAGACCATATCAAGCGCTAGCAAAATGCGCAATTCATATATCA 617
QY 196 AAGTATCCCTCAAGAGCTTCAGCGCTATGATGCTTAAGAAATGTAAGCCCTC 255

DB 618 AAGTGTCCCTGCAAGAGCTTCGCGCTATGATGCTTAAGAAATGTAAGCCCTC 677
QY 256 AGCCATCTGAGAGCAGTGTGTACAGCAATTCATCAAAAAAGAAACACAGGCCCTTCCC 315
DB 678 AGCCGCCCAAGAGCAGTGTGTACAGCAATTCATCAAAAAAGAAACACAGGCCCTTCCC 737
QY 316 CTTCCCCCATCTGATGATGAGAGCTTCCTTCATTCANAGTAAATTTCTAGATAC 375
DB 738 CTTCCCCCATCTGATGATGAGAGCTTCCTTCATTCANAGTAAATTTCTAGATAC 797
QY 376 AGCTGTAGAGCTCAAGTACTGAGAAAGCTCCATTCAGAAAGAAATTTATCTTAAG 435
DB 798 GTCTTGTAGAGCTCAAGTACTGAGAAAGCTCCATTCAGAAAGAAATTTATCTTAAG 857
QY 436 ATACTGTAATGATGATCTAA-TTTTGTGACATTTGGAATATATAGTTGT 483
DB 858 ATACTGTAATGATGATCTAA-TTTTGTGACATTTGGAATATATAGTTGT 906

RESULT 7

US-10-087-192-904/c
; Sequence 904, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 75252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-904

Query Match 6.0%; Score 375; DB 13; Length 75252;
Best Local Similarity 57.4%; Pred. No. 1.8e-75;
Matches 873; Conservative 0; Mismatches 625; Indels 23; Gaps 10;

QY 483 TTAGCCTGCGCGGCTGCTCAAGCCCTGTAATCCAGCCCTTTGGAGGCGCAAGTGGCA 542
DB 31345 TTGCTCGCGCGGCTGCTCAAGCCCTGTAATCCAGCCCTTTGGAGGCGCGGCGG 31286
QY 543 GATCATGAGTCAAGAGTTTGAGACCAAGCTTAGCCAACTGGTGAACCCCGTCTTACT 602
DB 31285 GATCATGAGTCAAGAGTTTGAGACCAAGCTTAGCCAACTGGTGAACCCCGTCTTACT 31226
QY 603 AAGATAC--AAAAATTAGCCAGGTGTGTGCGCACAAGCTGTAAACCCAGTGTGCA 660
DB 31225 AAAAAATACAAAAAAATTAATGACAGGCGGTGTGCGCGCGCTGTAGTCCAGCTACTCG 31166
QY 661 GAGAGTGAAGCGAGGAATTTGTTGAACCCAGAGGCGAAG--GTGAGAGAGCAAAAGATC 719
DB 31165 GAGAGTGAAGCGAGGAATTTGTTGAACCCAGAGGCGAAG--GTGAGAGAGCAAAAGATC 31106
QY 720 AACCAATGCACTGTAGCTGTGATGACAGGGCAAGCTCCAACTCAAAAAAATTAATTA 779
DB 31105 GACCACTGCACTGTAGCTGTGATGACAGGGCAAGCTCCGCTCGGAAAAAATTAATTA 31046
QY 780 AAAAATATGTAGTTGTGCT---TATTAACAATTAATAGCAAGTGAAGCAAAAGTGC 835
DB 31045 AATATCAAAATCTAGGTGCGGCGAGTGCAGAGCGCTGTGAATCCAGCTACTTAAGAGGC 30986
QY 836 TAAAGCTATGACATGTATATGAGAAATATCTGTGGAAACATATATAGGAACCTAAG 895

30985	TGAGGACAGGAAAGTGTGAACTCGGAGGCAAAAGTTGAG-TAAAGCAAGATCAAGCC	30927
QY	CCACTCTGGAAAGTAAAGCTTTTGGAAAAGAAATGTTTGAGGACAAAGGCTTAAAGAGATG	955
Db	30926 ACTGCACCTCCAGCCCTGGGTGACAGAGGGAACCTGTCTTCAAAACAAATTAATAATTA	30867
QY	956 AAAAAAAAAATTAATAATACAGTTTAACTGTGTGAGAAATGGATAGAGGTAGAGCTTAACTAGA	1015
Db	30866 ATATAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAATTA	30807
QY	1016 GAAATCAAATAGCAATGTTTCATGCTATGTTTAAAGACCTTGTAAGGGTGAAGACCATTA	1075
Db	30806 GTGGCTGAGACATGAGCCCTGTGGGTGATCTTAAAGTTTAAACTCATCGGGGTGGCTTACT	30747
QY	1076 CATATATCGACCACTCGCGGACCTTTTTTTTAAAGTAATGCTGTGCATTTTAAATAGAG	1135
Db	30746 GGCCTCTCTTGTGGGTGGGAAAGGAGCTTCAAG---AGTGGGCTCAGGGCATAGGAA	30690
QY	1136 GAGCAGAGAAATGTAGACAGTTGATTTGAGTCAAGATTTGAAGTTCTGCCAGACATGTGAA	1195
Db	30689 TGAGGCGAGCTGGAGGAGGATTTGGGGCTCGGACCTGGGTGACTCTTGCGCTGGTGTGG	30630
QY	1196 GGAAGACACAGTATGGGTAAGAGAGTGAAGATTTATCAAGACAGAAATTATGTCTGG	1255
Db	30629 GAAAGAGAGAGAGGGGATACCTGACAAACAGACAAAGAAACAGAGGTGTGGACCC	30570
QY	1256 CCAATGACATCTAGTCTGAAGTCTTAATCTGAGGAGAGAAAGTAAGAAAGACAGCTTGCTG	1315
Db	30569 CCAGGCCCTGACAGATCTGTCTACACCTCTCCCATGAGAGAGAG---GGCAGGGGA	30515
QY	1316 ATAGTTATGAAGAGTGTGAAGGCTTCAAGACCTTACAGGTGTGATTTAAATAGAAAT	1375
Db	30514 CATAAGCTGAAGATGTGGATTTTCTCAAGTGCACACCGAGATGTGCAGAACACCA	30455
QY	1376 GATTGAGAAAGAAATACTGTGAGAGAGTGAAGATTTTCAAGGCTTGAGTACTCTGACATA	1435
Db	30454 AGTGTGGGGCTGTGTGACCCAGAGAGACTGACAGCAT---CGATTATCATAGCTGAAC	30399
QY	1436 CCAGACACTGTGCTAAATGCTTCAAAAGACATGATCCCTGCTTCAAGGACCTTACAGCCA	1495
Db	30398 ACAGATGGAGTGTAGCCCAAAAGACGTAACGATTAGTGAAGGCTGAGGGAGTTTCAACAGCA	30339
QY	1496 AAAACAAGACATA-AGAAATPACACCAATACATTAATAGACACTGTGTGAATATCA	1554
Db	30338 GGGAACTTACCGAGGAGGAAGAACACACTTCTCAGACGAGATGGAGAAAGAGAG	30279
QY	1555 AGAAAGAAATACGATCTAGTACTGTAGATGTGCACGGCATCAAAATATCTTCTAGTT	1614
Db	30278 GGAAGAAAAAATAAACAATGTTTTCTGACATTTTGTGTAACCTTTTAGTCTT	30219
QY	1615 CAAGAAATTTCAATTCGGCCGGGCGGGGTGGCTCAAGCTCTGTAATCCACGACTTTGGGA	1674
Db	30218 CAAAAAAGAAATGCGGCCGGGSCACAGTGGCTCAAGCTGTAAATCCACGACTTTGGGA	30159
QY	1675 GGCAGAGCGGGTGTATCACAAGGTCAAGAGATCAAGACCATCTCTGTTAACAGGTGA	1734
Db	30158 GGCAGAGTGGGTGTATCAAGAGTCAAGAGATCAAGACCATCTCTGTTAACAGGTGA	30099
QY	1735 ACCCCCTCTTAC-AAAAATATTAATAATTAGCCAGCGGTGGTGGCGGCGCTGTAGT	1793
Db	30098 ACCCCGCTCTTACTTAATAATAAATAAATAAATTAGCCGGGTGTGGCGGSCACTGTAGT	30039
QY	1794 CCGAGCTACTCAGAGGCTGAGGACAGAGAAATGGCGTGAACCGGGAGGTAGAG-TTGGC	1852
Db	30038 CCGAGCTACTTGGAGGCTTGGACAGAGAAATGGCGTGAACCGAGAGGCGGAGCTTTCA	29979
QY	1853 GTAGCCGAGATCGCGCACTGGGCTCCAGCCTGGGCGACAGAGTGAAGCTGCTCA	1912
Db	29978 GTAGCCGAGATCGACAGACTGACCTCAGCCTGGGCGACAGAGGAGACTCATCTCA	29919
QY	1913 AAAAAAAAAAAAAAAAAAATTTTCAATCTTAAACACTGCATTTCAACACTGTAG	1972
Db	29918 AAAAAAAAAAAAAAAAAAGATCTGAATAATTTATAGTAAATTTGTGACAAACATAA	29859

Qy 1973 AATAGGAGAGCATGTTACAGG 1993
 | | | | |
 Db 29858 AGGTGACTACATAGTACGGG 29838

```

RESULT 8
US-10-087-192-274/c
Sequence 274, Application US/10087192
Publication No. US2002018256A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITILE OF INVENTION: CANCER
FILE REFERENCE: 52945200012
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 274
LENGTH: 73145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(73145)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-274

```

Query Match	6.0%;	Score 373.6;	DB 13;	length 73145;
Best Local Similarity	51.7%;	Pred. No. 3.8e-75;		
Matches 1278;	Conservative	0;	Mismatches 1104;	Indels 92; Gaps 15;

QY	449	ACTAATATTTTGAACATTTTGGAAATATATATAGTTGTTAGGCTGCGCGGGGCTCAAGCCT	508
Db	43054	TGCCAATATTTTCAGTATATATATAGAGAGAAAACAAGGCTGGGCAAGTGGCTCAACCT	42999
QY	509	GTAATCCCAAGCCCTTTGGAGGCGAGAGTGGCAGAT--CATGAGTCCAGAGTTTGAGA	566
Db	42994	GCAATCCCAACATTGAGAGGCGCAATGGGAGAGTTGCTTGAGCCCAAGAGTTCAAGA	42935
QY	567	CCAAGCTTAGCGAACATAGTGTAAACCCCGCTCTACTAAAGATATCAAAAAATTAAGCCAGGT	626
Db	42934	CAAGCCTGGGCAACACAGTAGAGCCCACTCTCTCAAAAAAATATGAACAATTAGGCAGAT	42875
QY	627	GTCGTGGCGACACACTGTATACCCCAAGCTGCTCGAGAGTGAAGCGCAGAGAAATTGCTTGA	686
Db	42874	GATGTGTGATCCTCTGTATGTTCCAGCTACTTGAGGAGGCTGAGGTGGAGGATCTCTTGG	42815
QY	687	ACCGAAGAGCAGAGG--TGACGCGAGCAAAAGATATCAACCAATGCACTGTAGGCTGGATGA	745
Db	42814	GCCCAAGAGGTGAGGCTCAGTAGAGCCATGATCAACACATGCACTCAGCTT-----	42761
QY	746	CAGGCGAAGACTCCAACTCAAAAAAAGAAAAAAGAAATATGTAAATTGTGCTATGA	805
Db	42760	-----GTCTCAAAAAAAGAAAAAAGAAAAAAGAAAGAAAGAAAAAACATGGT	42709
QY	806	CAAAATTAATAGCAGTGAAGAGCAAAAGTCTTAAAGCTTATGACCATGTATCTAGAGATTA	865
Db	42708	GTTTCAACAATTAGAGGAGAAAAAGAAAGTATCAGCATGAGAAAGATTAACAATTAAGACAA	42649
QY	866	CTGTGGGAACACATATATAGGAAACCTTAACCAAGTCTGGAAGTAAAGGTTTGGAAAAGGA	925
Db	42648	AAATTTGAGTGGCTGAAGATTTBAAAAAATACAACT-----TAA	42611
QY	926	ATGTTTGAAGACAAAGGCTTAAAGAGAGTGAAGAAAAAATTAATAATACCAATTATGCTG	985
Db	42610	TTTCTGTGTATAAAGGCTTGCACTTCCAAAGAAAAAAGAAATCCAGCAATTAAGCT	42551

QY 986 TGTGGAATGGGATAGGAGCTAAGTAAGAAATCAATAGGAATGTTTCATGTATGT 1045
 DB 42550 GTGGGCAAGAGAGTCAATTAACAAATATAGGAAGCTAATAAGAGTTCAGTAATCT 42491
 QY 1046 TTAGGACCTGTGAAGGTGAAGACATTAATCATATCTGACACATGCGGACCTTTT 1105
 DB 42490 CAAGTATGTTGAAGGCTGGGATTCATATGTAATATAGCAAAAAATATATTTAGCA 42431
 QY 1106 TTAATGTAATGCTTGGCAATTTAATATAGAGACAGAAATATAGACATGTGATGAGT 1165
 DB 42430 AATATGTAATGTAATATAGAGAGATATCAGATATAGAGGCAATGGGTGGTGCACAT 42371
 QY 1166 CAGATTTGAATGTTCTCCAGACATGTGAAAGAAAGACAGGTAGGCAAGAGATTGA 1225
 DB 42370 ATTACATGGAATCTAATATCCATTAAGACAGACCAAAACATATATATCTCTGAG 42311
 QY 1226 AGATTATCAAGACAGAAATTAATGCTGGCCAGTGGCAATCTAGTCTGATCAATCTGA 1285
 DB 42310 AAAAAAGAGTGAATGATTAATAATATATATTAATAATTAATCTTCAATATCAACT 42251
 QY 1286 GGGAGAGAGTGAAGATTAAGCAGCTTGTGATGTTATGAAAGAGTGAAGGCTTCAAG 1345
 DB 42250 ACATTAAGAAATTCAGACACATTAAGAGAGCTGAAGATCAAAACA-AGTTAATTAATG 42192
 QY 1346 GACCTACAGGTGTTGATTAATATGAAGATGATTTGAGAAAGAAATCTGTGAGAGATG 1405
 DB 42191 GTTGTGTTGGTGGGATTAATTAATGAACAAACA---GATAATTTCTTCTTTTCAATAT 42135
 QY 1406 AGATTTTCAGGCTTGATGATCTCATATCCAGACATCTGTGTAATGCTTCAAGACA 1465
 DB 42134 CATTTATGTTTCAAAAAAGTCAATATATATAGTCTCAATCAATCTTCAATTAATA 42075
 QY 1466 TGTATCCCTGCTCCAGAGGACTTACAGCCAAAAAAGAGATTAAGATACA-CACCAAT 1524
 DB 42074 CAAAAGCAAAATGATTTCAAGCTACATTTCTCCCTACGCAAAAAAAGATTAAGAAC 42015
 QY 1525 ACTATATATAGGACACTTGTGTAGATATATCAAGAAAGAAATATAGATCTGTATGATG 1584
 DB 42014 AAACAGAAATATAGAAATATATATTTTAAATATATCTTAAGAAATAATTTGTCTGA 41955
 QY 1585 TGCAGAGGATCAAAATATCTTCTAGTTTCAAGAAATTTCAATGCGCGCGCGCGG 1644
 DB 41954 GAAAGAAATCAAGAAACATATCTGTCTGTAAAGAAATATCAATGCGCGCGCGG 41895
 QY 1645 GCTCAGGCTGTATCTCCAGACCTTTGGAGGCGGAGCGGTGATCAAGAGTCAAGA 1704
 DB 41894 GCTCAGGCTGTATCTCCAGACCTTTGGAGGCGGAGCGGATCAAGAGTCAAGA 41835
 QY 1705 GATCAAGACATCTGTGTAAACAGGTGAACCCGCTCTTACAAAAATATATTAAT 1764
 DB 41834 GATCGAGACATCTGTGTAAACAGGTGAACCCGCTCTTACAAAAATATATTAAT 41775
 QY 1765 AGCAGAGCGTGTGGGGGGGCTGTATGTCCTGATCTTCAAGAGAGCTGAGAGAGAA 1824
 DB 41774 AGCGGGCGGTGGGGGGGCTGTATGTCCTGATCTTCAAGAGAGCTGAGAGAGAA 41715
 QY 1825 TGGCGTGAACCCGAGAGTGAAGTTTGC-GTGAGCGAGATCGCGCACTGCGCTC-CA 1882
 DB 41714 TGGCGTGAACCCGAGAGGCGGAGCTTGCATGAGCGGAGCAATGCCACTGCACTC 41655
 QY 1883 CTTGGGCGACAGAGTGAAGTGGCTCTCAAAAAAATATATATATATATATATAT 1942
 DB 41654 TCTGGGCTGACAGAGTGAAGTCTCCGTCTCAAAAAAATATATATATATATATAT 41595
 QY 1943 TCTTAAACACATCTGATTTCAACAGTCTGAATATAGAGAGCATTTACAGGAGAGAAA 2002
 DB 41594 CTGACATATCAAAACCTATGAAGAGTGAATGAG-----GAAAG 41554
 QY 2003 TGTATTCAGCAAGATGACAGAGTGAAGAAATAGAGATATGTTCAAGAGAGAGACCCCA 2062
 DB 41553 TCCTTAGAGAAACATCAACAGCTTAATATGCTTTATTTTCAAGAAATATGAGAAA 41494

QY 2063 GAGTCATGTTGTTAGGTTAGAGAAACAGAGTGTTTGCAATCTCAGGTTCACTTA 2122
 DB 41493 AA-----TGATGAACCTAAGATTAATATATATCTTTAGAGAAAGAA 41453
 QY 2123 GTGCGTTGTAATCAATATGTTGTTAGCAACTGATTTTAAAAATGAATTAATG 2182
 DB 41452 CAATTTTAAAGAAAGGAAAGGAGGAGAGTGAAGTGAATTAAGCAAAAAA----- 41397
 QY 2183 ATGAGAGAGAAATGAAAAATATAGCATGATTTACATTTTGAAGACAGATTAATTT 2242
 DB 41396 CTGAGAAAGAACACGCTGATGCAAGAGTGGCTTATTTCTTAAAGCTCAAAAC 41337
 QY 2243 CTGCAACTTTTCTCCATATGTAATCTGATATATTTTATATATGATGTAATGACA 2302
 DB 41336 ATGTGGGTTCAATTAACAGTGGCTCTCAGTTCTTTGATGAATGAATATGATCTTA 41277
 QY 2303 GATACATATATATTTCTTCTAGTACCTGACATCAAAAAATCTTTAAAGCACTG 2362
 DB 41276 ACAGAGAAAGGAGGAGGAGAGAAACACACCAAAACAAAGTGAAGCATTAAGCTTG 41217
 QY 2363 TCTAATCTCTTATTTTGAAGAGAGAAATCCAGATCTGAAGAGCAAAATTTGCT 2422
 DB 41216 AGCTTAAGGATATTAACACGTAAGAAATCTATGACAGATGTTTCAGTTAATGAGA 41157
 QY 2423 GAGGTATTAAGACAGCTTATGCTATGCTAATGAAGATCTTGAATTAATTTCTTCC 2482
 DB 41156 AATCTGAAGACATGACCAATTAACACAGATGAAGATTAACGTTAAACAGAGCTAG 41097
 QY 2483 ACTAGGCCATCTGCACTTCTAGTTCTGTGGCTGAAATATAGAAATATTTAGTAA 2542
 DB 41096 AAGTCAAAATTAATATATATATGAGAGAAATTAAGAGAAAGAAATCCCCCAATTA 41037
 QY 2543 CAGCATACCAAGTCTGGGA--AATATATGAGTATGAGTGGCTGAGAGCTCAATTTCTA 2600
 DB 41036 GAGGTGATGATCTTATGATGAATTCATTCATACTTAAGAAATATGATATCTCAC 40977
 QY 2601 AGAATATGACCTTAAGAGAGGTATGTCGCTCACCTTAATATCCAGACTTTGGGA 2660
 DB 40976 ATCACAATTAATTTCTGCTGCTGATGATGCTGATGCTGATATCCAGACTTTGGGA 40917
 QY 2661 GGCAGATCAAGAGATGCTTGAACCCAGAGTTCAAGATCAAGATGAGGCAATAGCA 2720
 DB 40916 GGCAGAGGAGGTGATGATCTTGAAGCCAGAGTTTGAACAGCTGAGAAACAGAG 40857
 QY 2721 AGACTCATCTGTACAAAAATTTAAATATGCTGAGCATGAGTATGCTGATG 2780
 DB 40856 AAACCCATTTCTACAAAAATATTAAGCAAGCGGTGTGATGCTGATG 40797
 QY 2781 CCCACTTACTTGGGAAGCT-AGTGTGTGATATGCTTG-ACACAGAGTTTGAAGCTAAG 2838
 DB 40796 CCCAGTCTTCAAGAGGCTGAGAGGATGAGATCACTTGAACCAAGAGGTGAGTTGCA 40737
 QY 2839 GTGAGCATGATCAACAACATGCACTGAGCTTGAAGTCAAGAGAAAGACCTGTCCCTA 2898
 DB 40736 GTGAGCAAGATCAACCACTGATCTCAGCTGGGTGACACAGTGAAGCTGTCTCAA 40677
 QY 2899 AAAAAAGAAAT 2912
 DB 40676 AAAAAAATAAT 40663

RESULT 9
 US-10-265-071-22
 ; Sequence 22, Application US/10265071
 ; Publication No. US20030147875A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Steven D.
 ; APPLICANT: Hemmerlich, Stefan
 ; APPLICANT: Tomita, Megumi
 ; TITLE OF INVENTION: Sulfatases and methods of use thereof
 ; FILE REFERENCE: US/10/265,071
 ; CURRENT APPLICATION NUMBER: US/10/265,071
 ; CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: 60/258,577
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/267,831
PRIOR FILING DATE: 2001-09-02
PRIOR APPLICATION NUMBER: 10/025,966
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 268685
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_structure
LOCATION: (0)...(0)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: n = A,T,C or G
US-10-265-071-22

Query Match 5.9%; Score 365.2; DB 15; Length 268685;
Best Local Similarity 52.8%; Pred. No. 7e-73;
Matches 1289; Conservative 0; Mismatches 1043; Indels 108; Gaps 19;

QY 486 GCGTCGCGCGTGGCTGACCGCTGTAATCCAGCCCTTTGGAGGCGCAGGTGGCAGAT 545
DB 221964 GCGAGGCGCGTGGCTGCTGCTGCTGTAATCCAACTTTGGAGGCGCAGGTGGTGGAT 222023
QY 546 CATGAGGTGAGAGTTTGAAGCAGCCTAGCAGCAATGTAAGAAACCCGCTCTACTAA 605
DB 222024 CATGAGGTGAGAGTTTGAAGCAGCCTAGCAGCAATGTAAGAAACCCGCTCTACTAA 222083
QY 606 GATACAAAAATTAGCCAGGTGTGTGGCGCAGCAGCCTGTAACCCAGCTGCTGAGAGAG 665
DB 222084 AATACAAAAATTAGCTGAGTGTGTGGCGCAGCAGCCTGTAACCCAGCTGCTGAGAGAG 222143
QY 666 TGAAGCAGAGGATTTGCTTAACCCAGAGAGCAGAGG-TCGACGAGCAAAAGTCACACC 744
DB 222144 TGAAGCAGAGGATTTGCTTAACCCAGAGAGCAGAGG-TCGACGAGCAAAAGTCACACC 222203
QY 725 AATGCACTGAGCCTGGATGATACAGGCGCAAGCTCCAATCAAAAAAAGAAAAAAGA 784
DB 222204 ACTGCACTGAGCCTGGGCAACAGAGGAGATCTCGCTCAAAAAAAGAAAAAAGAAAAA 222263
QY 785 AATATGTAGTTGTGTATTAACAATTAATAGCAGTGAAGCAAAAGTCTAAAGCTTA 844
DB 222264 AATGCTTGGCCATATATTTATCTTCTATGACATATTCATTAGAAAAATCACTGAGA 222323
QY 845 TGAACATGTATCTAGAAATATCTGTGGAAACATTAATTAAGGAACTTAACCACTGCTG 904
DB 222324 AATGCAATTTGTTGGAAAACTCATGAGGCTTCTATGTGAAGAAAGTAAATTTCTGCAAAA 222383
QY 905 G-AAGTAAGGTTTGGAAAAAGAAATGTTTGAAGCAAAAGGTTTAAAGAGTGAAAAAAA 963
DB 222384 GCTACTGAGATTTAAAGGCACTAATTAATTAAGCTGACGAAATTAACACACAGTCT 222443
QY 964 AATTAATAATCAAGTTAGTGTGTGAGAAATGGATAGGAGCTTAATTAAGAAATCAA 1023
DB 222444 CAATTAATCTGTTAAATTCAGAAATTTAATGTGACAAAAATCTTAATTAAGCAGGG 222503
QY 1024 ATAGGAATGTTTCAATGTAATGTAAGGAACTTGTGAAGGTTGAAGCACTTAATTAATCT 1083
DB 222504 GGAAGCTAGGAAAAAGGATTAACGATTTCTGGAAGAAAGTAAATCTGTGACCTGCTG 222563
QY 1084 GCAACATCGGCGGACTTTTATTTATGTAATGCTTGGCAATTAATTAAGAGG--AGCAG 1141
DB 222564 CCAAAATTAACATGATTTTGTCTCAACACCTCTCTGTGATTTAGCCCTGGGCGACATG 222623
QY 1142 AGAATGTAGACAGTTGATTAAGTGAAGTTGAAGTTCTGCAAGACAT-GTGAAGGAGAG 1200
DB 222624 ACAAAATCAAAAAGATGTCCATTAATAAGTTTATTAATGAACATCACTGAGGACAGAG 222683

QY 1201 AGACAGTGAAGGAGAGTGAAGATTTATCAAGACAGAAATTATG-TGTGGCCAG 1259
DB 222684 ATAAATATATCCAGAGGTCAAAAAGTATAGATCTAGTTTAAATATATGTAATAC 222743
QY 1260 TGGCATCTAGTCTGAGTCTAATCTGTGAGGAGAAAGTGAAGTAAAGCAGCTGCTGATAG 1319
DB 222744 ACAAAGCATTTGATCTTCTGCTGGCAATTTTTTCTCCATCAGTCTGTTTCTTT 222803
QY 1320 TTAATGAAGAGTGAAGGCTTCAAGGACCTACAGGTGTTAATTAATGAAGATGATTT 1379
DB 222804 CATGCTTGGTAAATTTCTAATTTAATTAATAATGATACCTTATATATACGATGAGA 222863
QY 1380 GGAAGAAAGATTAAGTGAAGATGATGATTTTCAAGCTTGAAGTCTGATCATCCAG 1439
DB 222864 TAATTTTCAA-----AGATGCTACTTGTCTTAATTTGCTTAAGATATTTT 222907
QY 1440 ACACGTGCTAAATGCTTCAAGACATGATCCCTGCTCAAGGACCTTAACAGCCAAAA 1499
DB 222908 ATTTAGTATCTTCAGTAGCAATGTAACATGCTATTCAGATGAGAAATTAACCTGC 222967
QY 1500 CAAGAGATTAAGAAATACACACCAATATCTATTAAGACCTTGTGTAATCAAGAAA 1559
DB 222968 CAATCATTAAGAGTGCAGAGAAAGACT----CACTCTAAAGATTAATATATATATA 223023
QY 1560 GAAATACATCTAGTCTGATGATGCAACGCAATCAAGATATCTTCTAGTTCAAGA 1619
DB 223024 CAATGCTGTCACTATGTTTATCTGAGGAGTTAATACAGAAATTTTCAAATATTA 223083
QY 1620 AGTTTCAAGATCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1679
DB 223084 AGTAACATA-CAGCGGCGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 223142
QY 1680 AGCGGCGGTGATCAC--AAGTCAAGAGATCAAGACCATCTGTGTTAACAAGTGAACC 1737
DB 223143 AGCGAGGCGGATTTACCTGAGGTCAGGACTTGAAGCAGACCTGAGCCAAATGTGAACC 223202
QY 1738 CGCTCTCAAAAAATTAATAAAATTAAGCAGGCGTGTGCGGCGCTGATGCTCA 1797
DB 223203 CGCTCTCAAAAAATTAATAAAATTAAGCAGGCGTGTGCGGCGCTGATGCTCA 223262
QY 1798 GCTACTCAGAGGCTGAGGCGAGAGATGCGTGAACCCGAGAGGTGAGATTGCG-GTGA 1856
DB 223263 GCTACTCAGAGGCTGAGGCGAGAGATGCGTGAACCCGAGAGGTGAGATTGCG-GTGA 223322
QY 1857 GCGAGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1914
DB 223323 GCTGAGATGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 223382
QY 1915 AAAAAAAGAAAAAAGTTTCAAGTCTTAACACCTGATTTCAACAGTCTAGA 1974
DB 223383 AAAAAAAGTAAAC-----TCATTCAGCTTAAC 223413
QY 1975 TAGAGAGCATGTATCAGGAGAGAAATGTTTTCAGCAAGAGTACAGATAGGGAATA 2034
DB 223414 AAGATTAATCTGGAATTTCTCAAAATTAATCTTTGCTATCTTTAAATGTGAATAATTA 223473
QY 2035 GAGGATATGTTCAAGAGAGAGACCCAGAGTCAAGTGTGTTGTTAGGTTTGAAGAAACA- 2093
DB 223474 TCAAAATCTCAAGATAGTTTACATGATGCAATTAATTAATGATGACTGCAAAATAG 223533
QY 2094 CAGTGTGTTCAATCTCCAGGTTTCAATGATGCTGTTAATAATCAATATATGATGATGGA 2153
DB 223534 CAATATTTCTTTAAATATTTCTGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 223593
QY 2154 ACCTGCAATTTAAATAATGAATTAATGATGAGAGAGATTAAGAAATTAATTAAGATGCA 2213
DB 223594 ACATATATATGTAATGATATGCTATGTTTATATGATATCACTACCTCAATTTT----TATA 223649
QY 2214 TTAATTTGAAGAGCAAGTATTAATTTTCTGCAACTTTGCTCAATTTGATCTGATCT 2273
DB 223650 TCACTTTGTTAAAGTCCATTTGTAATAATTAAG-----TGTTAACAAAGCA 223695
QY 2274 TATATTTTATGATGATGATGATATACAGATATATATTTTCTTACTGATGCTGCA 2233

Db	223696	AAAGATACAGGCTAAGTACGACGACTCAGCTATAATTTTCTTATTAGCATGATCTTG	223755
Qy	2334	GTCAAAAATCTTTAAAGACCTGGCTGGTCTPACTTCTTATTTTGCAGAGAAATC	22393
Db	223756	GACATATACCCCAATCTCTGTCTCACAAGCTTCTGTTTCTTATATCTCGAGATGGGGCA---	223812
Qy	2394	CAAGATCTGAGGAGCAAAACATTTTGGCCCTGAGGTTATAGAACAGGTTATGCCATTGGCTA	2453
Db	223813	-----TATATGCAAAACCCCTTGGCATCCCATTTACCTTAAAGTGACATPAAGTA	223864
Qy	2454	AAAGTATCTTATGTTAAATCTTTCCACTAGTGCATCTGCACTTCTAGTCTGTT	2513
Db	223865	ACCTGGAAGGTAAATATAAATAATATATGTCACAGTGTTAATTTCAATATGATCTTAT	223924
Qy	2514	GGCCTGAATATACGAATATATTATGTAACAGCATACAAAGTCTGGGGAAATATATTGG	2573
Db	223925	CAACCAAGATGCTTTAATTTT-----TATTTCTATGATTAATAAATGG	223965
Qy	2574	GTAGGTGGCTGAGAGCCTCATTTTCTAAGAAATGTGACCTTATGAGAGGTATGTGCT	2633
Db	223970	CAGACAAAGATTGAATCACTAGGTTAGCTGCAAGAAATTAATCCCGGCCAAGACAGTGGCT	224029
Qy	2634	CACACTTAATTTCCAGCACTTTGGAGGCCAAGTCAAGAAAGATCGCTTGAACCCAGAG	2693
Db	224030	CACAACTGAATCCAGCATTTTGGAGGCTGAGGAGGAGTCACTTGAGGTCAAGAG	224089
Qy	2694	TTCAAGACTAGATGGGGCAACTAGCAAGACTCATCTCTACAAAATTTTAAAAATCAG	2753
Db	224090	TTGAGACCAAGCTGTGACAACTAGTGAAACCCCATCTTACTTAAAAATACAAAAAATTAG	224149
Qy	2754	CTGAGCATGTGGGCATPAGCCCTGTATGCCACCTACCTGGGAAAGTA--GGTGGTGGATC	2812
Db	224150	CCGGGCAATGTGTGCACGTGTCTGTATCCAACTGTTTGGAGGCCATGCGACAGAAAAATC	224209
Qy	2813	GCTTG--ACACAGAGATTGAGGCTAAGGTAGCCATGATCACAACTGCATCCAGCTT	2871
Db	224210	ACTTGAAACCAAGAGGTGAGGTTGATGAGCCGAGATCGACCAATGTGATCCAGCCT	224269
Qy	2872	GAGTGACAGAGGAAGACCTGTCTCTTAAAAAGAAAAA	2911
Db	224270	GGGCAACAGAGCMAAGACTTCGCTCTCAACAAAAA	224309
RESULT 10			
US-10-025-966A-22			
Sequence 22, Application US/10025966A			
Publication No. US20030148920A1			
GENERAL INFORMATION:			
APPLICANT: Rosen, Steven D.			
APPLICANT: Palmeri, Diana			
APPLICANT: Stefan, Hemmerich			
TITLE OF INVENTION: Sulfatases and methods of use			
FILE REFERENCE: UCAL230			
CURRENT APPLICATION NUMBER: US/10/025,966A			
CURRENT FILING DATE: 2002-12-21			
PRIOR APPLICATION NUMBER: 60/258,577			
PRIOR FILING DATE: 2000-12-27			
PRIOR APPLICATION NUMBER: 60/267,831			
PRIOR FILING DATE: 2001-09-02			
NUMBER OF SEQ ID NOS: 26			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 22			
LENGTH: 268685			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (1)_(268685)			
OTHER INFORMATION: n = A,T,C or G			
US-10-025-966A-22			

Query Match	Similarity	52.8%	Score 365.2	DB 15	Length 268685
Best Local Match	Similarity	52.8% <td>Pred. No. 76 <td>73</td> <td></td> </td>	Pred. No. 76 <td>73</td> <td></td>	73	
Matches 1289	Conservative	0	Mismatches 1043	Indels 108	Gaps 19
QY	486	GCTTGCGCGGTGCTCAGCCCTGTAACTCCAGCCCTTTGGAGGCGCAGATGGCGAGAT	545		
Db	221964	GCCAGGCGCGGTGCTCGGCTCGTAACTCCCAACATTTGGAGGCGCAGATGGCGAGAT	2220232		
QY	546	CATGAGGCTCAGAGCTTTTANAGACCAAGCTTACCAACATGTGAAACCCCGTCTCTACTTAA	605		
Db	222024	CATGAGGCTCAGAGAGTTTCAAGACCACTCTGCTAAATGTGTAAACCCCACTCTACTTAA	2220883		
QY	606	GATACAAAATAATTAGCCAGGTGTGTGGCGCACCTGTAAACCCAGCTGTGAGAGAG	665		
Db	222084	AATACAAAATAATTAGCTAGTGTGTGTGGCACCTGTAAACCCAGCTGTGAGAGAG	222143		
QY	666	TGAGGCGAGAGAAATTGCTTGAACCCAGAGCGAGAG-TGCAGCGACAAAGATCACACC	724		
Db	222144	TGAGGCGAGAGAAATTGCTTGAACCCAGAGCGAGAG-TGCAGCGACAAAGATCACACC	2222030		
QY	725	AATGACCTGTAGCTCTGATGACAGGGCGAAGACTCCACTCAAAAAAAAAAAAAAAAAA	784		
Db	222204	ACTGACCTCCAGCCCTGGGCAACAGCGCAGACTCGCTCAAAAAAAAAAAAAAAAAA	2222633		
QY	785	AATATGTAAAGTTGTCTATAAACAATAATAGCGAGTGAGAGCAAAAGTCTAAAGCTTA	844		
Db	222864	AAAGTCTTGCCCATATATATTATCTTTCTATACATATTTCAATTAGAAAACATATCTAAG	2223232		
QY	845	TGACCAGTGTAACTAGAAATACCTGTGGAAACATATATAGGAAACCTAACCCAGTCTG	904		
Db	222324	AAACCAATTTGTGTTGGGAAACATCATGGGCTCTATGTAAAGTAAATTTCTGCAAA	2223838		
QY	905	G-AGTAAAGTTTGGAAAGAAATGTTGAGACAAAGGCTTAAAGAGTGAAAAAAA	963		
Db	222384	GCTACTGAGATTAAAAAGCACTAATTGTAATGAGTGACAGAAATTAACCAACAGTTC	2224433		
QY	964	AATTTAAATACCAAGTTTACGTGTGTGAGAAATGGGATAGGGAGCTAACAGAGAAATCAA	1023		
Db	222444	CAATATCTGTTTAAAAATTCAGAAATTTTAAATGTATACCAAAATCTTATAGTACAGGG	2225038		
QY	1024	ATAGAAATGTTTCACTGATGTGTTAAGAACCCGTGTAAGGGTGAAGACATTAATATCT	1083		
Db	222504	GGAGCTTGGGAAAGGATTAACCCATTTCTGGGAAAGGTAAATCTGTGCACTCGTG	2225633		
QY	1084	GCACCATGCGGGACTTTTTTTTATGTGTAATGCTTGGCAATTTAAATAGAGG--AGCAG	1141		
Db	222564	CCCAAAATAGACATGATTTTGTCTCAACCACTCTCTGATGTTTAGCCTGGGCCACATG	2226233		
QY	1142	AGAAATGTAGACAGTTTGAATGTAGTCAAGAGTTGAAGTTCTGCCAGACAT-GTAAAGGAAG	1200		
Db	222624	ACAAATACAAACACAGATGCTCAATAAAAGTTTAAATGAAACACATAGAGACAGAAAG	2226838		
QY	1201	AGACAGTAGGCAAGAGATGTGAAGATTTATCAGACACAGAGTTTAATG-TGCTGGCCAG	1259		
Db	222684	ATTAATAATATCCCAAGAGGTCAAAAGTAAAGTGAATCTCAGTTTAAATATATGTATATC	2227433		
QY	1260	TGGCATCTAGTCTGAGTCTAACTGAGGGAAGAAAGTGAAGTAAGCAGCTTGTGATAG	1319		
Db	222744	ACAAAGCATTTGATCTTTCTTGCTTGGCAATTTTTTCTCATCAATGCTGTGTTTCTTT	2228038		
QY	1320	TTATGAGAGAGTGGAGAGCTTCAAGACCTTACAGGTGTGTAATTAATGAAAGATGATTT	1379		
Db	222804	CATGCTTGATTAATTTCTAATTTTAAATTAACATGATATCACTTTTAACTGTAGAGAA	2228633		
QY	1380	GGAGAAAGATTAACGTGAGAGAGTGAAGATTTTACAGGCTGTGAGCTGTCAATCCAG	1439		
Db	222864	TAAATTTTCAA-----AAGTGTACTTGCTTAAATTTGCTTAAAGATATTTT	222907		
QY	1440	AACTGTGCTAAATGCTTCAAAAGCATGATCCCTGCTCAAGGAGCTTACAGCCAAAA	1499		
Db	222908	ATTTAGTATCTTCAAGTACCAATATGTAACAATGCTATTTCAAGTGAAGAAATTAACCTGC	222967		
QY	1500	CAAGAGATTAAGAAATACACACCATACTATTTATAGACACTTGTGTAGAAATCAAGAAA	1559		

QY 196 AGATTCTCCTCAAGAGCTTCAGCGCTAATGATGCTAAGAAAATGCGAAAGCCCTC 255
DB 512 AAGTTCTCTGCAAGAGCTTCGCGCTAATGATGCTAAGAAAATGCGAAAGCCCTC 571
QY 256 AGCATCTGAAGAGAGCTGTTACAGCAATGATCAAAAAGAAAACACAGGCCCTTCCC 315
DB 572 AGCGGCGCAAGAGAGCTGTTACAGCAATGATCAAAAAGAAAACACAGGCCCTTCCC 631
QY 316 CTTCCCCCACTACTGATGTAAGAGCTCTTCCATTTCCATAGTAATTTCTAGATAC 375
DB 632 CTTCCCCCACTACTGATGTAAGAGCTCTTCCATTTCCATAGTAATTTCTAGATAC 691
QY 376 AGCTGTAGAGCTCAAGTAAGTAAGAGCTCCCATTCAGAGAAATTTACTTA 433
DB 692 GTCTGTAGAGCTCAAGTAAGTAAGAGCTCCCATTCAGAGAAATTTACTTA 749
RESULT 12
US-10-002-491-10
Sequence 10, Application US/10002491
Publication No. US20030109467A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Andrew T. Walt
TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
FILE REFERENCE: RTS-0239
CURRENT APPLICATION NUMBER: US/10/002,491
CURRENT FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 91000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 73772-74071
OTHER INFORMATION: n = A, T, C or G
NAME/KEY: Intron
LOCATION: (576) ... (19018)
OTHER INFORMATION: Intron 1
NAME/KEY: Intron
LOCATION: (19154) ... (19785)
OTHER INFORMATION: Intron 2
NAME/KEY: Intron
LOCATION: (19919) ... (37293)
OTHER INFORMATION: Intron 3
NAME/KEY: Intron
LOCATION: (37660) ... (58973)
OTHER INFORMATION: Intron 4
NAME/KEY: Intron
LOCATION: (59115) ... (61405)
OTHER INFORMATION: Intron 5
NAME/KEY: Intron
LOCATION: (61540) ... (63027)
OTHER INFORMATION: Intron 6
NAME/KEY: Intron
LOCATION: (63127) ... (63463)
OTHER INFORMATION: Intron 7
NAME/KEY: Intron
LOCATION: (63564) ... (67187)
OTHER INFORMATION: Intron 8
NAME/KEY: Intron
LOCATION: (67335) ... (87922)
OTHER INFORMATION: Intron 9
NAME/KEY: Intron
LOCATION: (88037) ... (89288)
OTHER INFORMATION: Intron 10
US-10-002-491-10
Query Match 5.5%; Score 338; DB 15; Length 91000;
Best Local Similarity 45.5%; Pred. No. 8, 2e-67;
Matches 1134; Conservative 0; Mismatches 1280; Indels 78; Gaps 13;

QY 471 ATATATAGTTGTTAGCCGCGCGGCTGACAGCCCTGTAATCCAGCCCTTTGGAGG 530
DB 72916 AATTCACGTCATTCATCCGCGCGGCTGACAGCCCTGTAATCCAGCACTTTGGAGG 72975
QY 531 CCAGAGTGGGAGATCATGAGTCAAGATTGAGACCAAGCTTCAATGATGTAAC 590
DB 72976 CTGAGCAGAGTGAATACAGAGTCAAGATTGAGACCAAGCTTGGCAATGTAAC 73035
QY 591 CCGCTCTACTAATGAATACAAAATTTAGCAGTGTGTGGGCAACCTGTAAACCC 650
DB 73036 CTGTGCTCTAATTAATAATTTAATAATTTAGCAGTGTGTGGGCAACCTGTAAACCC 73095
QY 651 AGCTGCTCAG 709
DB 73096 AGCTACTCAG 73155
QY 710 AGCAAGATCACACCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
DB 73156 AGCAAGATCAG 73215
QY 770 AAAAAAAAAAAAAAAAAAATGTAAGTTGCTAT-----AACAAATTA 812
DB 73216 ACAAACAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 73275
QY 813 ATAGAGAGTA--GAAGCAAGTCTAAGCCTATGACATGTAATCTGTAATCTG 870
DB 73276 CCGTCAAGCATTGATCTACTCTCTTTGCTGACACACATTTCTCTAGTACTG 73335
QY 871 GGAACATATATTAAGGAACCTAACCCAGCTCTGAA-----GTAAAGT 914
DB 73336 AGAGTTCGTGCTTCATCAATATGATATCTTTCTTATGATATTCACAGATATCTCA 73395
QY 915 TTTGGAAGAAATGTTTGAAGCAAAAGGTTAAAGAGTGAAGAAAATTTAAATATC 974
DB 73396 CTTTGCTTTCTTCACTAAGAAAACCTGCGCTGAGTGAAGTCTTAACTTAA 7455
QY 975 CAGTTAGCTGTGTGAAGATGGATAGGAGCTAATAGAAATCAATAGGAATGTT 1034
DB 73456 TCTGTGCTTGAAGCTGAGAACTGAACAGTATGATGCTTAAACCAAGTTATGATCA 73515
QY 1035 TCATGATATGTTAAAGAACCTGTAAGGTAAGACATTAATCTGACATCGCG 1094
DB 73516 AACTCTAGAGTGAAGCTGATCTTCCATGATATCCCTTTCTTACCAATCACTCTT 73575
QY 1095 GGAATTTTTTTTATGTAATGCTTGGCAATTT-----AATAGAGAGCA 1140
DB 73576 ATACTATGAAATATGCTTGTACCTTCTTTCTTCAATTTCCACATCTTCCCA 73635
QY 1141 GAGATGTGACAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 73636 CTCATTTCTCACTATTAATCTTTGTGAGAAAGTGTCTTTCAAGACATGCAATGAG 73695
QY 1201 AGACAGTAGGCAAGAGAGTTGAA-----GAGATTAACAAGACAGATTAATGCTG 1256
DB 73696 TGAAGCTCAAGATATGATGATCAACCCAGCTTCAAGAAATGTAATCAAGCTTGA 73755
QY 1257 CAGTGCACTAGTGTGATCTATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1316
DB 73756 AAGATGAATCCCGAG 73815
QY 1317 TACTATGAG 1376
DB 73816 NNN 73875
QY 1377 ATTGAGAAAGATACTGTGAGAGAGAGATTTTCAAGCTTGAAGTCACTCAATAC 1436
DB 73876 NNN 73935
QY 1437 CAGACATGTGTAAATGCTTCAAGACATGATCCCTGCTCAAGAGGACTTACAGCCAA 1496
DB 73936 NNN 73995
QY 1497 AAACAAGAGATTAAGAAATACACACCAATATCTTATAGAGACCTGTGTAGATATCAAG 1556


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QY 777 AAAAAAATATGTAAGTTGCTATACAAATTAATAGGCAAGCAAGTCT 836
DB 13420 AAAAAAAAACTGTAAATGGAAGCCAT--CAGTATATTAGTACTTAAAGACATGATTT 13363
QY 837 AAAGCTATGACCATGTAATCTAGGAATAGTGGGAACATTAATAGGAACTTAAC 896
DB 13362 AATGAGAAACAGCTTAAAGATTAATAGCATTGTATCTTCAATGAAAG--C 13309
QY 897 CAGTCTGGAAGTAAAGTTTGGAAAGAAATGTTTGGAGCAAAAGGTTAAAGAGTGA 956
DB 13308 AAGAAGTAATTAACAGGTGAAGATCTAAATATTTAAATTAATCAAGAGAAAT 13249
QY 957 AAAAAAATTAATAATCAAGTTTACGTGTGGAGAGATGGATAGGAGCTAATAGAG 1016
DB 13248 ATAGGAATATATTGGCAAGATCTTGGAGACAGAGAGTTCTTCCAAAGCATGATGAAAT 13189
QY 1017 AATCAATATAGAAATGTTTCATGATGTTAAAGACCTGTGAAGGTGAAGCAATTAC 1076
DB 13188 TCAAAAGCCAAATTTTACTTCAAGAAATTTCTCAATGGGAAAGACAAATATAA 13129
QY 1077 ATTATCTGACCACTCCGCGGACTTTTTTTTATGTAATGCTTGGCAATTTAATAGAG 1136
DB 13128 ATTAATGCTACTATTGTAACAAACAAAGTTAAATATCTGAAACACTAAGCTACT 13069
QY 1137 AGCAGAAATGTAACAGTTGATGATGATGAGTGAAGTTCTGCCAGACATGTAAAG 1196
DB 13068 CCAATTTACTAAGAAATTTTAAATACTAAAGAAA--TGGACAGATTAAGACTAGG 13012
QY 1197 GAAGACAGATGGAAGAGTTGAAGATTAACAGACAGAGTTAATGCTGCGC 1256
DB 13011 CAGATCCAG-----AAGAAATAAATGACTTAAACAAATAGAGCCTGTGACAGTA 12960
QY 1257 CAGTGCATCTAGTCTGAGTCTAATCTAGGGAAGAGATGAAGACGTTCTCTGA 1316
DB 12959 TTCAGCCTGTATATCCAGACATTTGGAGGCGGAGGACAGATCACTGAAGTTGGG 12900
QY 1317 TAGTTATGAAGAGATGGAAGGCTTCAAGACCTACAGGTGTTAATTAAGAAATG 1376
DB 12899 AGTTCAAGACAGCCTGACCAACATGAAACCCCATCTCTAATAAATAAATAATTA 12840
QY 1377 ATTTG-----GAGAAAGATTAATCTGAGAGATGAGATTTTCAGGCTTGAGTACTCA 1431
DB 12839 GCTGAGCGTGTGGCGCATGCTGTATATCCAGTACTCCAGAGGCTGAGGCAAGAAAT 12780
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8149
; LENGTH: 31474
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8149

Query Match
Best Local Similarity 5.2%; Score 334.4; DB 10; Length 31474;
Matches 755; Conservative 0; Mismatches 536; Indels 29; Gaps 7;

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FT      DR
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FT      XX
FT      New human kinase peptide and nucleic acid molecule, useful for treating
FT      PT disorders associated with abnormal expression of kinase protein, e.g.
FT      PT adenocarcinoma of uterus or lung, in drug screening assays and
FT      PT pharmacogenomic analysis.
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FT      Claim 4; Fig 3; 131pp; English.
FT      PS
FT      The present invention provides the protein, cDNA and gene sequences of
FT      CC two splice variants of a human pftaire family kinase. The sequences are
FT      CC specifically expressed in the human testis, brain, uterus endometrium
FT      CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and
FT      CC can be used to treat related diseases. The present sequence is the gene
FT      CC of the invention
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Db	22040	ATGTTCAAGAAAGACACCCCAAGTCAATGTTTGTATGAGGTTAGAGAAACACAGTGT	22099
Oy	2101	TTGCAATCTCAGGTTCCATTAGTGGGTTATGAAATCAATATGATGATGAGCACTGCA	2160
Db	22100	TTGCAATCTCAGGTTCCATTAGTGGGTTATGAAATCAATATGATGATGAGCACTGCA	22155
Oy	2161	TTTTTAAAAAATGAAATTAATGATGAGAAAGAAATGAAATTAATGATGATTAACATT	2220
Db	22160	TTTTTAAAAAATGAAATTAATGATGAGAAAGAAATGAAATTAATGATGATTAACATT	22219
Oy	2221	TTGAAAGACAGATTAATTTCTGCACTTTTGTCCAAATGTAACTGTACTTAATTT	2280
Db	22220	TTGAAAGACAGATTAATTTCTGCACTTTTGTCCAAATGTAACTGTACTTAATTT	22279
Oy	2281	TTATGTATGATGTGAATACCAATATCATATATTTCTATCTGTATGATGAGTCAAA	2340
Db	22280	TTATGTATGATGTGAATACCAATATCATATATTTCTATCTGTATGATGAGTCAAA	22339
Oy	2341	AATCTTTTAAAGCACTGGCTGTGCTAACTTCCTATTTTTCAGAGAGAAATCCAAATC	2400
Db	22340	AATCTTTTAAAGCACTGGCTGTGCTAACTTCCTATTTTTCAGAGAGAAATCCAAATC	22399
Oy	2401	TGAGAGGACAAACATTTTGGCTGAGGTTATGAAACAGCTTATGCAATTGCTPAAAGTGA	2460
Db	22400	TGAGAGGACAAACATTTTGGCTGAGGTTATGAAACAGCTTATGCAATTGCTPAAAGTGA	22455
Oy	2461	TTCTTACTTAAATTTCTTTCCCACTATGTCGCAATCTGCACTTCTATCTGTGGCTGA	2520
Db	22460	TTCTTACTTAAATTTCTTTCCCACTATGTCGCAATCTGCACTTCTATCTGTGGCTGA	22519
Oy	2521	AATACAGAAATATATATAGTAAACAGATACACAACTCTGGGGAATAATATTTGGTGTAGTG	2580
Db	22520	AATACAGAAATATATATAGTAAACAGATACACAACTCTGGGGAATAATATTTGGTGTAGTG	22579
Oy	2581	GCTGAGAGCTCATTTTCTTAAGAATGTGACCTTATGCAAGGATATGTGGCTCACACTT	2640
Db	22580	GCTGAGAGCTCATTTTCTTAAGAATGTGACCTTATGCAAGGATATGTGGCTCACACTT	22639
Oy	2641	ATATTTTCACACACTTTGGAGGCGCAAGTCAAGAAAGATCGCTTGAAACCAAGAGTTCAAA	2700
Db	22640	ATATTTTCACACACTTTGGAGGCGCAAGTCAAGAAAGATCGCTTGAAACCAAGAGTTCAAA	22699

QY	2701	CTACATGGGCAACATAGCAAGACCTCATCTCTCAAAAAATTTAAAAATCAGCTGAGCA	2760
Db	22700	CTACATAGGGCAACATAGCAAGACCTCATCTCTCAAAAAATTTAAAAATCAGCTGAGCA	22759
QY	2761	TGCTGGCATACGCTGTAGTCCACCTACCTGGAGCTAGGTGGTGGATCGCTTACA	2820
Db	22760	TGCTGGCATACGCTGTAGTCCACCTACCTGGAGCTAGGTGGTGGATCGCTTACA	22819
QY	2821	CAGGATTTTGAAGCTTAAGTGAAGCCATGATCACAACTGCACTCCAGCTTGAAGTGA	2880
Db	22820	CAGGATTTTGAAGCTTAAGTGAAGCCATGATCACAACTGCACTCCAGCTTGAAGTGA	22879
QY	2881	AGGAAGACCCCTGCTCCCTAAAAAGAAATGTGGATTTTATCTCTTAAACGCTAAGT	2940
Db	22880	AGGAAGACCCCTGCTCCCTAAAAAGAAATGTGGATTTTATCTCTTAAACGCTAAGT	22939
QY	2941	CATTAGTCATTAAAGTTTGAAGTGAAGAAATATATGATCAGAGAAATTTATATCACT	3000
Db	22940	CATTAGTCATTAAAGTTTGAAGTGAAGAAATATATGATCAGAGAAATTTATATCACT	22999
QY	3001	GTGTCTGTAGGATATTTGAAGAAATTAAGACCTAGCTCAGGGATTCGACTTAAAGT	3060
Db	23000	GTGTCTGTAGGATATTTGAAGAAATTAAGACCTAGCTCAGGGATTCGACTTAAAGT	23059
QY	3061	TTTGTGTTGTTGTTTGAAGACAGAGTCTCTTTTGTAAACGAGCTAGAGTGAAGTGTG	3120
Db	23060	TTTGTGTTGTTGTTTGAAGACAGAGTCTCTTTTGTAAACGAGCTAGAGTGAAGTGTG	23119
QY	3121	CAGTCATGAGTCAACCGAGCCTCAAACTCCAGCCTCAAAATTAATCTTCCAGCTCGGCT	3180
Db	23120	CAGTCATGAGTCAACCGAGCCTCAAACTCCAGCCTCAAAATTAATCTTCCAGCTCGGCT	23179
QY	3181	CCCAAGTGTGGAATTAACAGGTGTGAGCCAAAGGTTTATGATGTGTGTGCTGCTAAGT	3240
Db	23180	CCCAAGTGTGGAATTAACAGGTGTGAGCCAAAGGTTTATGATGTGTGTGCTGCTAAGT	23239
QY	3241	GCCTCTCAAACTTCAGTGAAGACAGCAAGTGAACGGGAACTGACTCAACAACTGGGTT	3300
Db	22420	GCCTCTCAAACTTCAGTGAAGACAGCAAGTGAACGGGAACTGACTCAACAACTGGGTT	23299
QY	3301	TAAAGCTGAGCCTCTGCTATTCATGATCAAGCTAGTGAAGTGTGTGTGCTGCAAG	3360
Db	23300	TAAAGCTGAGCCTCTGCTATTCATGATCAAGCTAGTGAAGTGTGTGTGCTGCTGCAAG	23359
QY	3361	GCCAGACCTGAGACGAGAGGATCTAGTGAATTAAGTGAATCAAGTGTGATTTATGTGT	3420
Db	23360	GCCAGACCTGAGACGAGAGGATCTAGTGAATTAAGTGAATCAAGTGTGATTTATGTGT	23419
QY	3421	AGTGAACATTAAGATGAGAGGATGTGAATCAGTAACAAAGAAAGATTCACCTTGG	3480
Db	23420	AGTGAACATTAAGATGAGAGGATGTGAATCAGTAACAAAGAAAGATTCACCTTGG	23479
QY	3481	GTAATGTGAGCATGAGAGGAGAAAGATGGGGCCAAACATTAATCTGTTTTGTGTGACT	3540
Db	23480	GTAATGTGAGCATGAGAGGAGAAAGATGGGGCCAAACATTAATCTGTTTTGTGTGACT	23539
QY	3541	GACGAGAGAAATTTGATGCTTATTAACAGAAATAGGAGAAAGTGTGTGAGAGAAA	3600
Db	23540	GACGAGAGAAATTTGATGCTTATTAACAGAAATAGGAGAAAGTGTGTGAGAGAAA	23599
QY	3601	GAGAGTCTCTGTTTCAAGCGTGTGAGTCCAGGTGAGACAGAGTCTCCAAAGGAAAT	3660
Db	23600	GAGAGTCTCTGTTTCAAGCGTGTGAGTCCAGGTGAGACAGAGTCTCCAAAGGAAAT	23659
QY	3661	GAGCACTAGGCAACCTTAAGAAATCTGTGCTCAAGAGGAGCTGTGAGCTGACGTGT	3720
Db	23660	GAGCACTAGGCAACCTTAAGAAATCTGTGCTCAAGAGGAGCTGTGAGCTGACGTGT	23719
QY	3721	AGATCTGAGGGTCAATGACCATAGAGTTTGAAGAACAGAGGTAGGCAACCAAGAGAC	3780
Db	23720	AGATCTGAGGGTCAATGACCATAGAGTTTGAAGAACAGAGGTAGGCAACCAAGAGAC	23779

QY	3781	AAATTAACAAGAGAGAGAGCTGATGATGAGACTTTTGCTTTTGAATGAGAGAGA	3840
Db	23780	AAATTAACAAGAGAGAGAGACTGATGATGAGACTTTTGCTTTTGAATGAGAGAGA	23839
QY	3841	ACAGAAATGAAGGATGAAGGGAAACAGCTGTGTAGAAATGTAGACATCTGAAAAAAA	3900
Db	23840	ACAGAAATGAAGGATGAAGGGAAACAGCTGTGTAGAAATGTAGACATCTGAAAAAAA	23899
QY	3901	ATACACCTGTCAATGGAAGTCAAGGGAGAGAAATTTCAAGAGAGAGGTATGTGTACA	3960
Db	23900	ATACACCTGTCAATGGAAGTCAAGGGAGAGAAATTTCAAGAGAGAGGTATGTGTACA	23959
QY	3961	GTAATTAACAAGCATCAGAAATTAACAGTAAAGTCAATCTTTGATCTGACATTTGACTGTG	4020
Db	23960	GTAATTAACAAGCATCAGAAATTAACAGTAAAGTCAATCTTTGATCTGACATTTGACTGTG	24019
QY	4021	ATTGTGAGGAGACACTAATAAATTAAGAAATTTATGTGGGTATATGAGAGCAAAAG	4080
Db	24020	ATTGTGAGGAGACACTAATAAATTAAGAAATTTATGTGGGTATATGAGAGCAAAAG	24079
QY	4081	GAAGAGTTATCCAAATCAAGCAAGGTGGAGTGGATGAGTCTCCAAAGGTGAGGCA	4140
Db	24080	GAAGAGTTATCCAAATCAAGCAAGGTGGAGTGGATGAGTCTCCAAAGGTGAGGCA	24139
QY	4141	TCAGTGAATGTGGGAAGGGGCAACAGACATCCATGCCATCCAGGCAAGCCCTCCA	4200
Db	24140	TCAGTGAATGTGGGAAGGGGCAACAGACATCCATGCCATCCAGGCAAGCCCTCCA	24199
QY	4201	GAAGCTCCATGAGAGTTGAGTATCCAGAAAGTCTGTGATCCCTAATCTTTCTGGGTT	4260
Db	24200	GAAGCTCCATGAGAGTTGAGTATCCAGAAAGTCTGTGATCCCTAATCTTTCTGGGTT	24259
QY	4261	TGATATAGCTTCAATGTGTAGGCAATGATTTATTAACATATGGCCACTGTGATCACTT	4320
Db	24260	TGATATAGCTTCAATGTGTAGGCAATGATTTATTAACATATGGCCACTGTGATCACTT	24319
QY	4321	AACTTTCAACCCCTCTCCCTCCCTAATCATCTTGTGCTTCCAGTGAACCAAGTCCCTA	4380
Db	24320	AACTTTCAACCCCTCTCCCTCCCTAATCATCTTGTGCTTCCAGTGAACCAAGTCCCTA	24379
QY	4381	TCTTAAGCTAACCAATGTGTGCGACGATCATGCTCAACTTCAAAAAAGACATCACTTTG	4440
Db	24380	TCTTAAGCTAACCAATGTGTGCGACGATCATGCTCAACTTCAAAAAAGACATCACTTTG	24439
QY	4441	GAGATTCCTAAGATTTTGAAGTGTGCGTGCAGAAATTAAGTGAAGATCAAAATATAT	4500
Db	24440	GAGATTCCTAAGATTTTGAAGTGTGCGTGCAGAAATTAAGTGAAGATCAAAATATAT	24499
QY	4501	TTCAACAATATCAAGTGTGCTAATTTATATCAGGCGCCATTAATGTTTAAACAAAG	4560
Db	24500	TTCAACAATATCAAGTGTGCTAATTTATATCAGGCGCCATTAATGTTTAAACAAAG	24559
QY	4561	AGGTATTAATTCAGATTTTCTTTTATTAAGCTTACATGATGACAGTGTGTGAATG	4620
Db	24560	AGGTATTAATTCAGATTTTCTTTTATTAAGCTTACATGATGACAGTGTGTGAATG	24619
QY	4621	ATTGGGAATGAGGGAATCTTTTTTGAATGTATATCCCTGACCCCACTTCTTC	4680
Db	24620	ATTGGGAATGAGGGAATCTTTTTTGAATGTATATCCCTGACCCCACTTCTTC	24679
QY	4681	CTTGTGTTCTTCTACCTCTCTCCCTCTACTCAACAGAAAACTTCTCCCTCTACAT	4740
Db	24680	CTTGTGTTCTTCTACCTCTCTCCCTCTACTCAACAGAAAACTTCTCCCTCTACAT	24739
QY	4741	TCCCTGAATGTGTGTCTGTTAAGTTTCAAGCTTGAACGTGAGGCTTAATCAAGAAC	4800
Db	24740	TCCCTGAATGTGTGTCTGTTAAGTTTCAAGCTTGAACGTGAGGCTTAATCAAGAAC	24799
QY	4801	AGTGTATCAGATGTGAGATGTGTGGGAGAAAGTGAACATATGAAACCAATTACTTA	4860
Db	24800	AGTGTATCAGATGTGAGATGTGTGGGAGAAAGTGAACATATGAAACCAATTACTTA	24859
QY	4861	GCCGGAATGACGGGAAAAACAAGAGTCAAGATATTTTTTCTGATCTGAGATTTAAA	4920

D	b		2460	GCCGGA	CTGACGGGAAAAACAAGTCAAGCATTTTTTTTCGTCTGATCTGATATTAA	2491
O	y		4921	ATGATATG	TGTCATTCACTGTGATAGAAATCAGAAAATAAATTTATTTTGAGAG	4980
D	b		24920	ATGATATG	TGTCATTCACTGTGATAGAAATCAGAAAATAAATTTATTTTGAGAG	24972
O	y		4981	ATACCATG	AATGTGTTTAGACACTGCTAAGTTAGAGTAATTAAGGATGTACAGCCA	5040
D	b		24980	ATACCATG	AATGTGTTTAGACACTGCTAAGTTAGAGTAATTAAGGATGTACAGCCA	25032
O	y		5041	GCTCCAGA	CTGTGTGGGCGCTTAAAGTAAAGGCACATCTGAGTTGGAATTAAGATTTGA	5100
D	b		25040	GCTCCAGA	CTGTGTGGGCGCTTAAAGTAAAGGCACATCTGAGTTGGAATTAAGATTTGA	25092
O	y		5101	AATCATCAGA	ATACGGTTGTTCAATTAGACACTGTCAGTGGGTAAAGTATGCTAAGGAGC	5160
D	b		25100	AATCATCAGA	ATACGGTTGTTCAATTAGACACTGTCAGTGGGTAAAGTATGCTAAGGAGC	25152
O	y		5161	ATGTGTAG	TGATTAACAAGAACCAAAGCCCTAAGAAATCAATATGTTATTA	5220
D	b		25160	ATGTGTAG	TGATTAACAAGAACCAAAGCCCTAAGAAATCAATATGTTATTA	25212
O	y		5221	TTTATTTA	TTTTATTAATTTTTATTTTATTTTATTTATTTATTTATTTATTTTATTTAG	5280
D	b		25220	TTTATTTA	TTTTATTAATTTTTATTTTATTTTATTTTATTTATTTATTTATTTATTTTATTTAG	25272
O	y		5281	ACGGAGTCT	CGCTCTGCGCCAGGCTGAGTGCAGTGGCGMACTCAGCTCACCTGCA	5340
D	b		25280	ACGGAGTCT	CGCTCTGCGCCAGGCTGAGTGCAGTGGCGMACTCAGCTCACCTGCA	25332
O	y		5341	ACCTCGCT	CTCTGGGTTCAAGGAGCCTCTGCTCAGCCTCTCAAGTACTGGGACTA	5400
D	b		25340	ACCTCGCT	CTCTGGGTTCAAGGAGCCTCTGCTCAGCCTCTCAAGTACTGGGACTA	25392
O	y		5401	CAGGCACC	CAACCTACCTAATTTTTGATTTTATAGTAAAGAGGGGTTTCAAC	5460
D	b		25400	CAGGCACC	CAACCTACCTAATTTTTGATTTTATAGTAAAGAGGGGTTTCAAC	25452
O	y		5461	ATGTGGCC	AGGCTGTCTTGAACTTCTGACCTTGAATTCACCTGCCCTTGGCCTTCC	5520
D	b		25460	ATGTGGCC	AGGCTGTCTTGAACTTCTGACCTTGAATTCACCTGCCCTTGGCCTTCC	25512
O	y		5521	AAAGTCTG	GGAATTACAGTATGAGCACTGTGCTGGCTAATTTTGTTTTATPAG	5580
D	b		25520	AAAGTCTG	GGAATTACAGTATGAGCACTGTGCTGGCTAATTTTGTTTTATPAG	25572
O	y		5581	ATGGGGCT	CTTGCTATGTTGCCAGGCTGTGTAATCTCTGGACTTAACAAATCTCTCT	5640
D	b		25580	ATGGGGCT	CTTGCTATGTTGCCAGGCTGTGTAATCTCTGGACTTAACAAATCTCTCT	25632
O	y		5641	GCTTTGGC	CTCTCAAGTTACAATGTAGTCCCTGCGCTGAGCCAGAAATAT	5700
D	b		25640	GCTTTGGC	CTCTCAAGTTACAATGTAGTCCCTGCGCTGAGCCAGAAATAT	25692
O	y		5701	CAATATAT	TTAGATTTAGTAGAAGTACCTATGAAGAACAAGCCAGAGGGGACAGAG	5760
D	b		25700	CAATATAT	TTAGATTTAGTAGAAGTACCTATGAAGAACAAGCCAGAGGGGACAGAG	25752
O	y		5761	AAAAATTA	AGAGATTGTGGAACAAAGAGAGTGTCTCAGAGAGGAAGGATGTCT	5820
D	b		25760	AAAAATTA	AGAGATTGTGGAACAAAGAGAGTGTCTCAGAGAGGAAGGATGTCT	25812
O	y		5821	ATGATGCA	AAATGCTGAAAGTAAAGATTAAGAAATACATTTGGTTTCATAGGAAA	5880
D	b		25820	ATGATGCA	AAATGCTGAAAGTAAAGATTAAGAAATACATTTGGTTTCATAGGAAA	25872
O	y		5881	GTCAATGG	AAACCATGTGTGAATTAAGAAATCAATGTGCAAAAGCATTTT	5940
D	b		25880	GTCAATGG	AAACCATGTGTGAATTAAGAAATCAATGTGCAAAAGCATTTT	25932
O	y		5941	TATAGGGG	ATGAATTTTGTATTTCAAGAGCAAAAGTTCCATACATGGCAAGATCTA	6000

Dd		25940	TATAGGGGGAATGAAATTGTGATTTTCACAGAGCAAAACAGTTCATACATATGCACAATCTA	25939
Oy		6001	GTCGTGTGACCACCGGAGTAGTGCTCTGAAGTGTGATTTGGANAAGAGATCATTTGAGCTGA	6006
Dd		26000	GTCGTGTGACCCACGGGAGTTAGTGTCTAAAGTGTGATGGAGAAGAGATCATTTGAGCTGA	26050
Oy		6061	GGTTGGCTAGAGCTGTTCTCATGTGACACTAATGTCATGTGAGTCAACAGCTGTGATCCAAG	6120
Dd		26060	GGTTGGCTAGAGCTGTTCTCATGTGACACTAATGTCATGTGAGTCAACAGCTGTGATCCAAG	26111
Oy		6121	TGCCACATCTTTCAGTGAAATGACAGAGGGGATTGAGAGTTCACTGATGATGACCGCTAAA	6180
Dd		26120	TGCCACATCTTTCAGTGAAATGACAGAGGGGATTGAGAGTTCACTGATGATGACCGCTAAA	26177
Oy		6181	GAAAGTAAATGGAAGATGTGG	6201
Dd		26180	GAAAGTAAATGGAAGATGTGG	26200
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RESULT 2				
ADJ84182/c				
ID	ADJ84182	standard; DNA;	76698 BP.	
AC	ADJ84182;			
XX	DT	06-MAY-2004	(first entry)	
DE	Human c-rafi genomic DNA which is a target for antisense therapy.			
XX	antimicrobial; antiinflammatory; cytostatic; infection; inflammation;			
KM	tumour formation; anticsease therapy; human; c-rafi; do; target.			
OS	Homo sapiens.			
PN	MO2004003134-A2.			
PD	08-JAN-2004.			
PF	12-JUN-2003; 2003WO-USO18481.			
PR	26-JUN-2002; 2002US-0392020P.			
PA	(ISIS-) ISIS PHARM INC.			
PI	Monia BP, Freier SM, Manoharan M, Gaarde WA;			
DR	WPI; 2004-083026/08.			
PT	Decreasing levels of a preselected cellular mRNA in a cell, useful for			
PT	treating or preventing a disease associated with a preselected cellular			
PT	mRNA, comprises binding to the mRNA an antisense compound targeted to a			
PT	splice site on the mRNA.			
PS	Example 14; SEQ ID NO 1; 174pp; English.			
CC	The invention relates to a novel method for decreasing levels of a			
CC	preselected cellular mRNA in a cell or tissue comprising binding to the			
CC	preselected cellular mRNA an antisense compound which is specifically			
CC	hybridisable with a splice site on the mRNA and which is not a substrate			
CC	for RNase H when bound to the RNA. The method of the invention has			
CC	antimicrobial, antiinflammatory and cyostatic applications and may be			
CC	useful for decreasing levels of a preselected cellular mRNA in a cell or			
CC	tissue and thus for treating or preventing a disease or condition			
CC	associated with a preselected cellular mRNA or with a preselected target			
CC	cellular protein, particularly infection, inflammation or tumour			
CC	formation. The current sequence is that of the human C-rafi genomic DNA of			
CC	the invention which is a target for antisense therapy.			
SQ	Sequence	76698 BP;	21036 A;	16662 C; 17183 G; 21716 T; 0 U; 101 Other;
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Query Match	6.8%;	Score	419.8;	DB 12; Length 76698;
Best Local Similarity	52.3%;	Pred. No.	7.9e-65;	
Matches 1329; Conservative	0;	Mismatches	1152;	Indels 58; Gaps 16;

OY	449	TACTAATTTTGTGACATTTGGAAATTAATAAGTTTGTACCTGGCGGCTCACGCT	508
Db	5718	TACTAAAAATAAAAAAATTTTAAAAAAATTTTAAAAAACCGCGCGGCTCACGCT	5659
OY	509	GTAATCCAGCCCTTTGGAGGCGCCAGATGGGCGAGATCATGAGGTCAAGATTTTGAAC	568
Db	5658	GTAATCCAGCACTTTGGGAGGCCAAGGCAAGCGGATACAGAGGTCAAGATTCAGAAC	5599
OY	569	AGCTTACGCAACATGTGTAAACCCCGTCTTACTTAAGATTCAAAAATTAGCAGGTG	628
Db	5598	ATCTCGGCTTAACACGCTGAAATCCCATCTTAATAAAATCAAAAAATTAGCCGGGTG	5539
OY	629	GATGCGCAGACCTGTAAACCCAGCTGTGTGAGAGAGTGAAGGCGAGAAATTTGTTAAC	688
Db	5538	GTGCGCGGCTGTGTAGTCCCGCTTACTGGAAGCTGAAGCGAGGAATGGGTGAAC	5479
OY	689	CCAGAGGCGAGG- GTGACGCGAGCAAGATCACCAATGCACCT---GTAGCTGTAGT	744
Db	5478	CCAGAGGCGAGGCTTACATGAGGCAAGATGGGCGCACTGCACCTCCGTCTGGGCG	5419
OY	745	ACAGGCGCAAGCTCCAATCAAAAAAAAAAAAAAAAAAAAAAATGTAGTTGTCTATA	804
Db	5418	ACAGGCGCAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGACTAGAAAGTGTGGA	5359
OY	805	ACAAATAAATAGGCGGTGAGAGGCAAGGTGCTAAAGCCTATGACCATGTGTATCAAGAA	864
Db	5358	ATGTGATGATGATGAGGGGGAATTTTAAATGGGAATATATGCGCAGGCAACGGTGTCA	5299
OY	865	ACTGTGGAAACA- TAATAAGGAACCTAACCCAGTCTTGAAGTAAGTTTGA---	920
Db	5298	TGCTGTATCCAGCACTTTGGGAGCTGAGGACGAGATCACTGAGGTTGGAGTT	5239
OY	921	AAGAAATCTTGAGAGCAAAAGGTTTAAAGAGTGAATAAAAAAAAAATTAAATACAGTT	980
Db	5238	CGAAGCAGCCTGACCAACATGAGAAACCCCAATGTCTAATAAAATAAATAATTAACCG	5179
OY	981	AGCTGTGTGAGAAATGGGATAGGAGCTTAATGAGAAATCAATATAGAAATGTTCAAG	1040
Db	5178	GGCATTGGGCTGTATATCTCAGCTACTCGGAGGCTGAGGCAAGAACTGTTGAAC	5119
OY	1041	TATGTAAAGACCTGTGAAGGTGAAGACCATTAATAT-----	1081
Db	5118	TGGAGGCGAAGTTGACGAGCGGAGATGTGCCATTGCACTTGAGCTTGGGCAACA	5059
OY	1082	--CTGACCAATCGGGGACTTTTTTTTATGTATATATGCTTGGCAATTTAAATAGAGAC	1139
Db	5058	GGGTGAATCTCCGTCTCAATAAATAAATAAATAAATAAATAAATAAATAAATGGGATA	4999
OY	1140	AGAGATGTGACAGATTTGGATTTGAGTGAAGTGAAGTTCTGCAGACATGTGAAGAA	1199
Db	4998	ATAACACTTTCCTTGCAGGATTAATAGATTAACCTGAGAGCACTTGTGTGAGAGCC	4939
OY	1200	GAGACAGGTAGGCAAGAGATTGAAGATTAACAAGAAAGTAATGTCTGGCAG	1259
Db	4938	TGTGTGTGAGACTTCAGTGCCCTAGAGTGTGACTTGCCTGGGTTCAAAATTTGACCTG	4879
OY	1260	TGGCATCTAGCTAGGTCTATCTGAAGGAAGAAAGTGAAGATTAAGACGTTGTGATAG	1319
Db	4878	CATTTCCCTATCTGTGACTTGAAGACTCAATTTAACTTCAATTTTCCATTTCCCTCA	4819
OY	1320	TTATGAAGAGTGAAGGCTTCAAGACCTACAGGTGTGATTAATTAAGAAATGAT	1379
Db	4818	TCTATATGGAAG--TGAATGATACATCTCTTGAAGTTGTGAAGATTTATGTAAGTTT	4761
OY	1380	GGAGAAAGATTACTGTGAAGAG---TGAATTTTCAGGCTTGAAGTCACTCAATA	1435
Db	4760	AGAGTAAAGTACTTGAACAGTCCCTCTCTCATATTAACATGTGTGAAGTGTAGCTG	4701
OY	1436	CCAGACACTGTGCTAAATNGCTTCAAAAC-ATGATCCCTGCTTCAAGGACTTACAGCC	1494
Db	4700	TAAATTAAGAGCTATCTCCCTCTTTTCTTAAATAAACACTGTTTTCAGAAACCAAA	4641

QY	1495	AAAAA	CAAGATATGAAATACACCAAACTCTTTATAGAGACCTTGATGAATATCA	155
Db	4640	GAGTCAATATTAATACATCTTAATATATCATTTATCTTAATCTTGAGCAGATTC	4581	
QY	1555	AGAAAGAAATACATCTAATGTACTGTAGATGCAACGGCATCAAAAGATATCTTAGTT-	1613	
Db	4580	GAAAGCAACATTTGGTCAACCTTCTGATTAATCTCTTCAACATCCCAAGCTGATATTGG	4521	
QY	1614	-TCAAGATTTCAAGATTCGGCCGGGCGGGGGCTACGCTCTGTATATCCAGCATTTGG	1672	
Db	4520	CCCGACATTTAATCTTAAGAAATTTAAGGTGCTCAGCTGTAAATCCAGCATTTGG	4461	
QY	1673	GAGGCCGAGCGGGTGCATCAAGAGTCAGAGATCAAGACATCTGTGTAAACGGTG	1732	
Db	4460	GAGGCCGAGCGGGGGGATCAAGAGTCAGAGATCAAGACATCTCGGCTAAACGGTG	4401	
QY	1733	AAACCCGCTCTCTACAAAAATATTAATAATTTAGCCAGCGGTGGCGGGCGCTGTAG	1792	
Db	4400	AAACCCGCTCTCTCTAATAATAAAAAATTTACCGGGCGGTAGTGGCGGGCGCTGTAG	4341	
QY	1793	TCCGAGCTACTCAGAGGCTGAGGCAGAGATAGCGGTGAACCCGGGAGGTAGAGTTGC	1852	
Db	4340	TCCGAGCTACTCGGAGGCTGAGGCAGAGATAGCGGTGAACCCGGGAGCGAGCTTGC	4281	
QY	1853	-GTAGCCGAGATCGCGCACTGCGCTCCAGCTGGGCGACAGAGTGAAGTGGCTCA	1911	
Db	4280	AGTAGCCGAGATCGCGCACTGCACTCCAGCTGGGCGACAGAGCAAGCTCGTCTCA	4221	
QY	1912	AAAAAAAAAAAAAAAAAAAAA- - - -TTTCAGATTTAAACACACTGCATTTCAACAG	1967	
Db	4220	AAAAAAAAAAAAAAAAAAAAAAAAAATTTAAGAGCTGTGCTCATTTCAACTTTTCA	4161	
QY	1968	TCTAAGATAGAGAGCATGTTCACAGAGAGAAAAATGTTTCACAAAGGTACAGATAG	2027	
Db	4160	GCTCACTCGAAGATGGTACTCATTTTAAAAAATTTATGAGTGAATGAACCA	4101	
QY	2028	GGAATAGAGATATGTTCAAGAGAGAGACCCAGAGTCATGTTGTTAGGTTAGAG	2087	
Db	4100	TTTTAACTGAACATTTAGTGGCATTTAGTACATTCAGTCTTTTACAGCCACACCCCTA	4041	
QY	2088	GAACACAGATGTTTGCATCTCCAGGTCCTCATTAAGCGTAAATCAATATGTGG	2147	
Db	4040	GTTCAAAAATTTCCATTACTCCAAAGTAAACCCCTTAACATCAAGCATTTCTCC	3981	
QY	2148	TTAGCAACCTGCATTTTAAAAAATGAATTAATAGATGAGAAGAAATAGAAATATTAG	2207	
Db	3980	CCAATCC-CTGAAAGCTGTGCATACCAATATGCAATTCGTCTATGGAATTTTCTAT	3922	
QY	2208	CATCATTTACATTTTGAAGAGCAAGATTAATTTTTCGAACTTTCTCTCAA- - - -TTG	2263	
Db	3921	TCGTGATATTAATTAATAAATGAGACTCACAAATATGTGGCTTTTGTGACTGACTTTT	3862	
QY	2264	TAACTGACTTAATTTTATATGATAGGATGGAATACAGATACATATATATTTCTTACT	2323	
Db	3861	CACCTGGCAATATGTTTTCAGAGGTCATCCACATGTGAGCATGTGTCAACTTATTCA	3802	
QY	2324	GTAACTGAGTCAAAAATC- - - -TTTAAAGCATGCGCTGTGCTAACCTCTTATTGG	2380	
Db	3801	TTTTCACTGCTGAATTAATATCCCATGTAAATGTTATGCAACATTTGTATATCCATTCAT	3742	
QY	2381	CAGAGGAATATCCAAATCTGAGAGACAAACATTTTGGCTGAGGTTATAGAACACGCT	2440	
Db	3741	CTGTGTGTGACATTTGGGCTGTTTCCATTTTGGGCATCGTGTGTCTAAAAACATGTG	3682	
QY	2441	T- - - -ATGCCATTTGCTAAAAAGGATTTCTTAGTTAAATTTCTTTCCACTAGTGCATAC	2495	
Db	3681	TGTTACATGTGGGTGTCATATCCCTCACTTTAGATACCTCTGTGTTGGTGTAGAGAG	3622	
QY	2496	TGCATCTTAATCTGTGTGGCTGAATAACAGATATATTTAGGAACAAGCATACACAAG	2555	
Db	3621	GTCAAGTGTCTAAAGTATTTAGGAAGAAGTCTCAAGAAAGTATATAGAGAGAAGAAATGAG	3562	
QY	2556	TTGGGGAAATATATTTGGGTAGTGGCTGAGAGCTCATTTTCTAAGAAATGTGACCTT	2615	

Db 3561 TCTGAATGCTTGAAGGAATAGACATGCCCATGATGTCAGATCAGGAGGAAAT 3502
 Qy 2616 AGGACAGGATGATGATGCTCACAACCTAATTCAGACATTTGGGAGGCCAAGTCAAGAA 2675
 Db 3501 AGGCGGGGGGCGATGGCTCAGCCTTGTATCCCAACATTTGGAGGCTGAGGCAAGGCA 3442
 Qy 2676 ATGCGTTGAACCCAGATTCAAGACTAGCAGTGGGCAACATAGCAAGACCTCATCTTAC 2735
 Db 3441 ATCATCTGAGCTCAGAGATTAAAGACACAGCTGGCAACATGCAAAATCCCATCTCTAC 3382
 Qy 2736 AAAAAATTTAAATATAGCTAGCAGATGATGATGATGATGATGATGATGATGATGAT 2795
 Db 3381 TAAAAATACAAAATATAGCTGAGGATGATGATGATGATGATGATGATGATGATGAT 3322
 Qy 2796 AGCTAGTGGGTGA--TCGCTTGACACAGAGATTGAGGCTAAGGTGAGCCATGATCAC 2853
 Db 3321 GGCTGAGGCAAGAAATGCTTGAACCGGGGAGTTGAGGTTGCACTGAGCCAAAGTTGT 3262
 Qy 2854 ACACTGCACTCCAGCTTGAATGACAGAGAGAGACCCCTGCTTAAAGAAAGAAATG 2913
 Db 3261 GCCACTGCACTCCAGCTGGGCGACAGAGGAGACCTGCTCAAAAAAAGAAAAA 3202
 Qy 2914 TGGATTTTATCTCTTAC 2932
 Db 3201 AAAAAGATGTACCTTGGC 3183

RESULT 3

AA15610 standard; cDNA, 1930 BP.

AA15610;

25-JUN-1996 (first entry)

CROC-1 cDNA encodes c-fos promoter activating protein.

CROC-1; CROC-4; c-fos promoter activating protein; signal transducer; polyomavirus large T antigen; ds.

Homo sapiens.

Key Location/Qualifiers
 CDS 1..516
 FT /tag= a
 FT /product= "CROC-1"

W09601899-A1.

25-JAN-1996.

05-JUL-1995; 95WO-US007874.

08-JUL-1994; 94US-00272412.

(SCHE) SCHERING CORP.

Lin SL, Rothofsky ML;

WPI; 1996-097629/10.

P-PSDB; AAR90769.

Mammalian cell lines contg. recombinant vectors encoding c-fos promoter activating proteins - used to identify nucleic acids encoding signal transducing molecules which activate promoters.

Claim 13; Page 29-31; 41pp; English.

CC CROC-1 cDNA encodes a c-fos promoter activating protein of approx. 19 kD
 CC with an acidic amino terminal half and a basic carboxy terminus. The
 CC protein includes a kinase target domain which contains phosphorylation
 CC sites for a variety of kinases involved in signal transduction. CROC-1

CC mRNA is approx. 2.3 kb in length and present in all tissues examined. The
 CC cDNA is used in vectors, operatively linked to a nucleic acid encoding a
 CC polyomavirus large T antigen. Mammalian cell lines contg. these vectors,
 CC and vectors comprising a polyoma origin of replication and a nucleic acid
 CC suspected to encode and activating protein of the promoter, can be used
 CC to identify signal transducing molecules

SQ Sequence 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 U; 0 Other;

Query Match 6.5%; Score 402.6; DB 2; Length 1930;

Best Local Similarity 92.5%; Pred. No. 6.5e-62; Matches 444; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

Qy 16 CAATTTATGAAGAACCAATATACAGCTTAAATGAATGTGAGCTTAATATCCAGAG 75
 Db 245 CAATTTATGAAGAACCAATATACAGCTTAAATGAATGTGAGCTTAATATCCAGAG 304
 Qy 76 AACTCCCCCTTGTATGATTTGTAACAAAATTAATATGATGATGATGATGATGATGATGAT 135
 Db 305 CACCCCCCTTGTATGATTTGTAACAAAATTAATATGATGATGATGATGATGATGATGATGAT 364
 Qy 136 GAT 195
 Db 365 GAT 424
 Qy 196 AAGTTATCTTCAAGAGCTTACAGCGCTTAATGATGATGATGATGATGATGATGATGATGAT 255
 Db 425 AAGTTATCTTCAAGAGCTTACAGCGCTTAAATGATGATGATGATGATGATGATGATGATGAT 484
 Qy 256 AGCCATCTGAAGAGAGCTTACAGCAATTAATGATGATGATGATGATGATGATGATGATGAT 315
 Db 485 AGCCGCGCGAGAGAGAGCTTACAGCAATTAATGATGATGATGATGATGATGATGATGATGAT 544
 Qy 316 CTTCCTCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
 Db 545 CTTCCTCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
 Qy 376 AGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
 Db 605 GCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664

RESULT 4

AA16738 standard; cDNA, 1930 BP.

AA16738;

25-MAR-2003 (revised)

18-JUN-1998 (first entry)

cDNA encoding human CROC-1 protein.

CROC-1; activating protein; promoter; proto-oncogene; c-fos; antagonist; ds.

Homo sapiens.

Key Location/Qualifiers
 CDS 1..516
 FT /tag= a
 FT /product= "CROC-1"

US5736331-A.

07-APR-1998.

18-OCT-1995; 95US-00544900.

PR	08-JUL-1994 ;	94US-00272412.
PR	05-JUL-1995 ;	95MO-US007874.
XX		
XX	(SCHE) SCHERING CORP.	
PA		
XX		
XX	Rothofsky ML, Lin SL;	
PI		
DR	WPI, 1998-239204/21.	
DR	P-FEDB; AAM46892.	
XX		
PT	c-fos Promoter-activating proteins - assay for nucleic acids encoding	
PT	such proteins, assay for antagonists, etc.	
XX		
XX	Claim 16; Col 15-18; 12pp; English.	
XX		
CC	The present sequence encodes a novel human protein, designated CROC-1.	
CC	The protein is an activating protein of promoter of the proto-oncogene c-	
CC	fos. The specification describes a mammalian cell line whose cells	
CC	contain a recombinant expression vector comprising a reporter operatively	
CC	linked to a human c-fos promoter and a second expression vector	
CC	comprising a nucleic acid encoding that activates the human c-fos	
CC	promoter (e.g., CROC-1). Antigenic fragments of the CROC-1 protein can be	
CC	used to prepare antibodies, which are used to assay for or purify the	
CC	activating protein. Antagonists of the CROC-1 protein bind to, but do not	
CC	activate, the human c-fos promoter. (Updated on 25-MAR-2003 to correct PR	
CC	file.)	
SQ	Sequence 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 U; 0 Other;	
Query Match	6.5%; Score 402.6; DB 2; Length 1930;	
Best Local Similarity	92.5%; Pred. No. 6,5e-62;	
Matches 434; Conservative	0; Mismatches 34; Indels 1; Gaps 1;	
QY	16 CAATTATGAAAGCCAAATATACAGCCTTAAATAGATGTGACCTTAATACCGAAG	75
Db	245 CAATTATGAAAGCCGAATATACAGCCTTAAATAGATGTGACCTTAATACCGAAG	304
QY	76 AACTCCCTTTGTGAAGATTGTGAACAAATAATATATAGATGAGTTAATAGTTCAATG	135
Db	305 CACCCCTTTGTGAAGATTGTGAACAAATAATATAGATGAGTTAATAGTTCAATG	364
QY	136 GAATGATGAACCCCAAGAGCCATATCAGGCTTAGCAAAATGGCAGAAATTCATATATCATCA	195
Db	365 GAGTGTGACCCCAAGAGCCATATCAGGCTTAGCAAAATGGCAGAAATTCATATATCATCA	424
QY	196 AAGTTATCTTCAAGAGCTTCAGCGCTTAATGATGTCTTAAAGAAATGTGAACGCGCTC	255
Db	425 AAGTTATCTTCAAGAGCTTCAGCGCTTAATGATGTCTTAAAGAAATGTGAACGCGCTC	484
QY	256 AGGCATCGAAGGACAGGTGTAACAGCAATGATGCAAAAAGAAAAACCAAGCGCTTCCC	315
Db	485 AGCGCGCCGGAAGGACAGGTGTAACAGCAATGATGCAAAAAGAAAAACCAAGCGCTTCCC	544
QY	316 CTTCCTCCCATCTTGATGATGAAGCAGCTCTCAATTTTCCATAGTAAATTTTCTAGATAC	375
Db	545 CTTCCTCCCATCTTGATGATGAAGCAGCTCTCAATTTTCCATAGTAAATTTTCTAGATAC	604
QY	376 AGCTTTGAGACTCAAGTACTCGAAGAAAGAAAGCTCCCAATTCAAGAAATTTATCTTAAG	435
Db	605 GTCCTTGAGACTCAAGTACTCGAAGAAAGAAAGCTCCCAATTCAAGAAATTTATCTTAAG	664
QY	436 ATACTGTAATGATACTCA-TTTTTGTGATTTGGAATATATTAAGTTGT 483	
Db	665 ATACTGTAATGATACTCAATTTTGTGATTTGGAATATATTAAGTTGT 713	
RESULT 5		
ADP61827	standard; DNA; 2394 BP.	
XX	ADP61827;	
XX		
XX	12-FEB-2004 (first entry)	

DE	Human ubiquitin-conjugating enzyme E2 variant 1 DNA.
XX	
XX	cell cycle arrest; cyrostatic; antiproliferative; antitumor; antineoplastic;
KW	vasectomized; antithyroid; melanoma; breast; ovarian; lung;
KW	gastrointestinal; colon cancer; Grave's disease; psoriasis;
KW	atherosclerosis; restenosis; vasoproliferative; human; ds; gene;
XX	ubiquitin-conjugating enzyme E2 variant 1; UBE2V1.
XX	
OS	Homo sapiens.
XX	
PN	WO2003088910-A2.
XX	
PD	30-OCT-2003.
XX	
PF	15-APR-2003; 2003WO-US011867.
XX	
PR	15-APR-2002; 2002US-00123566.
PR	15-APR-2002; 2002US-00123731.
PR	16-APR-2002; 2002US-0373366P.
XX	
PA	(RIGEL-) RIGEL PHARM INC.
XX	
PI	Hitoshi Y, Jenkins Y;
XX	
DR	WPI; 2003-865396/80.
DR	P-PSDB; ADF61828.
XX	
PT	Identifying a compound that modulates cell cycle arrest, for treating
PT	e.g. cancer, comprises contacting a cell comprising a target polypeptide
PT	and determining the chemical or phenotypic effect of the compound upon
PT	the cell.

PS	Claim 16; SEQ ID NO 11; 176pp; English.	
XX		
CC	The invention relates to a novel method for identifying a compound that	
CC	modulates cell cycle arrest comprising contacting a target polypeptide	
CC	within a cell with a compound and determining the chemical or phenotypic	
CC	effect of the compound upon the cell. The method of the invention has	
CC	cytostatic, antiproliferative, antiarteriosclerotic, vasotropic and	
CC	anti-thyroid applications and may be useful for identifying a compound	
CC	that modulates cell cycle arrest. Such compounds may subsequently be used	
CC	for developing therapeutic reagents to treat melanoma, breast, ovarian,	
CC	lung, gastrointestinal or colon cancer, as well as other proliferative	
CC	diseases such as Graves disease, psoriasis, atherosclerosis, restenosis	
CC	and other vasoproliferative diseases. The current sequence is that of the	
CC	human ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) DNA of the	
CC	invention.	
XX		
SQ	Sequence 2394 BP; 658 A; 605 C; 481 G; 650 T; 0 U; 0 Other;	
	Query Match	6.5%; Score 402.6; DB 10; Length 2394;
	Best Local Similarity	92.5%; Pred. No. 6.66-62;
	Matches 434; Conservative 0; Mismatches 34; Indels 1; Gaps 1;	
QY	16 CAATTTTGAAGCAATATATACAGCCTTAAATAGATGTGAGCCTTAATATCCAGAG	75
Db	464 CAATTTATGAAACCGAATATACAGCCTTAAATAGATGTGAGCCTTAATATCCAGAG	523
QY	76 AACTCCCTTGTAGATTGTATACAAAATTAATATAGAGATGTAATAGTTCTAATG	135
Db	524 CACCCCTTTGTAGATTGTATACAAAATTAATATAGATGTGAGTAAATAGTTCTAATG	583
QY	136 GAATGTGAACCCCAAGAGCATATACACGCTGACGAAATGGACAATTCATATATCA	195
Db	584 GAGTGTGAGNCCCAAGAGCATATACATGTCTAGCAAAATGGCAGAAATTCATATGACATCA	643
QY	196 AAGTTATCTTCAAGAGCTTCAAGCGCTTAATGATGTCTAAAGAAATGTGAACGCGCTC	255
Db	644 AAGTTGTCTGCAAGAGCTTCAGGCGCTTAATGATGTCTAAAGAAATATGAAATCTCCTC	703
QY	256 AGCCATCTGAAGACAGTGTTCACGCAATGATCAAAAAGAAAAACACAGCGCTTCC	315

Db 704 AGCCCCGAGAGACAGTCTTACAGCAATTAATCAAAAAACACAGGCCCTTCCC 763
 Qy 316 CTTCCCCCACTGATGATGACAGTCTTCAATTTCCATAGTAAATTTTCTAGATAC 375
 Db 764 CTTCCCCCAATTCATTAATCAAGTCTTCAATTTCCATAGTAAATTTTCTAGATAC 823
 Qy 376 AGCTGTAGAGCTCAAAAGTCTGGAAGAAAGAAAGCTCCCATCAAGGAATTTATCTTAG 435
 Db 824 GTCTGTAGAGCTCAAAAGTCTGGAAGAAAGAAAGCTCCCATCAAGGAATTTATCTTAG 883
 Qy 436 ATACTGTAATGATGACTAA-TTTTGTACATTTGGAATATATAGTTGT 483
 Db 884 ATACTGTAATGATGACTAAATTTTGTCCATTTGAATATATAGTTGT 932

RESULT 6
 ADL62300
 ID ADL62300 standard; DNA; 3802 BP.

XX ADL62300;
 AC 20-MAY-2004 (first entry)
 DT 20-MAY-2004 (first entry)
 XX Human ovarian cancer DNA marker #20512.
 XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX Homo sapiens.
 XX WO200170979-A2.
 PD 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009126.
 PF 21-MAR-2001; 2000US-0191031P.
 PR 25-MAY-2000; 2000US-0207124P.
 PR 15-JUN-2000; 2000US-0211940P.
 PR 07-JUL-2000; 2000US-0216820P.
 PR 25-JUL-2000; 2000US-0220661P.
 PR 21-DEC-2000; 2000US-0257672P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Lee J, Lillie J;
 PI WPI; 2001-611502/70.
 DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 XX cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.
 XX used to characterize stage, grade, histological type of ovarian cancer.
 PS Disclosure; SEQ ID NO 20512; 106pp; English.
 XX The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the

CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention.

XX Sequence 3802 BP; 979 A; 967 C; 837 G; 1019 T; 0 U; 0 Other;

Query Match 6.5%; Score 402.6; DB 5; Length 3802;
 Best Local Similarity 92.5%; Pred. No. 6.9e-62;
 Matches 434; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

Qy 16 CAATTTAGAAAGCCAAATATACAGCTTAAATATGATGTGACCTTAATACCGAAG 75
 Db 438 CAATTTAGAAAGCCAAATATACAGCTTAAATATGATGTGACCTTAATACCGAAG 497
 Qy 76 AACCCCTTGTAGATTTGTGAACAAATTAATATGAGTAGAGTTAAGTTCTAATG 135
 Db 498 CACCCCTTGTAGATTTGTGAACAAATTAATATGAGTAGAGTTAAGTTCTAATG 557
 Qy 136 GAATGTGAACCCAGAGCCATATCAGCGCTAGCAAAATGGCAGAAATCATATATCATCA 195
 Db 558 GAGTGTGAACCCAGAGCCATATCAGCGCTAGCAAAATGGCAGAAATCATATATCATCA 617
 Qy 196 AAGTTATCTTCAAGAGCTTCAGCGCTAATGATGTCTTAAAGAAATGTGAAACGCCCTC 255
 Db 618 AAGTTATCTTCAAGAGCTTCAGCGCTAATGATGTCTTAAAGAAATGTGAAACGCCCTC 677
 Qy 256 AGCCATCGAAGGAGAGTGTACAGCAATGTATCAAAAAGAAAACACAGGCCCTTCCC 315
 Db 678 AGCCATCGAAGGAGAGTGTACAGCAATGTATCAAAAAGAAAACACAGGCCCTTCCC 737
 Qy 316 CTTCCCCCACTGATGATGACAGTCTTCAATTTCCATAGTAAATTTTCTAGATAC 375
 Db 738 CTTCCCCCAATTCATTAATCAAGTCTTCAATTTCCATAGTAAATTTTCTAGATAC 797
 Qy 376 AGCTGTAGAGCTCAAAAGTCTGGAAGAAAGAAAGCTCCCATCAAGGAATTTATCTTAG 435
 Db 798 GTCTGTAGAGCTCAAAAGTCTGGAAGAAAGAAAGCTCCCATCAAGGAATTTATCTTAG 857
 Qy 436 ATACTGTAATGATGACTAA-TTTTGTACATTTGGAATATATAGTTGT 483
 Db 858 ATACTGTAATGATGACTAAATTTTGTCCATTTGAATATATAGTTGT 906

RESULT 7
 AAS63021
 ID AAS63021 standard; cDNA; 2144 BP.

XX AAS63021;
 AC 29-JAN-2002 (first entry)
 DT 29-JAN-2002 (first entry)
 XX Cell death protective sequence CNT-00726.
 DE Human; protective sequence; cell death; cerebral edema; infection;
 XX meningitis; degenerative disease; Alzheimer's disease; heart disease;
 XX motor neuron disease; demyelinating disease; multiple sclerosis; asthma;
 XX nutritional condition; peripheral nervous system disorder; ischemia;
 XX diabetic neuropathy; autoimmune hemolytic anaemia; respiratory system;
 XX oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;
 XX polycystic renal disease; urinary tract; genitalia; endometriosis;
 XX breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;
 XX adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;
 XX osteoporosis; cancer; autoimmune disease; ss.

OS Homo sapiens.
XX
XX WO200176532-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011655.
XX
XX 11-APR-2000; 2000US-00547596.
XX
XX (COGE-) COGENT NEUROSCIENCE INC.
XX
XX Barney S, Thomas MB, Portbury SD, Pirnam K, Katz LC, Lo DC;
XX
XX WPI; 2002-017408/02.
XX
XX Novel nucleic acids referred as protective sequences and their encoded
XX products for diagnosing, treating diseases involving cell death,
XX including neurological disorders e.g. stroke and for identifying
XX modulators.
XX
XX Claim 2; Fig ID; 256p; English.
XX
XX The invention relates to isolated protective sequence polypeptides (I)
XX and polynucleotides (II). (II) is useful for transferring a protective
XX sequence into a cell, which delays and/or prevents the cell from
XX undergoing cell death. Protective sequences, their products or antibodies
XX are useful diagnostically, prophylactically, therapeutically or as
XX targets for treatment and diagnosis of conditions, disorders or diseases
XX involving cell death. The protective sequences and their products are
XX useful for preventing or treating disorders of the central nervous system
XX including neurological and psychiatric conditions, cerebral oedema,
XX infections such as meningitis, degenerative diseases such as Alzheimer's
XX and motor neuron disease, demyelinating diseases such as multiple
XX sclerosis, nutritional conditions, disorders of the peripheral nervous
XX system including diabetic neuropathy, disorders which cause cell death in
XX organ systems including blood vessels, heart (ischaemia), blood cells
XX (autoimmune haemolytic anaemia), respiratory system (asthma), oral
XX cavity, gastrointestinal tract, liver (cirrhosis), pancreatitis,
XX polycystic renal disease, urinary tract, genitalia (congenital
XX anomalies), endometriosis, breast (chronic mastitis), thyroid gland
XX (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),
XX musculoskeletal system (muscular atrophy), bone marrow or bone
XX (osteoporosis). The compositions promote cell death and are useful for
XX treating and/or ameliorating cancer and autoimmune diseases. The
XX compounds are further useful for treating physiological impacts on organs
XX caused by infection which induce cell death. (I) is useful to raise an
XX immune response, as a reagent in assays designed to quantitatively
XX determine levels of the protein in biological fluids, as markers for
XX tissues in which the corresponding protein is expressed and to isolate
XX receptors or ligands. AAs62967-AAs63142 represent the protective
XX polynucleotide sequences as described in the invention
XX
XX Sequence 2144 BP; 608 A; 511 C; 434 G; 591 T; 0 U; 0 Other;
XX
XX Query Match 6.5%; Score 401.6; DB 6; Length 2144;
XX Best Local Similarity 92.3%; Pred. No. 9.9e-62;
XX Matches 434; Conservative 0; Mismatches 34; Indels 2; Gaps 1;
XX
QY 16 CAATTTATGAAAGCCAAATATACAGCCTTAATAATAGAGTGGACCTTAATACCGAAG 75
DB 195 CAATTTATGAAAGCCAAATATACAGCCTTAATAATAGAGTGGACCTTAATACCGAAG 254
QY 76 AACTCCCTTTGTAAGATTTGTAACAAATTAATATATGAGTGAATTAAGTTCTAATG 135
DB 255 CACCCCTTTGTAAGATTTGTAACAAATTAATATATGAGTGAATTAAGTTCTAATG 314
QY 136 GAATGTTGAACCAAGGACATATGACGCTAGCAAAATGGCAATTAATATATATATCA 195
DB 315 GAGTGTGACCAAGGACATATGAGTGTGACCAAAATGGCAATTAATATATATATCA 374
QY 196 AAGTATCTTCAGAGGCTTACAGCGCTATATGATGTCTAAAGAAATGTGAACGCGCTC 255
|||||

DB 375 AAGTGTCTCTGCAAGAGCTTCGGCGCTAATATGATCTTAAGAAAAATATGAATCTCCCTC 434
QY 256 AGCCATCTGAGAGACAGTGTTCACAGCAATTTGATCAAAAAAGAAAAACACAGGCCCTTCCC 315
DB 435 AGCCGCCGAGAGACAGTGTTCACAGCAATTTGATCAAAAAAGAAAAACACAGGCCCTTCCC 494
QY 316 CTTTCCCCCATCTGATGATGATGACAGTCTTCATTTTCCATGATGATTAATTTTCTAGATAC 375
DB 495 CTTTCCCCCATCTGATGATGATGACAGTCTTCATTTTCCATGATGATTAATTTTCTAGATAC 554
QY 376 AGCTGTAGAGCTCAAGTACTGAAAGAAAGAGCTCCATTCAGAAAGAAATTTATCTTAAG 435
DB 555 GCTTGTAGACCTCAAGTACTGAAAGAAAGAGCTCCATTCAGAAAGAAATTTATCTTAAG 614
QY 436 ATACTGTAAATGATATCTAATTTT--GTACATTTGGAATATATAAGTTGT 483
DB 615 ATACTGTAAATGATATCTAATTTTTCGTCATTTGGAATATATAAGTTGT 664
|||||
RESULT 8
ABK84356
ID ABK84356 standard; cDNA; 3335 BP.
XX
XX ABK84356;
XX
XX 14-AUG-2002 (first entry)
XX
XX Human cDNA differentially expressed in granulocytic cells #927.
XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
XX viral infection; parasitic infection; protozoal infection;
XX fungal infection; sterile inflammatory disease; psoriasis;
XX rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
XX cardiac reperfusion injury; renal reperfusion injury; ARDS;
XX adult respiratory distress syndrome; inflammatory bowel disease;
XX Crohn's disease; ulcerative colitis; periodontal disease;
XX granulocyte activation; chronic inflammation; allergy.
XX
XX OS Homo sapiens.
XX
XX WO200228999-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US030821.
XX
XX 03-OCT-2000; 2000US-0237189P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression of
XX PT genes associated with granulocyte activation, which serves as diagnostic
XX PT markers that is useful for monitoring disease states and drug toxicity.
XX
XX PS Claim 1; SEQ ID NO 927; 114p; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
XX (GCA), by detecting the level of expression of gene(s) (Gs) identified by
XX CC DNA chip analysis as given in the specification, and comparing the
XX CC expression level to an expression level in an unactivated GC, where
XX CC differential expression of Gs is indicative of GCA. Also included are
XX CC modulating (M2) GA by contacting GC with an agent that alters the
XX CC expression of at least one gene in Gs; (2) screening (M3) for an agent
XX CC capable of modulating GCA or an inflammation (especially chronic) in a
XX CC tissue, an allergic response in a subject, exposure of a subject to a
XX CC pathogen or sterile inflammatory disease using the gene expression
XX CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
XX CC tissue, an allergic response in a subject, exposure of a subject to a
XX CC pathogen or sterile inflammatory disease, by detecting the level of

expression in a sample of the tissue of gene(s) from G6, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from G6 in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 3335 BP; 839 A; 857 C; 715 G; 924 T; 0 U; 0 Other;

Query Match 5.9%; Score 365.8; DB 6; Length 3335;

Best Local Similarity 92.3%; Pred. No. 2.2e-55; Matches 396; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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OY 56 TGGACCTAAATATCCCGAAGAAATCCCTTTGTAAGTTTGTAAACAAAATTATATATGAG 115
DB 1 TGGACCTAAATATCCCGAAGAAATCCCTTTGTAAGTTTGTAAACAAAATTATATATGAA 60
OY 116 TAGAGTTAATAGTTCTTAATGGAATGGAACCAAGAGCCATATCAAGCTAGCAAAATG 175
DB 61 TGGAGTAATATAGTTCTTAATGGAATGGAACCAAGAGCCATATCAAGCTAGCAAAATG 120
OY 176 GCAGAAATCATATATCATCAAAAGTTATCTTCAAGAGCTTCAAGGCTTATATGATCTAA 235
DB 121 GCAGAAATCATATATCATCAAAAGTTATCTTCAAGAGCTTCAAGGCTTATATGATCTAA 180
OY 236 AGAAATATGAAAGCCCTCAAGCATCTAAGAGAGAGCTTATAGCAATGATCAAAAG 295
DB 181 AGAAATATGAAAGCCCTCAAGCATCTAAGAGAGAGCTTATAGCAATGATCAAAAG 240
OY 296 AAAAACAAGAGGCTTCCCTCCCTCCCAATCTGATGTAAGAGAGCTTCAATTTCCATA 355
DB 241 AAAAACAAGAGGCTTCCCTCCCTCCCAATCTGATGTAAGAGAGCTTCAATTTCCATA 300
OY 356 GATGTAATTTTCTAGATACAGCTTGTAGAGCTCAAAAGTACGAAAGAAAGCTCCCAT 415
DB 301 GATGTAATTTTCTAGATACAGCTTGTAGAGCTCAAAAGTACGAAAGAAAGCTCCCAT 360
OY 416 CAAAGGAATTTTCTTAAGATACGTAATATGATATCTAA-TTTTGTACCTTTGGAATAT 474
DB 361 CAAAGGAATTTTCTTAAGATACGTAATATGATATCTAA-TTTTGTACCTTTGGAATAT 420
OY 475 ATAAAGTTGT 483
DB 421 ATTAAGTTGT 429

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RESULT 9

ADN16203 standard; DNA; 264965 BP.

ADN16203;

01-JUL-2004 (first entry)

Human sulfatase SULF2 gene.

Human; sulfatase; SULF2; enzyme; cytosolic; thrombolytic;

antiinflammatory; chromosome 20q12-13.2; gene; ds.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 91625..190625
 FT /tag= a "Human SULF2"
 FT /product= "Human SULF2"
 FT /note= "Contains many introns"
 PN WO200401365-A2.
 PD 15-APR-2004.
 XX 02-OCT-2003; 2003WO-US031442.
 XX 03-OCT-2002; 2002US-00265071.
 PR (REGC) UNIV CALIFORNIA.
 PA (THIO-) THIOS PHARM INC.
 XX Rosen S, Hemmerich S, Tomita M;
 PI MPI: 2004-330173/30.
 DR P-PSDB; ADN16191.
 XX New sulfatase polypeptide, useful in diagnosing and treating tumor,
 PT inflammation and thrombosis.
 XX Example 5; SEQ ID NO 22; 326bp; English.

The present sequence is that of the novel human sulfatase SULF2 gene on chromosome 20q12-13.2. The gene was isolated from a database search using human SULF2 cDNA ADN16190. It comprises 21 exons. The encoded sulfatase exhibits glucosamine-6-sulfatase activity, is an endosulfatase, removes a sulfate group from glycoproteins and/or proteoglycans, is secreted from eukaryotic cells, acts on extracellular matrix (ECM) components to remove a sulfate group resulting in release from the ECM of extracellular CC differentiation factors and/or growth factors, is secreted in greater abundance from a cancer cell than from a non-cancerous cell of the same CC type, removes 6-sulfate groups from heparin and is pro-angiogenic. mRNA encoding the sulfatase shows elevated expression in tumours. Novel human CC and murine sulfatase polypeptides and polynucleotides of the invention can be used in diagnostic applications, for therapeutic agent screening CC and in the treatment of a variety of disease conditions, including CC tumours, inflammation and thrombosis. Methods are provided of modulating CC sulfatase activity and of treating disease conditions using such CC modulators, particularly by administering inhibitors of the novel sulfatases.

Sequence 264965 BP; 71910 A; 62351 C; 63451 G; 67116 T; 0 U; 137 Other;

Query Match 5.9%; Score 365.2; DB 12; Length 264965;

Best Local Similarity 52.8%; Pred. No. 4.1e-55; Matches 1289; Conservative 0; Mismatches 1043; Indels 108; Gaps 19;

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OY 486 GCCTGCGCGGTGCTCAAGCCTGTATCCAGCCCTTGGAGGCGCAGATGGCGAGAT 545
DB 218244 GCCAGGCGGCGGTGCTCGTGGCTGTATCCAAACTTTGGAGGCGCAGATGGCGAGAT 218303
OY 546 CATGAGCTCAGAGATTGAGACCAAGCTTACCAACATGATGAAACCCGCTCTTACTTAA 605
DB 218304 CATGAGCTCAGAGATTGAGACCAAGCTTACCAACATGATGAAACCCGCTCTTACTTAA 218363
OY 606 GATACAAAATTTAGCAGATGAGTGGGCGCACACTGTATACCCCGCTGCTGAGAGAG 665
DB 218364 AATTACAAAATTTAGCAGATGAGTGGGCGCACACTGTATACCCCGCTGCTGAGAGAG 218423
OY 666 TGAGGCAAGAGATTGCTTGAACCAAGAGGAGAGG-TGACGAGCAAGAAAGATCACACC 724
DB 218424 TGAGGCAAGAGATTGCTTGAACCAAGAGGAGAGG-TGACGAGCAAGAAAGATCACACC 218483
OY 725 AATGCACTGTAGCTGTGATGACAGGGCAAGACTCCAACTCAAAAAAAAAAAAAAAAAA 784

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Db	218484	ACTGCACCTCCACCTCTGGGCACACAGACCGAGACTCCCTCTCTCAAAAAAAAAAAAAAAAAAAAAA	218543
OY	785	AATATGTAACTTTGTGCTATTAACAATTAATAGGCATGTAGAAAGCAAGTCTAAAGCCTTA	844
Db	218544	AAAGCTCTGCCCCCATATATTTATCTCTTCTATGACATATTTCAATTAGAAAAACATCTAGAACG	218603
OY	845	TGACCATGGTAACTAGGAATACGTGTGGGAACAATTAATAGGGAACCTAACCCAGTCTCG	904
Db	218604	AAACCAAGTTTGGTTTGGAAAAAATCATATGGGCTTATATGTGAAGTAATTTTGGCAAAA	218663
OY	905	G-AAGTAAAGTTTGGAAAAAGAAATGTTTAGGACAAAGGGTTTAAAGAGTGAAAAAAAAA	963
Db	218664	GCTACTGGAGATTTTAAAGGCACTAATATTGAATAAGCTGACGAATAATAAACCAACAGTTC	218723
OY	964	AATTAATAATCAAGTTTACGTGTGTGGAAATATGGGTATAGGAGCTAACTTAGAAAAATCAA	1023
Db	218724	CAATATATCTGTTTAAATAATTCAGAAATTTTAATGTGTGCAAAAATCTTAATTAATGACAGGG	218783
OY	1024	ATAGGAATGTTTCATGCTATGTAAAGAACCTGTATAGGGTGAAGACCAATTAATATCT	1083
Db	218784	GGAGACTAGGAAAAAGGATTAACGATTTCTGGAAAAAGATTAATATCTGTGCACTCGTG	218843
OY	1084	GCACCATGCGGGGACTTTTATTTTATGTAAATGCTTGGCAATTTAATAATAGAG--AGCA	1141
Db	218844	CCCAAAATAGACATGATTTGTCTCAACCACTCTCTGATGTATAGCCCTGGGCCCATATG	218903
OY	1142	AGATGTAGACAGCTTGGATTTGAGTGCAGAGTTGAAGTTCTGCCAGACAT-GTGAAGAAAG	1200
Db	218904	ACAAATACAAAACAATATGCCATTAATAAAGTTTATTAATAGAAACACATCAGGACAGAAAG	218963
OY	1201	AGACAGTAAAGGCAAGAGATTGAAGATTTACAAGACGAAGTTAATG-TGCTGGCCAG	1259
Db	218964	ATTAATATATCCCAAGAGGTCAAAAGTAAGTAGATCTCAGTTTAAATATATGTAAATCAC	219023
OY	1260	TGGCACTAGTCTGAGTCAATCTGAGGGAAGAGTAAGTAAGACACTGCTGCATATG	1319
Db	219024	ACAAAGCATTTGATCTTCTTGCTTGGCAATTTTTTCTCCACATGCTCTGTTTCTTT	219083
OY	1320	TTATGAAAGAGGTGAAGGCTTCAAGAACCTTAACAGTGTGTATTAATAGAAATGAT	1379
Db	219084	CATGCTTGTAATTTCTAATCTTTTATTAATAACATGATCACCTTTATATATCATGATGAGA	219143
OY	1380	GGAGAAATAATTAATCTGTAGAGAGTGAATTTTCAGGCTTGAGTACTCTCATATCCAG	1439
Db	219144	TAAATTTCAA-----AGATGCTACTGTGTAATTTGCTTAAAGATATTTT	219187
OY	1440	ACACTGTGCTAAATGCTTCAAAAGACATGATCCCTGCCCTCAAGGACCTTACAGCCAAAA	1499
Db	219188	ATTATGTAATCTTCAATAGAAATATGAACAATGGCATTTCAAGTGAAGAAATTAACATGCTGC	219247
OY	1500	CAAGAGATTAAGAAATACACCAATATCTTATTAAGAACCTTGTGTGAATATCAAGAAA	1559
Db	219248	CAAAATCAATAAAGGCGCAGAGAAAGACT---CACTCTAAAGAAATTAATAATATATTA	219303
OY	1560	GAATAACATCTAGTAATCTGTAGATGTGCAAGCGCAATCAAGAATATCTTCTAATTTCAAGA	1619
Db	219304	CAATTTGCTGTACATATGTTTATCTAGGGGATTAATACAGGAAAAATGTTCAAAATATTA	219363
OY	1620	AGTTTCAGATCGGCGGCGCGCGGTGCTCAAGCCTGTATATCCACAGACTTTTGGAGCGCG	1679
Db	219364	AGTAACATA-CAGCGGCGCATGTGTGCTCATCTGTATATCCCAACACTTTGGAGGCGCG	219422
OY	1680	AGGGGGGTGAGTAC--AAGGTACAGAGATCAAGACATCTGTGTTAACAGGTGAATCC	1737
Db	219423	AGGCAAGGCGGATTAATCTGAGGTCAAGAACTTTGAAGCACAGCTGACCAACATTTGTAAACC	219482
OY	1738	CCGTCTCTACAAAAATTAATAAATTAATGACGAGGCTGTGGCGGCGCCTTAGTCCCA	1797
Db	219483	CTGTCTCTACTAAAAATGTAAAAAATTAAGCCAGGCGGTGTGTATAGGCGCCTGTATTTCA	219542
OY	1798	GCTACTCAGAGAGGCTGAGGCAAGAGATATGGGTGAATCCCGGAGGTGAATTTGC-GTGA	1856

Db	219543	GCCTACTGGGAGGCTGAGCAGAGGAATTCACCTTGAAACCCAGAGGACGAGCTGCAGTGA	219602
QY	1857	GCCGAGATCGGCGCACTGCGCTCCAGCTG3GG--CGACAGAGTGAGCTGCGTCTCAAA	1914
Db	219603	GCTGAGATCAATGCATTTGCACTCCAGCGTGG3GCGACAGAGCAAACTCCGCTCAAA	219662
QY	1915	AAAAAAAAAAAAAAAAAGTTTCAGATCTTAAACACACTGCATTTCAACGCTTGAA	1974
Db	219663	AAAAAAAAAATTAACA-----TCATTCAGGTTAAC	219693
QY	1975	TAGAGAGCATGTTTACAGGAGAGAAATGTTTTACGAAAGGTACAGACTAGGAAATA	2034
Db	219694	AAGATTATACGTGAATGTTCAAAATAATCTTTGCTACTTTTAATGTGAAAATTATC	219753
QY	2035	GAGGATATGTTCAAGGAAGAGAGCCCAAGTCAATGTTTGTAGGGTTAGAGAAAACA-	2093
Db	219754	TCAAAAATCCTGGAAGATAGGTTACTGATGCGATMAATGATTTATATGATCAGAAAATAG	219813
QY	2094	CAGTGTTTGCAATCTCCAGGTTCCATTAGTGGCTTATGAAATCAATATGCTGTTAGCA	2153
Db	219814	CAATATTTCTTTAAAAAATATTCGCAATTATGTAATATATATATATATATACATTTACAAACAC	219873
QY	2154	ACTGCATTTTAAAAATGAAATATGATGAGAGAGAAATAGAAAATATTTAGCATGCA	2213
Db	219874	ACATACATATGTAATATGATAGCTATGTTTATATATACCTACTCATATTT---TATA	219929
QY	2214	TTACATTTTGAAGAGAGATATATTTTGTGCACTTTTGCTCCAAATGTAATCTGACT	2273
Db	219930	TCATCTGTTAAAGTCCACATTTGTAATATAG-----TGTTACCAAAAGCA	219975
QY	2274	TATATTTTATATGATGATGTGAATATACAGATACATATATATTTCTTACTGTAAGCTGCA	2333
Db	219976	AAGATATCAGGCTTAAGTCAGGACAGACTCAGCTTAAATTTCTTATATAGCATGATCTTG	220035
QY	2334	GTCAAAAATCTTTAAAGCACTGGCGTGCCTAATCTCTATTTTGCAGAGGAAGAAATC	2393
Db	220036	GACATATACCCAAATCTCTGTACACAAAGCTTCTGTTCTTATCTGTAGATGG3GCA---	220092
QY	2394	CMAATCTGAGAGACAAACATTTTGCTGAGGTTATAGAACCCAGCTTATGCAATTGCTA	2453
Db	220093	-----TATATGACAAACCCTTGGCATCCCATTTTACCTTAGGTGACATATPAAGATA	220144
QY	2454	AAAGTGAATCTTATGTTAAAAATCTTTCCCACTAGTGCCATATCTGCACCTTCTGTT	2513
Db	220145	ACCTGTGAAGTAAATATAATAATATTTGCCACAGTGTTTATTTCAATATATGATCTTAT	220204
QY	2514	GGCTGTAAATATACGAATATATATAGTGAAACAGATACACAAGCTGTGGGAAATATATTTGG	2573
Db	220205	CAACCAAGATGTCCTTAAATTTT-----TATTTCTATGATTAATAAAATGG	220249
QY	2574	GTAGTGGCTGAGAGCTCAATTTTCTAAGAAATGTGGAACCTTAGCAGGGTATGTGGCT	2633
Db	220250	CAGACCAAGATTGAATCTCAGTGTGACGTTCAMAAATTAATCCCGGCAAGCACAGTGGCT	220309
QY	2634	CACACCTAATATTCGAGCACTTTGGGAGGCGCAAGTCAAGAAATGCGCTTGAACCCAAAG	2693
Db	220310	CACACTGTATATCCACGCAATTTTGGAGGCTGAGGCGAGGCACTCACTTGAGGTCAAGAG	220369
QY	2694	TTCAAGACTAGCATGGGCAACATAGCAAGACTCATCTCTACAAAAAATTTAAAAATCAG	2753
Db	220370	TTGAGAGACAGCCTGAGCAACATGTGTAACCCCATCTCTAATTAATAATACAAAATTAG	220429
QY	2754	CTGAGCATGCTGGCAATACGCTCTTATCTCCACTACTTGGGAAGCTA--GCTGGGTGATC	2812
Db	220430	CCGGGCAATGTGGCAGCTGCTGTATGATCCAAATGTTTGGAGGCGCATGGCAGGAAAATC	220489
QY	2813	GCTTG--ACAAGAGATTGAGCTTAAGCTGAGGCTCATGATCACACAATCTCACTCCAGTT	2871
Db	220490	ACTTTGAACCCAAAGATGAGATGTGAGATGAGCCGAGATCGACATTCATCCACAGCT	220549
QY	2872	GAGTGACAGAGAAACCTGTCTCTTAAAAAAGAAAGAA	2911
Db	220550	GGGCAACAGAGCAAGACTCGTCTCAACAAAAA-----220589	

ID	ABSS56563	standard; DNA; 26865 BP.
AC	ABSS56563;	
DT	27-JAN-2003	(first entry)
XX	Human SUF2 genomic DNA sequence.	
DE		
XX	SUF2, de; glucosamine-6-sulphatase; cancer; ischaemia; tumour;	
KW	angiogenesis; coronary; carotid; arterial occlusive disease;	
KW	peripheral arterial disease; atherosclerosis; myointimal hyperplasia;	
KW	thromboangiitis obliterans; thrombotic disorder; vasculitis;	
KW	heart attack; myocardial infarction; vascular death; inflammation;	
KW	rheumatoid arthritis; asthma; adult respiratory distress syndrome;	
KW	sarcoidosis; hypersensitivity pneumonitis; multiple sclerosis;	
KW	allergic rejection; lymphoma; thrombosis; sulphatase;	
XX	chromosome 20q12-13.2.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	misc_feature	8160..8701
FT		/tag= a
FT		/note= "This sequence represents 540 nucleotides not
FT		shown in the specification as the result of a printing
XX		error"
XX		
PN	NO2002559327-A2.	
XX		
XX	01-AUG-2002.	
PD		
XX		
PF	26-DEC-2001; 2001WO-US049793.	
XX		
PR	27-DEC-2000; 2000US-0258577P.	
PR	09-FEB-2001; 2001US-0267831P.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
XX	Rosen SD, Hemmerich S, Tomlita M, Palmeri D;	
PI	WPI; 2002-636541/66.	
DR		
XX		
PT	New sulfatase polypeptides having glucosamine-6-sulfatase activity,	
PT	useful in screening, discovery and preparation of diagnostic and	
PT	therapeutic agents for treating cancer, ischemic conditions,	
XX	inflammation, or thrombosis.	
PS	Example 5; Page 110-180; 293pp; English.	
XX		
CC	This invention relates to the DNA and protein sequences of a novel	
CC	polypeptide having glucosamine-6-sulphatase activity. The sulphatases	
CC	are useful in screening, discovery and preparation of diagnostic and	
CC	therapeutic agents for treating cancer, ischemic conditions,	
CC	inflammation, or thrombosis. The nucleic acids are useful in preparing	
CC	the sulfatase polypeptides, identifying the expression of genes in a	
CC	biological specimen, or generating transgenic non-human animals or site-	
CC	specific gene modification in cell lines. The host cells are useful in	
CC	replicating and/or expressing the polynucleotides or nucleic acids. The	
CC	agents are useful in treating the disorders cited above by reducing	
CC	tumour growth, inflammation, and thrombosis, or increasing angiogenesis,	
CC	e.g. by treating coronary, carotid, or arterial occlusive disease,	
CC	peripheral arterial disease, atherosclerosis, myointimal hyperplasia,	
CC	thromboangiitis obliterans, thrombotic disorders, vasculitis; or	
CC	preventing ischemic conditions, heart attack (myocardial infarction), or	
CC	other vascular death. The sulphatases and/or agents are also useful in	
CC	treating rheumatoid arthritis, asthma, adult respiratory distress	
CC	syndrome, sarcoidosis, hypersensitivity pneumonitis, multiple sclerosis,	
CC	allergic rejection, and spread of lymphomas to cutaneous sites. The	
CC	present sequence represents the human SUF2 genomic DNA sequence of the	

CC	XX	Sequence	268685-BP, 7218 A; 6315 C; 6417 G; 6796 T; 0 U; 679 Other;
CC	XX	invention. This gene maps to human chromosome 20q12-13.2	
Query Match		5.9%; Score 365.2; DB 6; Length 268685;	
Best Local Similarity		52.8%; Pred. No. 4.1e-55;	
Matches 1289;		Conservative 0; Mismatches 1043; Indels 106; Gaps 19;	
QY	486	GCCCTGGCGGGGTGGCTCAAGCTCTGTAATCCCAAGCCCTTTGGAGGCCAGAGTGGGCAGAT	545
DB	221964	GCCAGGGCGGGGTGGCTCGTGGCTGTAAATCCCAACCTTTGGAGGCCAGAGTGGGTGAT	2220233
QY	546	CATAGAGTCAGAGATTGAGACCAAGCCCTAGCCCAATGGTGAACCCCGCTCTACTTAA	605
DB	222024	CATAGAGTCAGAGATTGAGACCAAGCCCTAGCCCAATGGTGAACCCCGCTCTACTTAA	2220833
QY	606	GATACAAAATAATGACGAGTGTGTGGCGCACCTGTAAACCCAGCTGCTGAGAGAG	665
DB	222084	AATACAAAATAATGAGTGTGTGGCGCACCTGTAAACCCAGCTGCTGAGAGAG	2221433
QY	666	TGAGGCAAGAGATTGCTTGAACCCAGAGCGAGG--TGACGCGAACAAGATCACACC	724
DB	222144	TGAGGCAAGAGATTGCTTGAACCCAGAGCGAGG--TGACGCGAACAAGATCACACC	2222030
QY	725	AATGCACTGTGACCTGATGACAGGCGAAAGCTCCACCTCAAAAAAAAAAAAAAAAAA	784
DB	222204	ACTGCACTCCAGCCCTGGCGAACAGCGAGACTCGCTCAAAAAAAAAAAAAAAAAA	2222853
QY	785	AATATGTAAAGTTGTGCTAATAAATAATATGAGCTAGAGAAAGCAAGTGTAAAGCCTA	844
DB	222264	AATATGTAAAGTTGTGCTAATAAATAATATGAGCTAGAGAAAGCAAGTGTAAAGCCTA	2223233
QY	845	TGACCAATGTAACTAGAGAAATCTGTGGACACATATATAGGAACTTAACCAAGTCTG	904
DB	222324	AAACCAAGTTGGTTGGGAAACCTCATGGGCTTCAATGTAAGATTAATCTGCAGAAA	2223838
QY	905	G-AAGTAAGTTTGGAAAGAAATGTTGAGAGCAAAAGGTTAAAGAGTAAAAA	963
DB	222384	GCTACTGAGATTAAAGGAACTAAATATTAATTAAGCTGACAGAAATTAACCAAGCTC	2224433
QY	964	AATTAATAATACAGATTATAGTGTGTGGAGAAATGGGATAGGAGCTAACTAGAGAAATCAA	1023
DB	222444	CATTAATCTGTTTAAATATTCAGAAATTTTAAATGTGTAACAAAATCTTATTAAGTGAAGG	2225030
QY	1024	ATAGAAATGTTTCAATGTATGTAAAGACCTGTGTAAGGTGAAGACATTAATATCT	1083
DB	222504	GGAACATAGGAAAGGATTAAGGATTAAGCATTTGGGAAAGGTAAATACGTGCATCTGCTG	2225633
QY	1084	GCACCAATCGCGGACTTTTTTTTATGTGTAATGCTTGGCAATTTAAATAGAG--AGCA	1141
DB	222564	CCCAAAATAGACATGATTTTGTCTTCAACACCTCTCTGATGTTTGGCCCTGGGCCATG	2226233
QY	1142	AGAATGTAGACATGTGATGTAGTCAGAGTTGAAGTTCTGCCAGACAT-GTAAAGGAG	1200
DB	222624	ACAAATACAAACAGATGTCATTAAGAAATTTTAAATGAACATATAGGACAGAAAG	2226833
QY	1201	AGACAGGTAGCAAGATTGAGAGATTTAACAAGACAGAGATTAAATG--TGCTGGCCAG	1259
DB	222684	ATTAATATATCCCAAGAGGTCAAAAGTAAAGTATGATCTCAAGTTTAAATGATTTATATC	2227433
QY	1260	TGGCATCTAGTCTGATGCTAATCTGAGGGAAGAAATGAAGTAAAGACCTTGTGATAG	1319
DB	222744	ACAAAGCATTTGATCTTCTTCTGTGGCAATTTTTTCTCCATCAATGCTCTGTTTTCTT	2228030
QY	1320	TTATGAGAGAGTGGAGGCTTCAAGACCTACAGTGTGATTTAAATAGAAATGATTT	1379
DB	222804	CATGCTTGTATTTCTTAACTTTTAAATTAACAATGATCACTTTTATATATCTGATGAGA	2228633
QY	1380	GGAAGAAAGAAATTAACGTGAGAGAGTGAAGATTTTCAGCTTGAGTCACTTCATACCA	1439
DB	222864	TAAATTTTCAA-----AGATGCTACTTGTAAATTTGCTTAAAGATATTTT	2229077
QY	1440	ACACTGTGCTAATATGCTTCAAAAGCATGATCCCTGCTCAAGGACTTACAGCCAAAA	1499

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Db      222908 ATTAGATCTTCGATGACCAATATTAACAATGCGCTATTCAAGTAGAATAATTAACACTGC 222967
Qy      1500 CAAGAGATTAAGAAATACACCAATACTATTATAGACACTTGTGTGAATATCAAGAAA 1559
Db      222968 CAATCATTAAGAGGTGACAGAAAAGACT---CACTCTAAAAGGATAAAATATATATTA 223023
Qy      1560 GAAATAGATCTACTGTAATGTGTGCAACGCGATCAAGATATCTTTAAGTTTCAAGA 1619
Db      223024 CAATGCTGTCACTATGTTTATCTGAAGGGAGTTAATACAGAGAAAATGTTCAAAATTA 223083
Qy      1620 AGTTTCAGATCGCGCGCGCGGTGCTACGCTGTATATCCAGCACTTTGGAGGCGC 1679
Db      223084 AGTAAACATA-CAGCCGGGCAATGTGTGCTCAATGCTGTATATCCAAACCTTTGGAGGCGC 223142
Qy      1680 AGCGGGGTGATCAC--AAGTCAGAGATCAAGACCATCTGTGTAAACAGGTGAACC 1737
Db      223143 AGCGAGGCGGTTTACTGAGGGTCAGACTTTAGAACAGCCTGACCAATTTGTGAACC 223202
Qy      1738 CCGTCTCTACAAAATAATTAATAATTAAGCAGCGCTGTGTGGCGGCGCTGTATGCCA 1797
Db      223203 CTGTCTCTACTAAAATGTAATAATAATTAAGCAGCGGTGTGTGGCGGCTGTATTTCA 223262
Qy      1798 GCTACTCAGAGGCTGAGCAGAGAGATGCGTGAACCCGGAGGTAGAGTTTGC--GTGA 1856
Db      223263 GCTACTCGGAGGCTGAGCAGAGAGATCACTTGAAACCCAGAGGCGAGAGGTTGCACTGA 223322
Qy      1857 GCGGAGATCGCGCCACTGCGCTCAGCGCTGAG--CGACAGAGTGAAGCTGCTCAAAA 1914
Db      223323 GCTGAGATCAATGCGCATTCGACTCGAGCGTGGGCGACGACAGCAAACTCCGCTCAAAA 223382
Qy      1915 AAAAAAAAAAAAAAAAAAGTTTCAATCTTAACAACACTGCACTTTCACAGCTTAGAA 1974
Db      223383 AAAAAAAAAAGTACA-----TCCATCAGCTTAAC 223413
Qy      1975 TAGAGAGCATGTTACAGGAGAGAAAATGTTTTCAGCAAAAGGTACAGATAGGAAAAT 2034
Db      223414 AAGTTTACTGTGAATGTCAAAATTAATCTTTGCTACTTTAATTTGTGAATAATTAATC 223473
Qy      2035 GAGGATTTGTTCAAGAGAGAGACCCAGAGTCAATGTTTGTGAAGGTTAGAGAAAACA- 2093
Db      223474 TCAAAATCTGAAGATAGGTTTCTGATGCAATTAATGATTAATGACATGCAAAAATAG 223533
Qy      2094 CAGTGTTCGCAATCTCAGGTTCCATTAGTGCGTTATGAATCAATATGCTGTAGCA 2153
Db      223534 CAATATTTCTTTAAAAATATCTGCATTATGTAATTAATTAATTAATTAACAAACACAC 223593
Qy      2154 ACCTGCAATTTAAAAAATGAATTAATGATGAAGAGATGAAGAAAATTTAGCATGCA 2213
Db      223594 ACATACATATGTAATAGTAGTAGTATTTTATGTAATACCTATCTCATTTT---TATA 223649
Qy      2214 TTACATTTTGAAGAGCAATTAATTTTCTGCAACTTTGCTCAATTTGTAATCTGTAAT 2273
Db      223650 TCACCTGTAAAGTCCACATTTGAAATTAAG-----TGTTACCAAAAGCA 223695
Qy      2274 TATATTTTATGATGATGTGAATACAGATACATATATTTCTTACTGTAGCATGCA 2333
Db      223696 AAGATATCAGGCTTAAGTCAGGCACTCAGCTTAATTTTCTTATTAAGCATGATCTTG 223755
Qy      2334 GTCAAAAAATCTTTAAAGCATGCGCTGTCTTAATCTTATTTTTCAGAGAGAGAAATC 2393
Db      223756 GACAATTAACCAATCTCTGTCACCAAGCTTCTGTTCTTATCTGAGATGAGGCG--- 223812
Qy      2394 CAGATCTGAGAGCAAAATTTTGGCTGAGGTATAGAACAGCTTATGCAATTCCTA 2453
Db      223813 -----TATATGACAAACCTTGGATCCCATTTACCTTAGGTGACCATTAAGTA 223864
Qy      2454 AAGATGATCTTAGTAAATATCTTTCCACATGTCGCACTTCTAGTTCGTT 2513
Db      223865 ACCCTGAAGTTAATTAATTAATTAATTTGCAAGTGTTTAATTTCAATTAATGATCTTAAT 223924
Qy      2514 GGCCTGAATATACGAATATATTTAGTGAACAGCATACACAGTCTGGGGAATATATTTGG 2573

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Db      223925 CAACCAAGATGCTTTAATTTT-----TATTTCTATGATTAATAAATGG 223969
Qy      2574 GTAGGTGCTGAGAGGCTCATTTTCTAAGAAATGTGGAACCTTAGCGAGGATATGTGCT 2633
Db      223970 CAGACCAAGATTGAACCTCAGGTTGACGTCAAGAAATTAATCTCCCGGCCAAGCAGTGGCT 224029
Qy      2634 CACACCTATTAATTCACGACTTTTGGAGGCCCAAGTCAAGAAATGCTCTTGAACCCAAAG 2693
Db      224030 CACAACTGTAAATCCCGACATTTTGGAGGCTGAGGCGAGCTCACTTAGAGTCAAGAG 224089
Qy      2694 TTCAAGACTAGCATGAGGCAACAATAGCAAGACCTCATCTCTACAAAAAATTTAAATTCAG 2753
Db      224090 TTGGAACCAAGCTGAGCAACAATGTGGAATCCCATCTCTATTAATAATTAATTAAG 224149
Qy      2754 CTGAGCATGTTGGCATACGCTGTAGTCCACCTTACTTGGGAAAGCTA--GTTGGGTGATC 2812
Db      224150 CCGGCGATGTTGACAGTCTGTAGTCCAACTGTTTGGAGGCGCATGCGAGAAAATTC 224209
Qy      2813 GCTTG-ACACAGAGTTTGAAGCTAAGTGAGCCATGATCACACAACTGCACTCCAGCTT 2871
Db      224210 ACTTGAAACCAAGAGTGAAGGTGTGCAATGAGCCGAGATCGACATTCACCTCAGCT 224269
Qy      2872 GAGTGACAGAGGAAGACCTGCTCCCTAATAAAGAAAGAA 2911
Db      224270 GGGCAACAGAGCAAGACTCCGCTCAACAAAAA 224309

RESULT 11
AAH72636
ID AAH72636 standard; cDNA; 2724 BP.
AC
XX AAH72636;
AC
XX
XX 19-SBP-2001 (first entry)
XX
XX Human cervical cancer marker nucleic acid 3910.
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000MO-US033312.
XX
XX 08-DEC-1999; 99US-0169681P.
XX
XX 21-DEC-1999; 99US-0171350P.
XX
XX 14-MAR-2000; 2000US-0189315P.
XX
XX 12-MAY-2000; 2000US-0203791P.
XX
XX 09-JUN-2000; 2000US-0210600P.
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PI Schlegel R, Deeds J, Berger A, Zhao X;
XX
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX
XX PT for assessing and detecting compounds for treating the cancer.
XX
XX
XX Claim 1; Page 774; 1051p; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX
XX cervical cancer with cytoskeletal activity. The nucleic acids and encoded
XX
XX polypeptides are useful to assess if a patient is afflicted with
XX
XX cervical cancer or has a pre-malignant condition; to monitor the
XX
XX progression of cervical cancer or a premalignant condition in a patient;
XX
XX and to select and/or assess the efficacy of a compound or therapy for
XX
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX
XX useful for gene therapy

```

XX Sequence 2724 BP; 906 A; 552 C; 605 G; 661 T; 0 U; 0 Other;
SQ
Query Match 5.5%; Score 338; DB 4; Length 2724;
Best Local Similarity 88.0%; Pred. No. 1.8e-50;
Matches 368; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 16 CAATTATGAAAGCCAAATATACAGCTTTAAATAGATGTGGACCTAAATACCCAGAAG 75
DB 332 CAATTATGAAAGCCAAATATACAGCTTTAAATAGATGTGGACCTAAATACCCAGAAG 391
QY 76 AACTCCCTTTGTAAGATTGTGACAAAATTAATGATGAGTTAATAGTTCTTAAG 135
DB 392 CACCCCTTTGTAAGATTGTGACAAAATTAATGATGAGTTAATAGTTCTTAAG 451
QY 136 GATGTGAAGCCCAAGAGCATATCAGCGCTAGCAAAATGCGAATTCATATATCATCA 195
DB 452 GAGTGTGAGCCCAAGAGCATATCAGTGTAGCAAAATGCGAATTCATATATGATCA 511
QY 196 AAGTTATCCTTCAAGAGCTTCAAGCGCTTAATGATGTCTTAAGAAAATGTGAAAGCCCTC 255
DB 512 AAGTTGTCTTCAAGAGCTTCAAGCGCTTAATGATGTCTTAAGAAAATGTGAAAGCCCTC 571
QY 256 AGCCATCTGAAGAGACAGTGTACAGCAATTGATCAAAAAGAAAACACAGGCGCTTCCC 315
DB 572 AGCCGCGCGAAGAGACAGTGTACAGCAATTGATCAAAAAGAAAACACAGGCGCTTCCC 631
QY 316 CTTCCCCCACTTGTATGTAAGACAGTCTTCATTTCCATAGTATGTAATTTTCTAGATAC 375
DB 632 CTTCCCCCACTTGTATGTAAGACAGTCTTCATTTCCATAGTATGTAATTTTCTAGATAC 691
QY 376 AGCTGTAGAGCTCAAAAGTACTGGAAGAAAGAGCTCCCATTCAAAGAAATTTATCTTA 433
DB 692 GTCTGTAGAGCTCAAAAGTACTGGAAGAAAGAGCTCCCATTCAAAGAAATTTATCTTA 749

RESULT 12
AAH72784
ID AAH72784 standard; cDNA; 2725 BP.
XX
AC AAH72784;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human cervical cancer marker nucleic acid 4058.
XX
KW Human cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200142467-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033312.
XX
PR 08-DEC-1999; 99US-0169681P.
XX
PR 21-DEC-1999; 99US-0171350P.
XX
PR 14-MAR-2000; 2000US-0189315P.
XX
PR 12-MAY-2000; 2000US-0203791P.
XX
PR 09-JUN-2000; 2000US-0210600P.
XX
PR 21-JUL-2000; 2000US-0220114P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Deede J, Berger A, Zhao X;
XX
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX
XX PT for assessing and detecting compounds for treating the cancer.
XX
XX PS Claim 1; Page 850; 1051p; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
SQ Sequence 2725 BP; 906 A; 552 C; 605 G; 662 T; 0 U; 0 Other;
Query Match 5.5%; Score 338; DB 4; Length 2725;
Best Local Similarity 88.0%; Pred. No. 1.8e-50;
Matches 368; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 16 CAATTATGAAAGCCAAATATACAGCTTTAAATAGATGTGGACCTAAATACCCAGAAG 75
DB 332 CAATTATGAAAGCCAAATATACAGCTTTAAATAGATGTGGACCTAAATACCCAGAAG 391
QY 76 AACTCCCTTTGTAAGATTGTGACAAAATTAATGATGAGTTAATAGTTCTTAAG 135
DB 392 CACCCCTTTGTAAGATTGTGACAAAATTAATGATGAGTTAATAGTTCTTAAG 451
QY 136 GATGTGAAGCCCAAGAGCATATCAGCGCTAGCAAAATGCGAATTCATATATCATCA 195
DB 452 GAGTGTGAGCCCAAGAGCATATCAGTGTAGCAAAATGCGAATTCATATATGATCA 511
QY 196 AAGTTATCCTTCAAGAGCTTCAAGCGCTTAATGATGTCTTAAGAAAATGTGAAAGCCCTC 255
DB 512 AAGTTGTCTTCAAGAGCTTCAAGCGCTTAATGATGTCTTAAGAAAATGTGAAAGCCCTC 571
QY 256 AGCCATCTGAAGAGACAGTGTACAGCAATTGATCAAAAAGAAAACACAGGCGCTTCCC 315
DB 572 AGCCGCGCGAAGAGACAGTGTACAGCAATTGATCAAAAAGAAAACACAGGCGCTTCCC 631
QY 316 CTTCCCCCACTTGTATGTAAGACAGTCTTCATTTCCATAGTATGTAATTTTCTAGATAC 375
DB 632 CTTCCCCCACTTGTATGTAAGACAGTCTTCATTTCCATAGTATGTAATTTTCTAGATAC 691
QY 376 AGCTGTAGAGCTCAAAAGTACTGGAAGAAAGAGCTCCCATTCAAAGAAATTTATCTTA 433
DB 692 GTCTGTAGAGCTCAAAAGTACTGGAAGAAAGAGCTCCCATTCAAAGAAATTTATCTTA 749

RESULT 13
ABV30259
ID ABV30259 standard; cDNA; 2725 BP.
XX
AC ABV30259;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker CDNA 30250.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-01833319P.
XX
PR 16-MAR-2000; 2000US-0189862P.
XX
PR 25-MAY-2000; 2000US-0207454P.
XX
PR 09-JUN-2000; 2000US-0213141P.
XX
PR 18-JUL-2000; 2000US-0219007P.
XX
PR 13-DEC-2000; 2000US-0255281P.
XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6566; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX

SQ Sequence 2725 BP; 905 A; 552 C; 606 G; 662 T; 0 U; 0 Other;

Query Match 5.5%; Score 338; DB 5; Length 2725;

Best Local Similarity 88.0%; Pred. No. 1.8e-50; Mismatches 0; Gaps 0;

Matches 368; Conservative 0; Indels 0; Gaps 0;

QY 16 CAATTATGAAGCCAAATATACAGCTTAATTAATGAGTGAATCCCAAG 75

DB 332 CAATTATGAAGCCAAATATACAGCTTAATTAATGAGTGAATCCCAAG 391

QY 76 AACTCCCTTTGTAAGTTGTAACAAAATTAATGAGTGAATGTTCTAATG 135

DB 392 CACCCCTTTGTAAGTTGTAACAAAATTAATGAGTGAATGTTCTAATG 451

QY 136 GAATGTGAACCCAAAGCCATATCAGCGCTAGCAAAATGCGAATTCATATCATCA 195

DB 452 GACTGTGAGCCCAAGCCATATCAGCGCTAGCAAAATGCGAATTCATATCATCA 511

QY 196 AAGTTATCCTTGAAGGCTTCAAGCGCTTATGATGCTTAAGAAATGGAACCGCTTC 255

DB 512 AAGTTATCCTTGAAGGCTTCAAGCGCTTATGATGCTTAAGAAATGGAACCGCTTC 571

QY 256 AGCCATCTGAAGAGAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 315

DB 572 AGCCGCGGAGAGAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 631

QY 316 CTTCCCTTGAAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 375

DB 632 CTTCCCTTGAAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 691

QY 376 AGCTTGAAGCTCAAAAGTCTGAGAAAGAGTCCCATTCAGAAAGAAATTTATCTTA 433

DB 692 GTCTTGAAGCTCAAAAGTCTGAGAAAGAGTCCCATTCAGAAAGAAATTTATCTTA 749

RESULT 14
ABV27562
ID ABV27562 standard; cDNA; 2725 BP.

XX ABV27562;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 27553.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX pharmacogenomic marker; gene; 88.

XX

OS Homo sapiens.

PN WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-018319P.

XX 16-MAR-2000; 2000US-0189862P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0235281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5630-5631; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (c) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX

SQ Sequence 2725 BP; 905 A; 552 C; 606 G; 662 T; 0 U; 0 Other;

Query Match 5.5%; Score 338; DB 5; Length 2725;

Best Local Similarity 88.0%; Pred. No. 1.8e-50; Mismatches 0; Gaps 0;

Matches 368; Conservative 0; Indels 0; Gaps 0;

QY 16 CAATTATGAAGCCAAATATACAGCTTAAATGATGAGTGAATCCCAAG 75

DB 332 CAATTATGAAGCCAAATATACAGCTTAAATGATGAGTGAATCCCAAG 391

QY 76 AACTCCCTTTGTAAGTTGTAACAAAATTAATGAGTGAATGTTCTAATG 135

DB 392 CACCCCTTTGTAAGTTGTAACAAAATTAATGAGTGAATGTTCTAATG 451

QY 136 GAATGTGAACCCAAAGCCATATCAGCGCTAGCAAAATGCGAATTCATATCATCA 195

DB 452 GACTGTGAGCCCAAGCCATATCAGCGCTAGCAAAATGCGAATTCATATCATCA 511

QY 196 AAGTTATCCTTGAAGGCTTCAAGCGCTTATGATGCTTAAGAAATGGAACCGCTTC 255

DB 512 AAGTTATCCTTGAAGGCTTCAAGCGCTTATGATGCTTAAGAAATGGAACCGCTTC 571

QY 256 AGCCATCTGAAGAGAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 315

DB 572 AGCCGCGGAGAGAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 631

QY 316 CTTCCCTTGAAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 375

DB 632 CTTCCCTTGAAGTGTTCAGCAATGATCAAAAAGAAACCAAGGCTTCC 691

QY 376 AGCTTGAAGCTCAAAAGTCTGAGAAAGAGTCCCATTCAGAAAGAAATTTATCTTA 433

DB 692 GTCTTGAAGCTCAAAAGTCTGAGAAAGAGTCCCATTCAGAAAGAAATTTATCTTA 749

RESULT 15
 ID ABV21740 standard; cDNA; 2725 BP.
 XX ABV21740;
 AC ABV21740;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21731.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-018319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 3668-3669; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (1) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 2725 BP; 905 A; 552 C; 606 G; 662 T; 0 U; 0 Other;
 XX
 Query Match 5.5%; Score 338; DB 5; Length 2725;
 Best Local Similarity 88.0%; Pred. No. 1,8e-50;
 Matches 368; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 16 CAATTATGAAAGCCAAATATACAGCCTTAATAATAGATGTGACCTAATAATCCAGAAG 75
 DB 332 CAATTATGAAAGCCAAATATACAGCCTTAATAATAGATGTGACCTAATAATCCAGAAG 391
 QY 76 AACTCCCTTTTGAAGATTGTGAACAAATTAATATGAGTAACTTAAGTTCTTAATG 135
 DB 392 CACCCCTTTTGAAGATTGTGAACAAATTAATATGAGTAAATAGTTCTTAATG 451
 QY 136 GAATGATGAACCAAGACCATATACAGCCTAGCAAAATGCGAATTCATATATCATCA 195
 DB 452 GAGTGTGACCAAGACCATATACAGCCTAGCAAAATGCGAATTCATATATCATCA 511

QY 196 AAGTATCCTTCAAGAGCTTCAGCCCTTAATATGTCTTAAGAAATGTGAACGCCCTC 255
 DB 512 AAGTGTCTCTGCAAGAGCTTCGCGCCTTAATATGTCTTAAGAAATATGAACCTCCCTC 571
 QY 256 AGCCATCTGAAGACAGTGTTCACGCAATTGATCAAAAAAGAAAACACAGGCCCTTCCC 315
 DB 572 AGCCGCCGGAAGACAGTGTTCACGCAATTATCAAAAAAGAAAACACAGGCCCTTCCC 631
 QY 316 CTTCCCCCATTAAGTATGAGAGCTTTTCATTTTCCATAGTAGTAATTTTCTAGATAC 375
 DB 632 CTTCCCCCAATTGATTTAATCAGTCTTCATTTTCCACAGTAGTAATTTTCTAGATAC 691
 QY 376 AGCTGTAGAGCTCAAAAGTACTGGAAGAAAGCTCCCATCTCAAGGAATTTATCTTA 433
 DB 692 GTCTTGTAGACCTCAAGATGACGGGGGAAATCCACAGACAGAAATAGCCAGATCTCA 749

Search completed: December 26, 2004, 18:49:00
 Job time : 1806.57 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 10:56:59 ; Search time 22 Seconds
(without alignments)
1902.468 Million cell updates/sec

Title: US-10-786-065-5

Sequence: 1 MGEELCAKTVPGSCGYHCS.....CDLLASYGKHHPAPSKCW 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	39.5	496	2 S23385	protein kinase (EC
2	912	39.3	496	2 S30435	protein kinase PCT
3	908	39.1	496	2 JCS110	cyclin-dependent k
4	907.5	39.1	461	2 JCS111	cyclin-dependent k
5	900	38.8	451	2 S30436	protein kinase PCT
6	897	38.7	523	2 S23384	protein kinase (EC
7	876.5	37.8	380	2 S32831	serine/threonine-s
8	819	35.3	378	2 B87722	protein ZC123.4 (I
9	800.5	34.5	577	2 T15445	hypothetical prote
10	745.5	32.1	292	2 S40021	protein kinase (EC
11	745	32.1	302	1 OKB85	protein kinase PHO
12	743	32.0	292	1 A45091	protein kinase (EC
13	743	32.0	292	1 A45092	protein kinase (EC
14	743	32.0	293	2 JE0374	cyclin-dependent c
15	739	31.9	288	2 T41101	protein kinase (EC
16	737	31.8	292	1 A46365	protein kinase (EC
17	734	31.6	305	2 S23382	protein kinase (EC
18	731.5	31.5	291	2 S23386	protein kinase (EC
19	713	30.8	298	1 A44878	protein kinase (EC
20	713	30.7	288	1 A42566	protein kinase (EC
21	701	30.2	294	2 S51008	protein kinase (EC
22	701	30.2	296	2 S24386	protein kinase (EC
23	695.5	30.0	294	2 S23095	protein kinase (EC
24	694.5	29.9	294	1 S42049	protein kinase (EC
25	691.5	29.8	294	1 B40444	protein kinase (EC
26	691.5	29.8	294	2 S22440	protein kinase (EC
27	691.5	29.8	302	2 T17115	protein kinase cdc
28	690	29.7	308	1 S53538	protein kinase (EC
29	689.5	29.7	294	1 A40444	protein kinase (EC

30	689.5	29.7	294	2 T49271	CELL DIVISION CONT
31	688	29.7	292	2 S22441	protein kinase (EC
32	686	29.6	292	2 T25374	hypothetical prote
33	683.5	29.5	294	1 JQ2243	protein kinase (EC
34	681.5	29.4	291	2 A39107	protein kinase (EC
35	679.5	29.3	294	1 S57928	protein kinase (EC
36	679	29.3	298	2 A41227	protein kinase (EC
37	671	28.9	301	1 A48041	protein kinase (EC
38	663	28.6	293	2 T02922	protein kinase (EC
39	662.5	28.6	317	1 JC4827	protein kinase (EC
40	662	28.5	297	2 A37871	protein kinase (EC
41	662	28.5	301	1 S42101	protein kinase (EC
42	658.5	28.4	294	1 S31332	protein kinase (EC
43	652	28.1	346	1 I78840	protein kinase (EC
44	650	28.0	302	1 I50474	protein kinase (EC
45	646	27.8	346	1 I48157	protein kinase (EC

ALIGNMENTS

RESULT 1

S23385 protein kinase (EC 2.7.1.37) cdc2-related PCTAIRE-1 - human

C/Species: Homo sapiens (man)

C/Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #ext_change 16-Aug-2004

C/Accession: S23385; S22747

R/Meyerson, M.; Ender, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai

EMBO J. 11, 2909-2917, 1992

A/Title: A family of human cdc2-related protein kinases.

A/Reference number: S23382; PMID:92347325; PMID:1639063

A/Accession: S23385

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-496 <MEY>

A/Cross-references: UNIPROT:000536; EMBL:X66363; NID:G36618; PIDN:CAA47006.1; PID:G36619

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F/163-415/Domain: protein kinase homology <KIN>

F/171-179/Region: protein kinase ATP-binding motif

Query Match	39.5%	Score 916;	DB 2;	Length 496;
Best Local Similarity	44.7%	Pred. No. 5.8e-35;		
Matches	202;	Conservative	67;	Mismatches 121; Indels 62; Gaps 9;
QY	23	GENHSC---RSQPTTEAFAKL-TDLKASCSMTSFHRCGLQAAQKFKRPSNSD	78	
DB	54	GEIRSGRGLSSAPRIYHEDLMKSGSDQSATSDE--VQSPVVMRRHPRKIS-	110	
QY	79	CFQEDDLRGQFQWRSLP-----FGAAS	101	
DB	111	---TEDINK---RLSLPADIRLPEGYLEKLTLSNPFPDKPLRRRLRVSLSEIGGKUE	163	
QY	102	SVTLNLEKGEISVATYVKGISRLINGOLVALKYISMAEGVFTFARISLKGAGNI	161	
DB	164	TYIKDKGEGYATVYKSKSLTDNLVALKEIRLEHESGACPTAIRVSLDLGHANI	223	
QY	162	VLLHDIHTKETLTTFEFYMTDLAQYMSQHGGGLPHNVRLFQGLAYIHHQVYL	221	
DB	224	VTLHDIHTKESLTIVFEYLDKQYLDGNIINMHVVKFLPLGLAGLAYCHQKVL	283	
QY	222	HRDLKQNLILSHGLKADFGLARAKISPSQTVSSSEVYTLWYRPDALLGATRYSSSL	281	
DB	284	HRDLKQNLILSHGLKADFGLARAKISPKTVSNEVYTLWYRPDALLGATRYSSSL	343	
QY	282	DIWAGGCIPIEMFQGGPLPGVSNILEOLEKIMVYGVTEPTDTPGVSLPVNPEWPL	341	
DB	344	DMWGGCIFYEMATGRLPFG-STVEBQHLFIPLGLTPEETWGIISNEEFKTYNYK	402	
QY	342	PIPRSLHVWNRLLGRVP---EAEDLASQMLKGFPRDVSAAQALVHDYFSAAPLQYOL	397	
DB	403	YAAEHL-----LSHAPRLDSGADLLTKLQFEGGNRSASADAMKHPFLSGEIRIHL	456	

QY 398 PDESLFTVSGVRLKPEKMDLLASYQKGNHPA 429
 Db 457 PDTTISIFALKEIQLQKESASLRSSMPDGRPA 488

RESULT 2

S30435
 protein kinase PCTAIR-1 (EC 2.7.1.-) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004
 C/Accession: S30435
 R/Okuda, T.; Cleveland, J.L.; Downing, J.R.
 Oncogene 7, 2249-2258, 1992
 A>Title: PCTAIR-1 and PCTAIR-3, two members of a novel cdc2/CDC28-related protein kinase
 A/Reference number: S30435; MUID:93064701; PMID:1457147
 A/Accession: S30435
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-496 <OKU>
 A/Cross-references: UNIPROT:Q04735; EMBL:X69025; NID:953610; PIDN:CAA48787.1; PID:953611
 A/Intons: 68/1
 C/Superfamily: protein kinase homology
 C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:163-415/Domain: protein kinase homology <KIN>
 F:171-179/Region: protein kinase ATP-binding motif

Query Match 39.3%; Score 912; DB 2; Length 496;
 Best Local Similarity 45.8%; Pred. No. 8.8e-55;
 Matches 200; Conservative 64; Mismatches 111; Indels 62; Gaps 9;

QY 23 GEASRC---RSQPTTEAFKL-TDLKASCSMTSHPRGLQAAQAQKFKSRPSND 78
 Db 54 GELRSVRGPISSAPETVHEDMKSGSDQASATSSD--VQSPVRVMRMRHPRKIS- 110
 QY 79 CFEEDLRQGFQWRKSLP-----FGAAS 101
 Db 111 ---TEDINK-----RLSLPADIRLPEGLYEKLTINSPIFDKPLSRRLRVSLSIGGKYLE 163
 QY 102 SYNLLEKLGSGYATYTKGIRINGOLVALKVISMNAECPPTAIRASLLKGLKHANI 161
 Db 164 TYTKDKLKEGYATATYKGSKLTDLNLVALKEIRLHEEGAPCTAIRREVSLKDLKHANI 223
 QY 162 VLLHDIITTKETLTFFVEVYMTDLAQYMSQHPRGLPHNVRLMPOLLGLAYIHQVHL 221
 Db 224 VTLHDIITHEKSLTLVFEYIDKQLKQYLDCCGNVIMHNVKLPFLQGLGLAYCHQKVL 283
 QY 222 HRDLKQNLILSHLGLKADFGIARAKSIPSQTVSSEVTLWYRPDALLGATEYSSEL 281
 Db 284 HRDLKQNLILINERGLKTLADFGIARAKSIPTKTYSENVTLWYRPDILLSTGYSTQI 343
 QY 282 DLWGAGCIFIEMQGPPLFPQVSNILIEQLEKIWEVLCVPTEDTPGVSKLPVNPMPFL 341
 Db 344 DMWGVCICITFYKATGKPLFPFG-STVEEQHLFIIRLIGTPTLEETWPGILNNEERTYNYPK 402
 QY 342 PTPRSILHVVNRLGRVP---EAEDLASQWLKGFPRDRVSAOGLVHDYFSLPSQLYDL 397
 Db 403 YRAEAL-----LSHNPRLDSOGADLLTTLQLOPEGNRRISAEDAKHPFLSLGGERIKHL 456
 QY 398 PDESLFTVSGVRLKPE 414
 Db 457 PDTTISIFALKEVQLQKE 473

RESULT 3

UC5110
 cyclin-dependent kinase-related protein 1a - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Aug-2004
 C/Accession: UC5110
 R/Gao, C.Y.; Chauthaiwale, V.M.; Rampalli, A.M.; Zelenka, P.S.
 Gene 176, 243-247, 1996
 A>Title: Expression of alternatively spliced PCTAIR-1 mRNA in PC12 cells and neonatal

A/Reference number: UC5110; MUID:97075937; PMID:8918260
 A/Contents: PC12 cell
 A/Accession: UC5110
 A/Molecule type: mRNA
 A/Residues: 1-496 <GAO>
 A/Cross-references: UNIPROT:Q63686; GB:U36444; NID:91040966; PIDN:AAC52912.1; PID:9104096
 C/Comment: This protein plays a role in differentiation and in apoptosis of differentiated
 C/Superfamily: protein kinase homology
 C/Keywords: ATP
 F:163-415/Domain: protein kinase homology <KIN>
 F:171-179/Region: protein kinase ATP-binding motif

Query Match 39.1%; Score 908; DB 2; Length 496;
 Best Local Similarity 46.6%; Pred. No. 1.3e-34;
 Matches 200; Conservative 65; Mismatches 118; Indels 46; Gaps 10;

QY 23 GEASRC---RSQPTTEAFKL-TDLKASCSMTSHPRGLQAAQAQKFKSRPSND 77
 Db 54 GELRSVRGPISSAPETVHEDMKSGSDQASATSSD--VQSPVRVMRMRHPRKIST 111
 QY 78 ----DQFQ-EEDLR--QGFQWRKSLP-----FGAASYNLEKL 109
 Db 112 EDINKLSLPADIRLPEGLYEKLTINSPIGDKPLSRRLRVSLSIGGKLETYIKDL 171
 QY 110 GEGSYATYTKGIRINGOLVALKVISMNAECPPTAIRASLLKGLKHANIVLLHDIH 169
 Db 172 GEGYATATYKGSKLTDLNLVALKEIRLHEEGAPCTAIRREVSLKDLKHANIVTLHDIH 231
 QY 170 TKEITLTPFEVYMTDLAQYMSQHPRGLPHNVRLMPOLLGLAYIHQVHLRPLKPN 229
 Db 232 TEKSLTLVFEYIDKQLKQYLDCCGNVIMHNVKLPFLQGLGLAYCHQKVLHRDLKPN 291
 QY 230 ILISHLGEIKLADFGIARAKSIPSQTVSSEVTLWYRPDALLGATEYSSELDIWAGCI 289
 Db 292 ILINERGLKTLADFGIARAKSIPTKTYSENVTLWYRPDILLSTGYSTQIDMWGVC 351
 QY 290 PTEMQGPPLFPQVSNILIEQLEKIWEVLCVPTEDTPGVSKLPVNPMPFLPTPSILHV 349
 Db 352 FYEMATGRLFPFG-STVEEQHLFIIRLIGTPTEDTPGILNNEERTYNYKYRAEAL-- 408
 QY 350 VWNRLGRVPEAE---DLASQWLKGFPRDRVSAOGLVHDYFSLPSQLYDLPEESLFT 405
 Db 409 ----LRHNPRLDSOGADLLTTLQLOPEGNRRISAEDAKHPFLSLGGERIKHLPTTISIFA 464
 QY 406 VSGVRLKPE 414
 Db 465 LKEVQLQKE 473

RESULT 4

UC5111
 cyclin-dependent kinase-related protein 1b - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Aug-2004
 C/Accession: UC5111
 R/Gao, C.Y.; Chauthaiwale, V.M.; Rampalli, A.M.; Zelenka, P.S.
 Gene 176, 243-247, 1996
 A>Title: Expression of alternatively spliced PCTAIR-1 mRNA in PC12 cells and neonatal re
 A/Reference number: UC5110; MUID:97075937; PMID:8918260
 A/Contents: PC12 cell
 A/Accession: UC5111
 A/Molecule type: mRNA
 A/Residues: 1-461 <GAO>
 A/Cross-references: UNIPROT:Q63686; GB:U36444; NID:91040966; PIDN:AAC52913.1; PID:9104096
 C/Comment: This protein plays a role in differentiation and in apoptosis of differentiated
 C/Superfamily: protein kinase homology
 C/Keywords: ATP
 F:128-380/Domain: protein kinase homology <KIN>
 F:136-144/Region: protein kinase ATP-binding motif

Query Match 39.1%; Score 907.5; DB 2; Length 461;
 Best Local Similarity 55.6%; Pred. No. 1.3e-34;
 Matches 179; Conservative 52; Mismatches 80; Indels 11; Gaps 3;

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QY 97 FGAASYLNLKLEKGGSYATVYKGISRINGQVLAIVKISMNABGVPTAIRBASLLKGL 156
DB 124 FGLLEFYIKLDKLEGGSYATVYKGSKLTIDNLTALKEIRLEHEBGAPCTAIRREVSLIKDL 183
QY 157 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 216
DB 184 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 243
QY 217 HOHVLHRDLKPONLLISHLGEKLADFGIARAKSIPSGTYSSEVVTLMWRPPDALIGATE 276
DB 244 RQVHLHRDLKPONLLINERGELKADFGIARAKSIPSTKYSNVTLMWRPPDILIGSTD 303
QY 277 YSSELDIWAGGCTFIEMFGQPLPFGVSNILEQLEKIMEVLGVPTEDTWPVGSKLPPNYP 336
DB 304 YSQIDIMWGVCIFIEYMATGRPLFPG-STVEEQLHPIFRILGPTEDTWPVGLISNEEFPRT 362
QY 337 EMPPLPTPRSLHVMNRIGRVPAE---DLASQMLKGFPRDVSQOGLVHDYFSAIS 392
DB 363 YNPKYKRAAL-----LHAPRLBCDGDALTKLQFEGRNKISADAKHPFLSLGE 416
QY 393 QLYQLPDEESLFTVSGVRLKPE 414
DB 417 RIHKLPDTTISIFALKVQLKE 438

RESULT 5
S30436
protein kinase PCTAIR-3 (EC 2.7.1.1) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004
C:Accession: S30436
R:Okuda, T.; Cleveland, J.L.; Downing, J.R.
Oncogene 7, 2249-2258, 1992
A:Title: PCTAIR-1 and PCTAIR-3, two members of a novel cdc2/CDC2-related protein kinase
A:Reference number: S30435; UID:93064701; PMID:1437147
A:Accession: S30436
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-451 <OKU>
C:Cross-references: UNIPROT:Q04899; EMBL:X69026; NID:953612; PIDN:CAA48788.1; PID:953613
C:Superfamily: protein kinase homology
C:Keyword: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:119-371/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match 38.8%; Score 900; DB 2; Length 451;
Best Local Similarity 49.9%; Pred. No. 2.8e-34;
Matches 190; Conservative 54; Mismatches 87; Indels 50; Gaps 8;

QY 74 RNSNDFQOEEDLRQGFQWRKSLP----- 96
DB 59 RQNRFRSMEDLNK-----RLSLPMDIRLPQEFLOKQLENPGLPKPLTRMSRRASLSDIG 114
QY 97 FGAASYLNLKLEKGGSYATVYKGISRINGQVLAIVKISMNABGVPTAIRBASLLKGL 156
DB 115 FGLLEFYIKLDKLEGGSYATVYKGSKLTIDNLTALKEIRLEHEBGAPCTAIRREVSLIKDL 174
QY 157 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 215
DB 175 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 243
QY 216 HOHVLHRDLKPONLLISHLGEKLADFGIARAKSIPSGTYSSEVVTLMWRPPDALIGAT 275
DB 234 HHRKILHRDLKPONLLINERGELKADFGIARAKSIPSTKYSNVTLMWRPPDILIGSTD 293
QY 276 YSSELDIWAGGCTFIEMFGQPLPFGVSNILEQLEKIMEVLGVPTEDTWPVGSKLPPNYP 335
DB 294 EYSTPIDMVGVCIFIEYMATGRPLFPG-STVKEELHLIFRILGPTEDTWPVGLISNEEFPRT 352
QY 336 PEWFP--LPTPRSLHVMNRIGRVPAEDLASOMLKGFPDRDSAOGLVHDYFSAIS 393
DB 353 YNPKYKRAAL-----LHAPRLBCDGDALTKLQFEGRNKISADAKHPFLSLGE 408

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QY 394 LYQLPDEESLFTVSGVRLKPE 414
DB 409 VHQHDTASIFSLKEIQLQKD 429

RESULT 6
S23384
protein kinase (EC 2.7.1.37) cdc2-related PCTAIR-2 - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C:Accession: S23384; S22746
R:Heyerson, M.; Ender, G.H.; Wu, C.L.; Su, L.K.; Gorke, C.; Nelson, C.; Harlow, E.; Tsai
EMBO J. 11, 2909-2917, 1992
A:Title: A family of human cdc2-related protein kinases.
A:Reference number: S23382; UID:92347325; PMID:1639063
A:Accession: S23384
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-523 <MEY>
A:Cross-references: UNIPROT:Q00537; EMBL:X66360
R:Meyerson, M.L.
submitted to the EMBL Data Library, May 1992
A:Reference number: S22743
A:Accession: S22746
A:Molecule type: mRNA
A:Residues: 1-366, 'L', 368-432, 'E', 434-523 <MB2>
A:Cross-references: EMBL:X66360; NID:936616; PIDN:CAA47004.1; PID:936617
C:Superfamily: protein kinase homology
C:Keyword: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:190-443/Domain: protein kinase homology <KIN>
F:198-206/Region: protein kinase ATP-binding motif

Query Match 38.7%; Score 897; DB 2; Length 523;
Best Local Similarity 52.4%; Pred. No. 4.4e-34;
Matches 177; Conservative 62; Mismatches 81; Indels 18; Gaps 6;

QY 97 FGAASYLNLKLEKGGSYATVYKGISRINGQVLAIVKISMNABGVPTAIRBASLLKGL 156
DB 186 FKMFEYIKLEKGGSYATVYKGSKLTIDNLTALKEIRLEHEBGAPCTAIRREVSLIKDL 245
QY 157 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 216
DB 246 KANITVTLHDIIHTKKTLLFVFEVYMHDTLAQVMSQHPGGLHPHNVRLLPFWOLLRGLAYTH 305
QY 217 HOHVLHRDLKPONLLISHLGEKLADFGIARAKSIPSGTYSSEVVTLMWRPPDALIGATE 276
DB 306 RKVHLHRDLKPONLLINERGELKADFGIARAKSVPTKYSNVTLMWRPPDILIGSTD 365
QY 277 YSSELDIWAGGCTFIEMFGQPLPFGVSNILEQLEKIMEVLGVPTEDTWPVGS---KLPN 333
DB 366 YSQIDIMWGVCIFIEYMATGRPLFPG-STVEDELHLIFRILGPTEDTWPVGLISNEEFPRT 424
QY 334 YNPKYKRAAL-----LHAPRLBCDGDALTKLQFEGRNKISADAKHPFLSLGE 414
DB 425 YN--FPKYKRAAL-----LHAPRLBCDGDALTKLQFEGRNKISADAKHPFLSLGE 475
QY 390 LPSQLYQLPDEESLFTVSGVRLKPEWCDLASV--OKGH 426
DB 476 LGPRTHALPESVIFSLKEIQLQKDPGRFNSSYPETGH 513

RESULT 7
S32831
serine/threonine-specific protein kinase PCTAIR-3 (EC 2.7.1.1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Aug-2004
C:Accession: S32831
R:Heyerson, M.; Ender, G.H.; Wu, C.L.; Su, L.K.; Gorke, C.; Nelson, C.; Harlow, E.; Tsai
EMBO J. 11, 2909-2917, 1992
A:Title: A family of human cdc2-related protein kinases.
A:Reference number: S23382; UID:92347325; PMID:1639063
A:Accession: S32831

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A:Molecule type: mRNA
A:Residues: 1380 <MEY>
A:Cross-references: UNIPROT:Q07002; EMBL:X66362; NID:g297101; PIDN:CAA47005.1; PID:g2971
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:48-300/Domain: protein kinase homology <KIN>
F:56-64/Region: protein kinase ATP-binding motif

Query Match 37.8%; Score 876.5; DB 2; Length 380;
Best Local Similarity 54.2%; Pred. No. 2.8e-33;
Matches 175; Conservative 52; Mismatches 83; Indels 13; Gaps 5;

QY 97 FGAAASYLNLEKLGSGSYATVYKGISRINGQLVALKVISMAEEGVPTAIRBASLLKGL 156
DB 44 FGLKLETVYKLDKLGEGYATVAFGRSKLTENLVALKETLEHEEGAPCTAIRVSLKGL 103
QY 157 KHANIVLHDIHTKETLTFVEYMHDTDLAQYMSQHPGGL-HPHNVRLFMFOLLRLGLAYI 215
DB 104 KHANIVLHDLHTDRLSLTLVFEYLDSDLKQYL-DHCGNLSMHHNVKIFMOLLRLGLAYC 162
QY 216 HHQVHLHRLDKPQNLISHLGEIKLADFGIARAKSIPSOQYSSVVTLWYRPDALLGAT 275
DB 163 HTKRIIHRDLKPQNLINERGEIKLADFGIARAKSVPTKYSNEVVTLWYRPDPVLLGST 222
QY 276 EYSELDIMWAGCIFTEMFGQPLFPGVSNILEQLEKIMEVGLVPTEDTPGYSKLPNN 335
DB 223 EYSTPLAMGCVGCIHYEMATGRPLFPG-STVKEELHLIFRLGTPTSETPGVTAISERF 281
QY 336 PEMFPLPTPRSLHVVNRLGRVBEA---DLASQMLKGFPRDRVSAQELVHDYFSALP 391
DB 282 TYSEFCYLPQPL-----INHARLRLDTGDHILLSLLVYESSKRMABALSHSYRSISG 335
QY 392 SOLYQLPDESLFTVSGVRLKPE 414
DB 336 ERVHQLDPAISPLSKELQIQKD 358

RESULT 8

B87722
protein ZC123.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
C:Accession: B87722
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; NCID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: B87722
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <STO>
A:Cross-references: UNIPROT:Q45022; GB:chr.I; PIDN:AAB97606.1; PID:g2804502; GSPDB:GN000
C:Genetics: contains similarity to ser/thr protein kinases
A:Gene: ZC123.4
A:Map position: 1
C:Superfamily: discoidin I amino-terminal homology; fibronectin type III repeat homology
inase homology; SAM homology; SH2 homology; SH3 homology

Query Match 35.3%; Score 819; DB 2; Length 378;
Best Local Similarity 51.2%; Pred. No. 1.1e-30;
Matches 165; Conservative 53; Mismatches 92; Indels 12; Gaps 4;

QY 103 YLNLEKLGSGSYATVYKGISRINGQLVALKVISMAEEGVPTAIRBASLLKGLKHANTY 162
DB 60 YKRIDLKGGSYATVYKCGSKLDSIVALKETLQCGELPFAIRBASLLKGLRNLANTY 119
QY 163 LHHDIHTKETLTFVEYMHDTDLAQYMSQHPGGLHPHNVRLFMFOLLRLGLAYIHHQVHL 222
DB 120 SLHDIYQHHLTFVEYMHDTDLAQYMSQHPGGLHPHNVRLFMFOLLRLGLAYIHHQVHL 179

QY 223 RDLKPQNLISHLGEIKLADFGIARAKSIPSOQYSSVVTLWYRPDALLGATEYSSELD 282
DB 180 RDLKPQNLISHLGEIKLADFGIARAKSVPTKYSNEVVTLWYRPDPVLLGSTDYSLD 239
QY 283 IMWAGCIFTEMFGQPLFPGVSN---ILFQLEKIMEVGLVPTEDTPGYSKLPNNYP 337
DB 240 MWGVCIFAEICTGALAPFGSKDSHPGTRQDLDIMFISRGTPDEKRMPEVTLTROYTBE 299
QY 338 WEPPLPTPRSLHVVNRLGRV-DEADLASQMLKGFPRDRVSAQELVHDYFSALP 396
DB 300 LEPFRYELSEFIAVNPWFRLKLTGQELGMLQLTRPESRVSAAAMLHPYFASPREVAL 359
QY 397 LPDESLFTVSGVRLKPEKCDL 418
DB 360 LAPQSIF---RLK-ELKDL 375

RESULT 9

T15445
hypothetical protein C07G1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
C:Accession: T15445
R:Hawkins, J.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid C07G1.
A:Reference number: Z18352
A:Accession: T15445
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-577 <HAW>
A:Cross-references: UNIPROT:Q17794; EMBL:U58751; NID:g1326379; PID:g1326380; PIDN:AAB006;
A:Experimental source: strain Bristol N2; clone C07G1
C:Genetics:
A:Gene: CESP:C07G1.3
A:Map position: 4
A:Introns: 35/1; 101/2; 136/1; 168/2; 185/3; 267/3; 311/3; 449/2; 525/3
C:Superfamily: protein kinase homology

Query Match 34.5%; Score 800.5; DB 2; Length 577;
Best Local Similarity 49.3%; Pred. No. 1.1e-29;
Matches 167; Conservative 50; Mismatches 97; Indels 25; Gaps 6;

QY 97 FGAAASYLNLEKLGSGSYATVYKGISRINGQLVALKVISMAEEGVPTAIRBASLLKGL 156
DB 232 FGLKLETVYKLDKLGEGYATVAFGRSILTNKFAVAKETRLQEGEAPCTAIRVSLRL 291
QY 157 KHANIVLHDIHTKETLTFVEYMHDTDLAQYMSQHPGGLHPHNVRLFMFOLLRLGLAYI 216
DB 292 KHANIVLHDIHTDRLSLTLVFEYLDSDLKQYMSQHPGGLHPHNVRLFMFOLLRLGLAYI 351
QY 217 HHQVHLHRLDKPQNLISHLGEIKLADFGIARAKSIPSOQYSSVVTLWYRPDALLGATE 276
DB 352 QRVLHRLDKPQNLITAKGEIKLADFGIARAKSVPTKYSNEVVTLWYRPDPVLLGSTD 411
QY 277 YSELDIMWAGCIFTEMFGQPLFPGVSNILEQLEKIMEVGLVPTEDTPGYSKLPNNYP 336
DB 412 YSTHIDMMGVGCIHYEMATGRPLFPG-STVKEELHLIFRLGTPTSETPGVTAISERF 470
QY 337 ---EMFPLPTPRSLHVVNRLGRVBEA---DLASQMLKGFPRDRVSAQELVHDYFS 388
DB 471 YANRHYNDPLCR-----QIPRIDAHGFELIMKFLQYEGDKRVSAAEAHVHPLR 520
QY 388 ALPSQYQLPDESLFTVSGVRLKPEKCDLASVYKGNH 427
DB 521 TIAVVCCHLRDEQSVLEADGIHIRE---LNAS---DHN 553

RESULT 10

S40021
protein kinase (EC 2.7.1.37) cdcd homolog - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S40021; S39071
 R:Michaelis, C.E.; Weeks, G.
 submitted to the EMBL Data Library, August 1992
 A:Description: The unicellular organism *Dictyostelium discoideum* possesses a highly related
 A:Reference number: S40021
 A:Accession: S40021
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-292 <MIC>
 A:Cross-references: UNIPROT:P34117; EMBL:L00652; NID:g167695; PIDN:AAA16056.1; PID:g167695
 R:Michaelis, C.; Weeks, G.
 Biochim. Biophys. Acta 1179, 117-124, 1993
 A:Title: The isolation from a unicellular organism, *Dictyostelium discoideum*, of a highly
 A:Reference number: S39071; MUID:94032415; PMID:8218353
 A:Accession: S39071
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-18, 'V', 20-188, 'G', 190-292 <M12>
 A:Cross-references: EMBL:L00652
 C:Complex: In various organisms, cdc2 has been identified as a component of the M-phase
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine
 F:2-254/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:33,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 32.1%; Score 745.5; DB 2; Length 292;
 Best Local Similarity 52.2%; Pred. No. 1.9e-27;
 Matches 151; Conservative 49; Mismatches 84; Indels 5; Gaps 4;

QY 103 YLNLKLGEGSYATVYKIGSRINGQVALKYISNNAE-EGVPTAIRBASILKGLKRIANI 161
 Db 4 YSKIEKLEGEGYGVNNAKKNRTEGEIVALKRIRLDSDEGEVPCYAIRISILKELKRPNI 63
 QY 162 VLHLDIHTKKTLLFVEEYVHTDLAQYMSQHPGSLHDPHNRLFMFOLLGLATVHHQVLL 221
 Db 64 VRLHDVHTHKKTLLFVEEDYDQDKKTLDDCGGSIKPTTISFMYQLKGVAFCHDRVL 123
 QY 222 HRDLKPONLLISHLGEIKLADFGILARAKSIPSQTVSSBEVYTLWVRPPDALIGATEVSSSEL 281
 Db 124 HRDLKPONLLINRKGELKADFGILARAFGVIRVRYSHBVYTLWVRAPDVLMSRKYSTPI 183
 QY 282 DIMWAGCIFIEMFGQGPLFPGVSNILQLEKIMVNLGVPTEDTIPGYSKLPNYPENFPL 341
 Db 184 DIMWALCIFEMWAGRPFPFG-SCGSDQLFFRIFKILTPNEESWPSITLPEYKTD-FPV 241
 QY 342 PTPSLVHVWNRLLGRVPEAEADLASOMLKGPRDVSQAEALVHDPYSAL 390
 Db 242 HPAHQLSIVYHGDE--KGLNLLSKMLQYDPNQRITAAALAKHYFFGL 288

RESULT 11
 OKBAY85
 protein kinase PHO85 (EC 2.7.1.-) - Yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein P7102.18c-a; protein YPL031c
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 30-Jun-1991 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: S62043; S05853; J01063; PC4036
 R:Dieterich, F.S.; Allen, E.; Araujo, R.; Aparicio, A.; Carpenter, J.; Cherry, J.M.; Chun
 H.; Lin, A.; Lin, D.; Marathe, R.; Mitternacht, S.; Namath, A.; Oefner, P.; Petel, F.X.;
 submitted to the EMBL Data Library, December 1995
 A:Reference number: S62043
 A:Accession: S62043
 A:Molecule type: DNA
 A:Residues: 1-302 <DIE>
 A:Cross-references: UNIPROT:Q06888; EMBL:U44030; NID:g1171408; PID:g1171426; GSPDB:GN0000
 R:Uesono, Y.; Tanaka, K.; Toh-e, A.
 Nucleic Acids Res. 15, 10299-10309, 1987
 A:Title: Negative regulators of the PHO system in *Saccharomyces cerevisiae*: isolation and
 A:Reference number: S05853; MUID:88096566; PMID:3320965
 A:Accession: S05853
 A:Molecule type: DNA
 A:Residues: 1-95, 'A', 97-302 <UBS>

A:Cross-references: EMBL:Y00867; NID:g94169; PIDN:CMA6874.1; PID:g94170
A:Experimental source: strain DC5
R:Zhong, H.L.; Li, B.L.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 24, 523-529, 1992
A>Title: Cloning and high expression of yeast PHO85 gene in Escherichia coli.
A:Reference number: JCI1063
A:Accession: JC1063
A:Molecule type: DNA
A:Residues: 1-83, 'N', '86-95', 'A', '97-302 <ZHO>
A:Accession: PC4036
A:Molecule type: protein
A:Residues: 1-15 <ZH2>
C:Gene: SGD:PHO85; MIPS:YPL031C
A:Cross-references: SGD:S0005952; MIPS:YPL031C
A:Map position: 16L
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP, phosphotransferase; serine/threonine-specific protein kinase
F/2-58/Domain: protein kinase homology <KIN>
F/10-18/Region: protein kinase ATP-binding motif
F/33,50,130,132/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 32.1%; Score 745; DB 1; Length 302;
Best Local Similarity 51.7%; Pred. No. 2,1e-27;
Matches 152; Conservative 44; Mismatches 88; Indels 10; Gaps 4;

Dy 103 YLNLEKTLEGSAATYYKGIRINGQIVALKVISMNAEEGVPFAIREASLLKGLKHANIV 162
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 4 FKOLEKNGTAYIATYYKKINKTTGYVVAAKEYLDSEEGTPSAINEISLMKEIKHENIV 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Dy 163 LLADIIITKETITLVPEYMHFDLAQYMSSH----FGILHPNNRLMFOLLGLAYITH 217
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 RLVDYIHTEHNTKTLTFEFPMDNDLKRYMSRTVGNTPRGELNLVKYFQWDLLOGLAFCH 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Dy 218 QHVLRDLKPQWLISHGELKLADPGLARAKSIPSTQSSSEVVTLMYRPDALLGATEY 277
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 NKILHRDLKPQWLINRGQLKDGFLARAGIPNTSSSEVVTLMYRAPDVLMGSRTY 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Dy 278 SSELDIMGACGFIFEMFOQPPLFPGVSNILEQLEKIWEVLGVPTEDTPWCVSKLPYNPE 337
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 STSIDMCGCTIAEMINGKPLPPG-TNDEEQKLIFDIMGTGNESIMPVTCLKPKYNPN 242
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Dy 338 WPLPPTSLSHYVMNRIGRV---EAEDLASQMLKCFPPDRVAQEAOLVTDYS 368
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 243 IQGRP-PDLRQVLOPHHTETPLDGNLMDPLHGULQNPWRISAQALHHPWA 295
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 12
A45091
protein kinase (EC 2.7.1.37) cdcc-related ncik - bovine
N/A/Alternate names: cdcc-related protein kinase PSSALRB homolog, tau protein kinase II lat
C/Species: Bos primigenius taurus (cattle)
C/Gene: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A45091; S39453; S39454
J/Lew, J.; Winkfein, R.J.; Paudel, H.K.; Wang, J.H.
J. Biol. Chem. 267, 25922-25926, 1992
A>Title: Brain proline-directed protein kinase is a neurofilament kinase which displays p
A:Reference number: A45091; MUID:93100310; PMID:1464604
A:Accession: A45091
A:Molecule type: mRNA
A:Residues: 1-292 <LEM>
A:Cross-references: GB:L04798
A:Experimental source: brain
A>Note: Sequence extracted from NCBI backbone (NCBIN:120848, NCBIP:120849)
R: Kobayashi, S.; Ishiguro, K.; Omori, A.; Takamatsu, M.; Arioka, M.; Imahori, K.; Uchida,
FEBS Lett. 335, 171-175, 1993
A>Title: A cdcc-related kinase PSSALRB/cdks is homologous with the 30 kDa subunit of tau
A:Reference number: S39453; MUID:94074679; PMID:8253190
A:Accession: S39453
A:Molecule type: mRNA
A:Residues: 1-292 <KO>
A:Cross-references: GB:X82440; NID:9572618; PIDN:CMA57821.1; PID:9572619
A:Accession: S39454

A:Accession: T41101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-288 <PDB>
A:Cross-references: UNIPROT:O74456; EMBL:AL031535; PIDN:CAA02750.1; GSPDB:GN00068; SPDB
A:Experimental source: strain 972h-, cosmid c16c4
C:GeneticSB:
A:Gene: SPDB:SPCC16C4.11
A:Map position: 3
A:introns: 10/1
C:Superfamily: kinase-related transforming protein; protein kinase homology

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OM protein - protein search, using sw model

Run on: December 27, 2004, 12:15:39 ; Search time 355 Seconds
(without alignments)
440.045 Million cell updates/sec

Title: US-10-786-065-5
Perfect score: 2320
Sequence: 1 MGOELCAKTVOGCGSCYHCS.....COLLASYOKGHHAPGSKCW 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues
Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdp:*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdp:*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdp:*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdp:*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdp:*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdp:*
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8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdp:*
9:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pdp:*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdp:*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdp:*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdp:*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdp:*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdp:*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdp:*
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pdp:*
17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdp:*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdp:*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdp:*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2320	100.0	435	9	US-09-801-861-5 Sequence 5, Appl1
2	2320	100.0	435	14	US-10-224-562-5 Sequence 5, Appl1
3	2320	100.0	435	17	US-10-618-941-86 Sequence 86, Appl1
4	1784	76.9	343	9	US-09-801-861-2 Sequence 2, Appl1
5	1784	76.9	343	14	US-10-224-562-2 Sequence 2, Appl1
6	1659.5	71.5	321	15	US-10-466-759-7 Sequence 7, Appl1
7	1410	60.8	268	15	US-10-425-114-54124 Sequence 54124, A
8	1195	51.5	330	9	US-09-801-861-8 Sequence 8, Appl1
9	1195	51.5	330	14	US-10-224-562-8 Sequence 8, Appl1
10	1194.5	51.5	423	14	US-10-153-242-2 Sequence 2, Appl1
11	1194.5	51.5	423	17	US-10-723-860-407 Sequence 407, App
12	1191.5	51.4	423	14	US-10-153-242-4 Sequence 4, Appl1
13	1191	51.3	330	9	US-09-801-861-9 Sequence 9, Appl1

14	1191	51.3	330	14	US-10-224-562-9	Sequence 9, Appl1
15	1190	51.3	330	9	US-09-801-861-10	Sequence 10, Appl1
16	1190	51.3	330	14	US-10-224-562-10	Sequence 10, Appl1
17	1185.5	51.1	469	16	US-10-408-765A-1291	Sequence 1291, Ap
18	1000	43.1	245	9	US-09-801-861-7	Sequence 7, Appl1
19	1000	43.1	245	14	US-10-224-562-7	Sequence 7, Appl1
20	993	42.8	240	9	US-09-801-861-6	Sequence 6, Appl1
21	993	42.8	240	14	US-10-224-562-6	Sequence 6, Appl1
22	916	39.5	496	14	US-10-354-358-64	Sequence 64, Appl1
23	916	39.5	496	14	US-10-723-860-2263	Sequence 2263, Ap
24	910	39.2	527	9	US-09-925-298-450	Sequence 490, App
25	910	39.2	527	14	US-10-102-806-490	Sequence 490, App
26	909.5	39.2	482	15	US-10-112-944-586	Sequence 286, App
27	900	38.8	460	13	US-10-087-192-1299	Sequence 1299, Ap
28	897.5	38.7	502	17	US-10-256-106-13	Sequence 13, Appl1
29	897.5	38.7	504	17	US-10-618-941-85	Sequence 85, Appl1
30	897	38.7	437	15	US-10-296-115-1222	Sequence 1222, Ap
31	895	38.6	481	13	US-10-087-192-1302	Sequence 1302, Ap
32	893	38.5	472	17	US-10-851-921-8	Sequence 8, Appl1
33	890	38.4	523	14	US-10-354-358-86	Sequence 86, Appl1
34	876.5	37.8	374	14	US-10-325-430-6	Sequence 6, Appl1
35	876.5	37.8	380	17	US-10-757-262-50	Sequence 50, Appl1
36	861	37.1	519	13	US-10-087-192-1506	Sequence 1506, Ap
37	819	35.3	378	14	US-10-369-493-4977	Sequence 4977, Ap
38	800.5	34.5	577	14	US-10-369-493-6067	Sequence 6067, Ap
39	785.5	33.9	326	15	US-10-389-566-2455	Sequence 2455, Ap
40	763	32.9	334	14	US-10-368-493-3434	Sequence 3434, Ap
41	759	32.7	366	15	US-10-389-566-2114	Sequence 2114, Ap
42	752	32.4	320	15	US-10-389-566-2115	Sequence 2115, Ap
43	751	32.4	305	9	US-09-801-368-262	Sequence 262, App
44	751	32.4	305	15	US-10-389-566-1838	Sequence 1838, Ap
45	751	32.4	305	15	US-10-389-566-2066	Sequence 2066, Ap

ALIGNMENTS

RESULT 1
US-09-801-861-5
; Sequence 5, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001098
; CURRENT APPLICATION NUMBER: US/09/801, 861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Human
US-09-801-861-5

Query Match	100.0%	Score 2320;	DB 9;	Length 435;
Best Local Similarity	100.0%;	Pred. No. 6.2e-183;		
Matches 435;	Conservative	0;	Mismatches 0;	Indels 0;
Gap 0;				
QY	1	MGOELCAKTVOGCGSCYHCS	EGEBAHSCRRSPETTEAFAFKLTDLKEASCSMTSPHRL	60
DB	1	MGOELCAKTVOGCGSCYHCS	EGEBAHSCRRSPETTEAFAFKLTDLKEASCSMTSPHRL	60
QY	61	QAAAROKFKSKPRNSDCFOEEDLRGGFQWKSIPFGAASSYLNLKKGESYATVYKG	120	
DB	61	QAAAROKFKSKPRNSDCFOEEDLRGGFQWKSIPFGAASSYLNLKKGESYATVYKG	120	
QY	121	ISIRINGOLVALKVISMNAEEGVPTAIRASLLKGLKIANIVLHDIIHTKETTFFVEFY	180	
DB	121	ISIRINGOLVALKVISMNAEEGVPTAIRASLLKGLKIANIVLHDIIHTKETTFFVEFY	180	

FILE REFERENCE: CL001098
CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 343
TYPE: PRT
ORGANISM: Human
US-09-801-861-2

Query Match
Best Local Similarity 100.0%; Score 1784; DB 9; Length 343;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCELCAKTVQPCSCYHSGEGEASCRSROPETTEAFAFKLTDLEASCSMTSPHPRGL 60
DB 1 MGCELCAKTVQPCSCYHSGEGEASCRSROPETTEAFAFKLTDLEASCSMTSPHPRGL 60
QY 61 QARARQKFKSKRRNSDCFOEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
DB 61 QARARQKFKSKRRNSDCFOEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
QY 121 ISRINGQVALKVTSMNAEEGVFTAIRASLLKGLKHANIVLLHDIHTKETLTVEFY 180
DB 121 ISRINGQVALKVTSMNAEEGVFTAIRASLLKGLKHANIVLLHDIHTKETLTVEFY 180
QY 181 MHTDLAQVMSQHFGHLPNNVLFMFQQLRGLAYIHQHVLRDLKPKQLLSHIGELK 240
DB 181 MHTDLAQVMSQHFGHLPNNVLFMFQQLRGLAYIHQHVLRDLKPKQLLSHIGELK 240
QY 241 ADFGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSSSELDIWGACIFIEFQGPPLF 300
DB 241 ADFGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSSSELDIWGACIFIEFQGPPLF 300
QY 301 PGVSNLEOLEKIMEVLGVPTEDTPGVSGLPNYP 336
DB 301 PGVSNLEOLEKIMEVLGVPTEDTPGVSGLPNYP 336

RESULT 5
US-10-224-562-2
Sequence 2, Application US/10224562
Publication No. US20030022229A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001098DIV
CURRENT APPLICATION NUMBER: US/10/224,562
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 343
TYPE: PRT
ORGANISM: Homo sapiens
US-10-224-562-2

Query Match
Best Local Similarity 100.0%; Score 1784; DB 14; Length 343;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCELCAKTVQPCSCYHSGEGEASCRSROPETTEAFAFKLTDLEASCSMTSPHPRGL 60
DB 1 MGCELCAKTVQPCSCYHSGEGEASCRSROPETTEAFAFKLTDLEASCSMTSPHPRGL 60
QY 61 QARARQKFKSKRRNSDCFOEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
DB 61 QARARQKFKSKRRNSDCFOEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
QY 121 ISRINGQVALKVTSMNAEEGVFTAIRASLLKGLKHANIVLLHDIHTKETLTVEFY 180

DB 121 ISRINGQVALKVTSMNAEEGVFTAIRASLLKGLKHANIVLLHDIHTKETLTVEFY 180
QY 181 MHTDLAQVMSQHFGHLPNNVLFMFQQLRGLAYIHQHVLRDLKPKQLLSHIGELK 240
DB 181 MHTDLAQVMSQHFGHLPNNVLFMFQQLRGLAYIHQHVLRDLKPKQLLSHIGELK 240
QY 241 ADFGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSSSELDIWGACIFIEFQGPPLF 300
DB 241 ADFGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSSSELDIWGACIFIEFQGPPLF 300
QY 301 PGVSNLEOLEKIMEVLGVPTEDTPGVSGLPNYP 336
DB 301 PGVSNLEOLEKIMEVLGVPTEDTPGVSGLPNYP 336

RESULT 6
US-10-466-759-7
Sequence 7, Application US/10466759
Publication No. US20040081983A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION
APPLICANT: LEE, Ernestine A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: ISON, Craig H.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, Monique G.
APPLICANT: JACKSON, Jennifer L.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: TRAN, Bao
APPLICANT: DING, Li
APPLICANT: LU, Dyrung Aina M.
APPLICANT: LAL, Preeti G.
APPLICANT: WARREN, Bridget A.
TITLE OF INVENTION: KINASES AND PHOSPHATASES
FILE REFERENCE: PI-0344 USN
CURRENT APPLICATION NUMBER: US/10/466,759
CURRENT FILING DATE: 2003-07-17
PRIORITY APPLICATION NUMBER: PCT/US02/01369
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: US 60/263,083
PRIORITY FILING DATE: 2001-01-18
PRIORITY APPLICATION NUMBER: US 60/271,205
PRIORITY FILING DATE: 2001-02-23
PRIORITY APPLICATION NUMBER: US 60/271,117
PRIORITY FILING DATE: 2001-02-23
PRIORITY APPLICATION NUMBER: US 60/276,859
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: US 60/278,504
PRIORITY FILING DATE: 2001-03-23
PRIORITY APPLICATION NUMBER: US 60/278,522
PRIORITY FILING DATE: 2001-03-23
PRIORITY APPLICATION NUMBER: US 60/280,510
PRIORITY FILING DATE: 2001-03-29
PRIORITY APPLICATION NUMBER: US 60/280,266
PRIORITY FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 7494145CD1
US-10-466-759-7

Query Match
Best Local Similarity 83.6%; Score 1659.5; DB 15; Length 321;
Matches 321; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

ORGANISM: Mus musculus
US-10-224-562-8

Query Match 51.5%; Score 1195; DB 14; Length 330;
Best Local Similarity 68.2%; Pred. No. 3.6e-90;
Matches 225; Conservative 45; Mismatches 60; Indels 0; Gaps 0;

QY 97 PQAASSYLNLEKLGEGSYATVTKGISRINGQVYALKVISMABEGVPFAIRBASLLKGL 156
DB 1 PQAADSYELKLGEGSYATVTKGSKVNGKVALVIRLOEBEGGPFAIRBASLLKGL 60
QY 157 KXANIVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIH 216
DB 61 KXANIVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIH 120
QY 217 HOHVLHDLKPNLISHGELKADFGIARAKSIPQYSSSEVTLTWYRPPDALLGATE 276
DB 121 QRYIHRDLKPNLISHGELKADFGIARAKSVSHYTSNEVTLTWYRPPDALLGATE 180
QY 277 YSEELDIWAGCIFIEMFGQPLPGVSNILEQLEKIMVYLVPTEDTWPVSKLPNNVP 336
DB 181 YSTCLDMVGICIFVEMIGVAFPGMKDIOQLERIPLVLTGTPNEDTWPVSHLPHFRP 240
QY 337 EMFPLTPRSLHVNVRIGRVEAEADLASOMLKGPRDRVSAQEALVHDYFSALPSQLXQ 396
DB 241 ERFVYSSSLKROAMNKLSYVNHAEADLASKLQCSFKNLSAQAALSHYFSDLPRLWE 300
QY 397 LPDESLFTVSGVRLKPEMCDLLASYOKGH 426
DB 301 LTMDSITFVPRVRLQPEAGESMRARFGKN 330

RESULT 10

US-10-153-242-2
Sequence 2, Application US/10153242
Publication No. US20030166217A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Pot, David
APPLICANT: Kassam, Altaf
APPLICANT: Marenbach, Taasha
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRE)
FILE REFERENCE: PP-01429.103/200130.44501
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 423
TYPE: PRP
ORGANISM: Homo sapiens
US-10-153-242-2

Query Match 51.5%; Score 1194.5; DB 14; Length 423;
Best Local Similarity 60.5%; Pred. No. 5.5e-90;
Matches 234; Conservative 55; Mismatches 83; Indels 15; Gaps 2;

QY 51 SMTSPHPRGLQARAKQFKSKPRNSDCFOEDLRQGFQWRK-----SLPFGA 99
DB 30 TOSTPDPFKPANQVRYHSE---NNACINFTSTGKSPKVRHSSPSSTSPKFGK 85
QY 100 ASSYLNLEKLGEGSYATVTKGISRINGQVYALKVISMABEGVPFAIRBASLLKGLKIA 159
DB 86 ADSYELKLGEGSYATVTKGSKRVNGKVALVIRLOEBEGGPFAIRBASLLKGLKIA 145
QY 160 NVLVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIHQY 219
DB 146 NVLVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIHQY 205
QY 220 VLRDLKPNLISHGELKADFGIARAKSIPQYSSSEVTLTWYRPPDALLGATEYSS 279
DB 206 IHRDLKPNLISHGELKADFGIARAKSVSHYTSNEVTLTWYRPPDALLGATEYST 265

QY 280 ELDINGAGCIFIEMFGQPLPGVSNILEQLEKIMVYLVPTEDTWPVSKLPNNVPWF 339
DB 266 CLDMVGICIFVEMIGVAFPGMKDIOQLERIPLVLTGTPNEDTWPVSHLPHFRP 325
QY 340 PLPTPRSLHVNVRIGRVEAEADLASOMLKGPRDRVSAQEALVHDYFSALPSQLYQLPD 399
DB 326 TLYSSKNLRQAMNKLSYVNHAEADLASKLQCSFKNLSAQAALSHYFSDLPRLWE LTD 385
QY 400 EESLFTVSGVRLKPEMCDLLASYOKGH 426
DB 386 MSITFVPRVRLQPEAGESMRARFGKN 412

RESULT 11

US-10-723-860-407
Sequence 407, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Nataasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlocnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05982.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 407
LENGTH: 451
TYPE: PRP
ORGANISM: Homo sapiens
US-10-723-860-407

Query Match 51.5%; Score 1194.5; DB 17; Length 451;
Best Local Similarity 54.3%; Pred. No. 5.9e-90;
Matches 242; Conservative 61; Mismatches 106; Indels 37; Gaps 5;

QY 6 CAKTVQPGGSCY-----HCSEGBAHSRCSQ-----PETTEAARKLTDLKEASCS 51
DB 7 CNAABPGYSAFVGTPQICVTMTSTRNCGMDSYVKPLDTIEDKKVYQRT----- 58
QY 52 MTSFPHPRGLQARAKQFKSKPRNSDCFOEDLRQGFQWRK-----SLPFGA 100
DB 59 OSTPDPFKPANQVRYHSE---NNACINFTSTGKSPKVRHSSPSSTSPKFGA 114
QY 101 SSYLNLEKLGEGSYATVTKGISRINGQVYALKVISMABEGVPFAIRBASLLKGLKIAN 160
DB 115 DSYELKLGEGSYATVTKGSKRVNGKVALVIRLOEBEGGPFAIRBASLLKGLKIAN 174
QY 161 IYVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIHQY 220
DB 175 IYVLHDIHTKXTLTFVEFVYMTDLAQYMSOHPRGSLHPNVRLEFOLLRLGLAYIHQY 234
QY 221 IHRDLKPNLISHGELKADFGIARAKSIPQYSSSEVTLTWYRPPDALLGATEYSS 280
DB 235 IHRDLKPNLISHGELKADFGIARAKSVSHYTSNEVTLTWYRPPDALLGATEYST 294
QY 281 LDIWAGCIFIEMFGQPLPGVSNILEQLEKIMVYLVPTEDTWPVSKLPNNVPWF 340
DB 295 LDMVGICIFVEMIGVAFPGMKDIOQLERIPLVLTGTPNEDTWPVSHLPHFRPRT 354
QY 341 LPTPRSLHVNVRIGRVEAEADLASOMLKGPRDRVSAQEALVHDYFSALPSQLYQLPDE 400
DB 355 LYSSKNLRQAMNKLSYVNHAEADLASKLQCSFKNLSAQAALSHYFSDLPRLWE LTD 414
QY 401 EESLFTVSGVRLKPEMCDLLASYOKGH 426
DB 415 SSITFVPRVRLQPEAGESMRARFGKN 440

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RESULT 12
US-10-153-242-4
; Sequence 4, Application US/10153242
; Publication No. US20030166217A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Marenbach, Tasha
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRB)
; FILE REFERENCE: PP-01429.103/200130.44501
; CURRENT APPLICATION NUMBER: US/10/153,242
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: mouse
US-10-153-242-4

Query Match
Best Local Similarity 51.4%; Score 1191.5; DB 14; Length 423;
Matches 233; Conservative 55; Mismatches 84; Indels 15; Gaps 2;

QY 51 SMTSFHPRGLQAAQAQKFKSKRPRNSDCFOEEDLRQGFQWRK-----SLPFGA 99
DB 30 TSTFDPFEKPAQVQRVHSE---NNACINFKSSAGKSPKVRHSSPSPTSPKFGK 85
QY 100 ASSYLALEKLGSGSYATVYKGISRINGQVVALKVISMNAEEGVPFPAIRBASILKGLKA 159
DB 86 ADSYEKLEKLGSGSYATVYKGISKNGKVALKVIRLQEEEGTPTFAIRBASILKGLKA 145
QY 160 NIVLHDIHTKETTLPFEVEMHTDLAQYMSQHPGGLHPHNVLFWFOLLRLGLAYITHOH 219
DB 146 NIVLHDIHTKETTLPFEVEMHTDLAQYMDKHPGGLHPDNVNLFLFOLLRLGLAYITHOH 205
QY 220 VLRDLKPNQLLISHGLKDLADFGIARAKSIPSQTSSEVVTLMYRPDPALLGATEYSS 279
DB 206 IIRHDLKPNQLLISDGEIKLADFGIARAKSVPSHTYSNEVVTLMYRPDPVLLGSTEYGT 265
QY 280 ELDIMGAGCIFIEMFGQPLFPGVSNILQLEKIMEVLGVPTEDTPGVSKLPNNPDEMP 339
DB 266 CLDMGVGCI FVEMIQGVAAFPKMKDIOQLERIFLVLTGPNEEDTPGVASHLPKPERP 325
QY 340 PLPTPSLHVNNRLGRVPEADLASQMLKGPFRDRVSAQEAIVHDYFSALEPSQLYQLPD 399
DB 326 TVYNSKSLQANWKLSYVNHADLASKLLQCSFKRNLASQALSHHYFSDLPRLMELTD 385
QY 400 EBSLFTVSGVRLKPEKCDLLASYQKH 426
DB 386 MSIFTPVNVRLQPEAGESMRAFGKNN 412

RESULT 13
US-09-801-861-9
; Sequence 9, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 330
; TYPE: PRT

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; ORGANISM: Human
US-09-801-861-9

Query Match
Best Local Similarity 51.3%; Score 1191; DB 9; Length 330;
Matches 224; Conservative 46; Mismatches 60; Indels 0; Gaps 0;

QY 97 FGAASSYLALEKLGSGSYATVYKGISRINGQVVALKVISMNAEEGVPFPAIRBASILKGL 156
DB 1 FGAADSYEKLKLGSGSYATVYKGISKNGKVALKVIRLQEEEGTPTFAIRBASILKGL 60
QY 157 KQANIVLHDIHTKETTLPFEVEMHTDLAQYMSQHPGGLHPHNVLFWFOLLRLGLAYITH 216
DB 61 KQANIVLHDIHTKETTLPFEVEMHTDLAQYMDKHPGGLHPDNVNLFLFOLLRLGLAYITH 120
QY 217 HQHVLHDLKPNQLLISHGLKDLADFGIARAKSIPSQTSSEVVTLMYRPDPALLGATE 276
DB 121 QRYIILHDLKPNQLLISDGEIKLADFGIARAKSVPSHTYSNEVVTLMYRPDPVLLGSTE 180
QY 277 YSEELDIMGAGCIFIEMFGQPLFPGVSNILQLEKIMEVLGVPTEDTPGVSKLPNNP 336
DB 181 YSTCLDMGVGCI FVEMIQGVAAFPKMKDIOQLERIFLVLTGPNEEDTPGVASHLPKPERP 240
QY 337 EWFPLPTPSLHVNNRLGRVPEADLASQMLKGPFRDRVSAQEAIVHDYFSALEPSQLYQ 396
DB 241 ERFITLYSSKSLQANWKLSYVNHADLASKLLQCSFKRNLASQALSHHYFSDLPRLMELTD 300
QY 397 LPDEBSLFTVSGVRLKPEKCDLLASYQKH 426
DB 301 LTDMSSIFTPVNVRLQPEAGESMRAFGKNN 330

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RESULT 14
US-10-224-562-9
; Sequence 9, Application US/10224562
; Publication No. US20030022229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-562-9

Query Match
Best Local Similarity 51.3%; Score 1191; DB 14; Length 330;
Matches 224; Conservative 46; Mismatches 60; Indels 0; Gaps 0;

QY 97 FGAASSYLALEKLGSGSYATVYKGISRINGQVVALKVISMNAEEGVPFPAIRBASILKGL 156
DB 1 FGAADSYEKLKLGSGSYATVYKGISKNGKVALKVIRLQEEEGTPTFAIRBASILKGL 60
QY 157 KQANIVLHDIHTKETTLPFEVEMHTDLAQYMSQHPGGLHPHNVLFWFOLLRLGLAYITH 216
DB 61 KQANIVLHDIHTKETTLPFEVEMHTDLAQYMDKHPGGLHPDNVNLFLFOLLRLGLAYITH 120
QY 217 HQHVLHDLKPNQLLISHGLKDLADFGIARAKSIPSQTSSEVVTLMYRPDPALLGATE 276
DB 121 QRYIILHDLKPNQLLISDGEIKLADFGIARAKSVPSHTYSNEVVTLMYRPDPVLLGSTE 180
QY 277 YSEELDIMGAGCIFIEMFGQPLFPGVSNILQLEKIMEVLGVPTEDTPGVSKLPNNP 336
DB 181 YSTCLDMGVGCI FVEMIQGVAAFPKMKDIOQLERIFLVLTGPNEEDTPGVASHLPKPERP 240
QY 337 EWFPLPTPSLHVNNRLGRVPEADLASQMLKGPFRDRVSAQEAIVHDYFSALEPSQLYQ 396

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Db 241 ERFITLSSSKNLQKANKLSYVNHAEADLAKLQCSFKNRLSAQALSHYFSDLPRLWE 300
QY 397 LPDEESLFTVSGVRLKPEKCDLLASYQKH 426
Db 301 LTDMSISFTVPVNRLOPEAGESMRAFGKN 330

RESULT 15

US-09-801-861-10
; Sequence 10, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 330
; TYPE: PRP
; ORGANISM: Mus musculus
US-09-801-861-10

Query Match 51.3%; Score 1190; DB 9; Length 330;
Best Local Similarity 67.9%; Pred. No. 9, 3e-90;

Matches 224; Conservative 45; Mismatches 61; Indels 0; Gaps 0;

QY 97 FGAASSYLNLEKLGEGSVATVYKGISRINGQVALKVISMABEGVPTAIRBASILKGL 156
Db 1 FSKADSYELKELGEGSVATVYKGSKVNGKLVALKVRLOEBEGTPTAIRBASILKGL 60
QY 157 KHANIVLHDIHTKETLTFVEFEYMTDLAQYMSQHFGSLHFNVRLLFMFOLLRLGIATYH 216
Db 61 KHANIVLHDIHTKETLTFVEFEYMTDLAQYMDKHPGSLHFNVRLLFMFOLLRLGIATYH 120
QY 217 HOHVLHRLDKPONLISHLGEIKLADFGARAKSIPSTYSSSEVVTLMYRPPDALLGATE 276
Db 121 QRYIHLRLDKPONLISHLGEIKLADFGARAKSVPSHTYSNEVVTLMYRPPDALLGATE 180
QY 277 YSSELDIWGAGCIFIEMFGQPLFGVSNILBQLEKIMEVLGVPTEDTWPGVSKLPNYP 336
Db 181 YSTCLDMWGVCIFVEMIGVAAFGMKDIOQLERIPLVGTPNEDTWPVHSLPHFKP 240
QY 337 EMFPLPTPSLSLVNWRRLGRVPEADLASQMLKGFPRDVSAQELVHDYFSLPSQLYQ 396
Db 241 ERFITLSSSKNLQKANKLSYVNHAEADLAKLQCSFKNRLSAQALSHYFSDLPRLWE 300
QY 397 LPDEESLFTVSGVRLKPEKCDLLASYQKH 426
Db 301 LTDMSISFTVPVNRLOPEAGESMRAFGKN 330

Search completed: December 27, 2004, 12:25:43
Job time : 356 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 11:08:34 ; Search time 24 Seconds
(without alignments)
1202.014 Million cell updates/sec

Title: US-10-786-065-5

Perfect score: 2330
Sequence: 1 MGDELCAKTVPQGCSCYHCS.....CDLASVQKGMHPAPFSKCM 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2330	100.0	435	4	US-09-801-861-5
2	2330	100.0	435	4	US-10-224-562-5
3	1784	76.9	343	4	US-09-801-861-2
4	1784	76.9	343	4	US-10-224-562-2
5	1195	51.5	330	4	US-09-801-861-8
6	1195	51.5	330	4	US-10-224-562-8
7	1194.5	51.5	423	4	US-09-806-344-2
8	1191.5	51.3	423	4	US-09-806-344-4
9	1191	51.3	330	4	US-09-801-861-9
10	1191	51.3	330	4	US-10-224-562-9
11	1190	51.3	330	4	US-09-801-861-10
12	1190	51.3	330	4	US-10-224-562-10
13	1000	43.1	245	4	US-09-801-861-7
14	1000	43.1	245	4	US-10-224-562-7
15	993	42.8	240	4	US-09-801-861-6
16	993	42.8	240	4	US-10-224-562-6
17	916	39.5	496	4	US-09-538-092-1239
18	773.5	33.3	332	4	US-09-248-796A-18399
19	751	32.4	305	4	US-09-538-092-771
20	743	32.0	292	1	US-08-154-915-2
21	743	32.0	292	2	US-08-464-517-38
22	743	32.0	292	2	US-08-246-361A-38
23	743	32.0	292	3	US-08-463-772-38
24	743	32.0	292	4	US-09-538-092-1238
25	743	32.0	292	5	PCT-US93-09945-2
26	734	31.6	305	4	US-09-538-092-1236
27	691.5	29.8	294	2	US-08-874-347-26

28	691.5	29.8	294	3	US-09-093-522-26	Sequence 26, App1
29	685	29.5	544	4	US-09-417-197-115	Sequence 115, App
30	681.5	29.4	544	4	US-09-417-197-113	Sequence 113, App
31	680	29.3	298	2	US-08-874-347-25	Sequence 25, App1
32	680	29.3	298	2	US-08-969-106-2	Sequence 2, App1
33	680	29.3	298	3	US-09-093-522-25	Sequence 25, App1
34	680	29.3	298	4	US-09-338-125-2	Sequence 2, App1
35	680	29.3	298	4	US-09-266-225D-14	Sequence 14, App1
36	679	29.3	298	3	US-09-457-040B-29	Sequence 29, App1
37	679	29.3	298	4	US-09-538-092-1006	Sequence 1006, App
38	676	29.1	298	4	US-09-411-628-13	Sequence 13, App1
39	676	29.1	298	4	US-10-174-794-13	Sequence 13, App1
40	662.5	28.6	317	1	US-08-463-090B-9	Sequence 9, App1
41	662.5	28.6	317	2	US-08-874-347-18	Sequence 18, App1
42	662.5	28.6	317	3	US-09-093-522-18	Sequence 18, App1
43	662.5	28.6	317	3	US-09-248-796A-18426	Sequence 18426, App
44	657.5	28.3	300	2	US-08-874-347-10	Sequence 10, App1
45	657.5	28.3	300	3	US-09-093-522-10	Sequence 10, App1

ALIGNMENTS

RESULT 1									
US-09-801-861-5									
Sequence 5, Application US/09801861									
Patent No. 6492154									
GENERAL INFORMATION:									
APPLICANT: YAN, Chunhua et al.									
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC									
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES									
FILE REFERENCE: CLO01098									
CURRENT APPLICATION NUMBER: US/09/801,861									
CURRENT FILING DATE: 2001-03-09									
NUMBER OF SEQ ID NOS: 10									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 5									
LENGTH: 435									
TYPE: PRT									
ORGANISM: Human									
US-09-801-861-5									
Query Match									
Best Local Similarity 100.0%; Score 2320; DB 4; Length 435;									
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGDELCAKTVPQGCSCYHCS	EGEHAHSCRRSQPETTEAFAKLTDLKEASCMTSPFPRGL	60					
DB	1	MGDELCAKTVPQGCSCYHCS	EGEHAHSCRRSQPETTEAFAKLTDLKEASCMTSPFPRGL	60					
QY	61	QARAQKFKSKPRNSD	CFQEDLRQGFQWRKSLPFGAASSYLNEKLGESYATVYKG	120					
DB	61	QARAQKFKSKPRNSD	CFQEDLRQGFQWRKSLPFGAASSYLNEKLGESYATVYKG	120					
QY	121	ISIRINGQVALKVISMNA	EEGVPFTAIRASILKGIKXANIVLHDIITKETTTFVEY	180					
DB	121	ISIRINGQVALKVISMNA	EEGVPFTAIRASILKGIKXANIVLHDIITKETTTFVEY	180					
QY	181	MHTDIAQVMSQHPGGI	HPNNVLFPMQILRGALYIHQVLRHDKPOULL	180					
DB	181	MHTDIAQVMSQHPGGI	HPNNVLFPMQILRGALYIHQVLRHDKPOULL	180					
QY	241	ADFGIARAKISQTYSS	EVVTLWRRPPDALLGATESSSELDIMWAGCT	240					
DB	241	ADFGIARAKISQTYSS	EVVTLWRRPPDALLGATESSSELDIMWAGCT	240					
QY	301	PGVSNILEQLEKIWEY	LVGTEDTWPGVSKLPNNVPEWPLPTPR	300					
DB	301	PGVSNILEQLEKIWEY	LVGTEDTWPGVSKLPNNVPEWPLPTPR	300					
QY	361	EDLASQMKGFPRDRVS	QGEALVHDFSLPSQLVOLPDEP	360					
DB	361	EDLASQMKGFPRDRVS	QGEALVHDFSLPSQLVOLPDEP	360					

Db 361 EDLASQMLKGFPPDRVSAGDALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
QY 421 SYQKGHHPAQFSKWCW 435
Db 421 SYQKGHHPAQFSKWCW 435

RESULT 2

US-10-224-562-5
; Sequence 5, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-562-5

Query Match 100.0%; Score 2320; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 3,6e-226;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
Db 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
QY 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
Db 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
QY 121 ISRINGQVALVKVISMNAEEGVPTAIRASLLKGLKHANIVLHDIHTKETLTFVPEY 180
Db 121 ISRINGQVALVKVISMNAEEGVPTAIRASLLKGLKHANIVLHDIHTKETLTFVPEY 180
QY 181 MHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIHQVHLRDLKPQVLLISHLGEELK 240
Db 181 MHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIHQVHLRDLKPQVLLISHLGEELK 240
QY 241 ADEGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSELDIWAGCIFIEMFGQGPLF 300
Db 241 ADEGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSELDIWAGCIFIEMFGQGPLF 300
QY 301 PGVSNILEQLEKIMEVILGVPTEDTWPGVSKLPYNNDEWEPPLPTPRSLHVVVNNRLGVPEA 360
Db 301 PGVSNILEQLEKIMEVILGVPTEDTWPGVSKLPYNNDEWEPPLPTPRSLHVVVNNRLGVPEA 360
QY 361 EDLASQMLKGFPPDRVSAGDALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
Db 361 EDLASQMLKGFPPDRVSAGDALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
QY 421 SYQKGHHPAQFSKWCW 435
Db 421 SYQKGHHPAQFSKWCW 435

RESULT 3

US-09-801-861-2
; Sequence 2, Application US/09801861
; Patent No. 6432154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Human
US-09-801-861-2

Query Match 76.9%; Score 1784; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 4,8e-172;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
Db 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
QY 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
Db 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
QY 121 ISRINGQVALVKVISMNAEEGVPTAIRASLLKGLKHANIVLHDIHTKETLTFVPEY 180
Db 121 ISRINGQVALVKVISMNAEEGVPTAIRASLLKGLKHANIVLHDIHTKETLTFVPEY 180
QY 181 MHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIHQVHLRDLKPQVLLISHLGEELK 240
Db 181 MHTDLAQYMSQHPGGLHPHNVRLFMFQLLRGLAYIHQVHLRDLKPQVLLISHLGEELK 240
QY 241 ADEGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSELDIWAGCIFIEMFGQGPLF 300
Db 241 ADEGLARAKSIPQYSSSEVTLWYRPPDALLGATEYSELDIWAGCIFIEMFGQGPLF 300
QY 301 PGVSNILEQLEKIMEVILGVPTEDTWPGVSKLPYNNP 336
Db 301 PGVSNILEQLEKIMEVILGVPTEDTWPGVSKLPYNNP 336

RESULT 4

US-10-224-562-2
; Sequence 2, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-562-2

Query Match 76.9%; Score 1784; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 4,8e-172;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
Db 1 MGELCAKTVQPGCCSYHCSEGEAHS CRSPQETTEAAFKLTDLKEASCSMTSFHPRL 60
QY 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
Db 61 QAAARQKFKSKPRNSND CFQEDLRQGFQWRKSLPFGAASSYLNLKLGEGSYATVYKG 120
QY 121 ISRINGQVALVKVISMNAEEGVPTAIRASLLKGLKHANIVLHDIHTKETLTFVPEY 180

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Db 121 ISINGQVAVAKVISMNAEGVFTAIRBSLKLKLANIVLHDIHTKELTTFVEF 180
Qy 181 MHTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIHQHVHLRDLKPNLLISHLGEK 240
Db 181 MHTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIHQHVHLRDLKPNLLISHLGEK 240
Qy 241 ADPGLARASIPQTSSEVYTLWYRPPDALLGATYSSELDITWAGCIFIEMFGQPLF 300
Db 241 ADPGLARASIPQTSSEVYTLWYRPPDALLGATYSSELDITWAGCIFIEMFGQPLF 300
Qy 301 PGVSNILEQLEKIMEVLGVPTEDTWPVSKLPYNP 336
Db 301 PGVSNILEQLEKIMEVLGVPTEDTWPVSKLPYNP 336

RESULT 5
US-09-801-861-8
; Sequence 8, Application US/09801861
; Patent No. 6432154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-801-861-8

Query Match 51.5%; Score 1195; DB 4; Length 330;
Best Local Similarity 68.2%; Pred. No. 2e-112;
Matches 225; Conservative 45; Mismatches 60; Indels 0; Gaps 0;

Qy 97 FGAASSYLNLEKLGSGSYATVYKGISRINGQVAVAKVISMNAEGVFTAIRBSLKL 156
Db 1 FGAADSYEKLKLGSGSYATVYKGSKNVGLKVALKVIHQEBEGTPTAIRBSLKL 60
Qy 157 KLANIVLHDIHTKELTTFVEFYMTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIH 216
Db 61 KLANIVLHDIHTKELTTFVEFYMTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIH 120
Qy 217 HQHVHLRDLKPNLLISHLGEKLDLADFGIARAKSIPQTSSEVYTLWYRPPDALLGATE 276
Db 121 QRYIHLRDLKPNLLISHLGEKLDLADFGIARAKSVSHSHYSNEVYTLWYRPPDALLGATE 180
Qy 277 YSELDITWAGCIFIEMFGQPLFPGVSNILEQLEKIMEVLGVPTEDTWPVSKLPYNP 336
Db 181 YETCDLMGVGCIPIEMFGQVAFPMKDIQDLERIFVLGTPTEDTWPVSHSLPHFNP 240
Qy 337 EMFPLPTPRSLHVVNRLGRVPEADLASOMLKGPRDRVSAQELVHDFGSLPSOLYQ 396
Db 241 ERFYVSSKSLQAWNKLSYVNHAEADLASKLQCSKPNRLSAQALSHYFSDLPRLWE 300
Qy 397 LPDESILFTVSGVRLKPEMCDLLASYOKGH 426
Db 301 LTDMSSIFTVPNVRLQPEAGBSMRAFGKN 330

RESULT 6
US-10-224-562-8
; Sequence 8, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
```

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DITV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-224-562-8

Query Match 51.5%; Score 1195; DB 4; Length 330;
Best Local Similarity 68.2%; Pred. No. 2e-112;
Matches 225; Conservative 45; Mismatches 60; Indels 0; Gaps 0;

Qy 97 FGAASSYLNLEKLGSGSYATVYKGISRINGQVAVAKVISMNAEGVFTAIRBSLKL 156
Db 1 FGAADSYEKLKLGSGSYATVYKGSKNVGLKVALKVIHQEBEGTPTAIRBSLKL 60
Qy 157 KLANIVLHDIHTKELTTFVEFYMTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIH 216
Db 61 KLANIVLHDIHTKELTTFVEFYMTDLAQYMSQHPGGLHPHNVRLFMFOLLGLAYIH 120
Qy 217 HQHVHLRDLKPNLLISHLGEKLDLADFGIARAKSIPQTSSEVYTLWYRPPDALLGATE 276
Db 121 QRYIHLRDLKPNLLISHLGEKLDLADFGIARAKSVSHSHYSNEVYTLWYRPPDALLGATE 180
Qy 277 YSELDITWAGCIFIEMFGQPLFPGVSNILEQLEKIMEVLGVPTEDTWPVSKLPYNP 336
Db 181 YETCDLMGVGCIPIEMFGQVAFPMKDIQDLERIFVLGTPTEDTWPVSHSLPHFNP 240
Qy 337 EMFPLPTPRSLHVVNRLGRVPEADLASOMLKGPRDRVSAQELVHDFGSLPSOLYQ 396
Db 241 ERFYVSSKSLQAWNKLSYVNHAEADLASKLQCSKPNRLSAQALSHYFSDLPRLWE 300
Qy 397 LPDESILFTVSGVRLKPEMCDLLASYOKGH 426
Db 301 LTDMSSIFTVPNVRLQPEAGBSMRAFGKN 330

RESULT 7
US-09-206-344A-2
; Sequence 2, Application US/09206344A
; Patent No. 6432668
; GENERAL INFORMATION:
; APPLICANT: Christoph Reinhard
; APPLICANT: David Pot
; APPLICANT: Altaf Kassem
; APPLICANT: Tasha Marenbach
; APPLICANT: Lewis T. Williams
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (HPPFAIRE)
; FILE REFERENCE: 200103.445 / 1429.002
; CURRENT APPLICATION NUMBER: US/09/206,344A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-206-344A-2

Query Match 51.5%; Score 1194.5; DB 4; Length 423;
Best Local Similarity 60.5%; Pred. No. 3.3e-112;
Matches 234; Conservative 55; Mismatches 83; Indels 15; Gaps 2;

Qy 51 SNTSFHPRGLQAPRAQKRSKPRNSDCFOEBDLRQGFQWRK-----SLPFGA 99
Db 30 TQSTFDPKPKANQKRVHSE-----NNACINFKTSSTGKESPKYRRHSPSPSPKFGK 85
Qy 100 ASSYLNLEKLGSGSYATVYKGISRINGQVAVAKVISMNAEGVFTAIRBSLKLGLGHA 159
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Query Match 51.3%; Score 1191; DB 4; Length 330;
 Best Local Similarity 67.9%; Pred. No. 5e-112;
 Matches 224; Conservative 46; Mismatches 60; Indels 0; Gaps 0;

97 FGAASSYLNLKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 156
 1 FGKADSYELKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 60

157 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 216
 61 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 120

217 HOHVLHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 276
 121 QRYIILHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 180

277 YSESLDIMGAGCIFIEMFGQGPLFPGVSNILOLEKIMEVLGVPTEDTPGVSKLPNNVP 336
 181 YSTCLDMGVGCI FVEIMOGVAAPFGMKIIOQLERIFLVLTGPNEDTPGVHSLPHFKP 240

337 EWFPLPTPSLSLVNWRRLGRVPEADLASOMLKGPRDVSQAQALVHDYFSALEPSOLYQ 396
 241 ERFITYNSKSLRQANNKLSYVNHAEADLASKLQCSFKRLSLQAALSHYFSDLPRLWE 300

397 LPDESLFTVSGVRLKPEKCDLLASYOKGH 426
 301 LTDMSIFTVPNVRLQPEAGESMRAFGKNN 330

RESULT 11
 US-09-801-861-10

; Sequence 10, Application US/09801861
 ; Patent No. 6492154
 ; GENERAL INFORMATION:
 ; APPLICANT: YAN, Chunhua et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO01098
 ; CURRENT APPLICATION NUMBER: US/09/801,861
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-801-861-10

Query Match 51.3%; Score 1190; DB 4; Length 330;
 Best Local Similarity 67.9%; Pred. No. 6.4e-112;
 Matches 224; Conservative 45; Mismatches 61; Indels 0; Gaps 0;

97 FGAASSYLNLKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 156
 1 FGKADSYELKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 60

157 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 216
 61 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 120

217 HOHVLHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 276
 121 QRYIILHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 180

277 YSESLDIMGAGCIFIEMFGQGPLFPGVSNILOLEKIMEVLGVPTEDTPGVSKLPNNVP 336
 181 YSTCLDMGVGCI FVEIMOGVAAPFGMKIIOQLERIFLVLTGPNEDTPGVHSLPHFKP 240

337 EWFPLPTPSLSLVNWRRLGRVPEADLASOMLKGPRDVSQAQALVHDYFSALEPSOLYQ 396
 241 ERFITYNSKSLRQANNKLSYVNHAEADLASKLQCSFKRLSLQAALSHYFSDLPRLWE 300

QY 397 LPDESLFTVSGVRLKPEKCDLLASYOKGH 426
 DB 301 LTDMSIFTVPNVRLQPEAGESMRAFGKNN 330

RESULT 12

US-10-224-562-10
 ; Sequence 10, Application US/10224562
 ; Patent No. 6730506
 ; GENERAL INFORMATION:
 ; APPLICANT: YAN, Chunhua et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO01098DIY
 ; CURRENT APPLICATION NUMBER: US/10/224,562
 ; CURRENT FILING DATE: 2002-08-21
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-224-562-10

Query Match 51.3%; Score 1190; DB 4; Length 330;
 Best Local Similarity 67.9%; Pred. No. 6.4e-112;
 Matches 224; Conservative 45; Mismatches 61; Indels 0; Gaps 0;

97 FGAASSYLNLKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 156
 1 FGKADSYELKLEKGGSVATVYKGSIRINGOLVAKVISMNAEEGVPTAIRBASLLKGL 60

157 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 216
 61 KIANIVLHDIHTKETTLPFEVYMTDLAQYMSOHGGLHPHNVLFPOLLRLGLAYIH 120

217 HOHVLHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 276
 121 QRYIILHRDLKPNLLISHGELKADFGARAKSIPSQYSSSEVVTLMWRPPDALLGATE 180

277 YSESLDIMGAGCIFIEMFGQGPLFPGVSNILOLEKIMEVLGVPTEDTPGVSKLPNNVP 336
 181 YSTCLDMGVGCI FVEIMOGVAAPFGMKIIOQLERIFLVLTGPNEDTPGVHSLPHFKP 240

337 EWFPLPTPSLSLVNWRRLGRVPEADLASOMLKGPRDVSQAQALVHDYFSALEPSOLYQ 396
 241 ERFITYNSKSLRQANNKLSYVNHAEADLASKLQCSFKRLSLQAALSHYFSDLPRLWE 300

397 LPDESLFTVSGVRLKPEKCDLLASYOKGH 426
 301 LTDMSIFTVPNVRLQPEAGESMRAFGKNN 330

RESULT 13

US-09-801-861-7
 ; Sequence 7, Application US/09801861
 ; Patent No. 6492154
 ; GENERAL INFORMATION:
 ; APPLICANT: YAN, Chunhua et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO01098
 ; CURRENT APPLICATION NUMBER: US/09/801,861
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 245
 ; TYPE: PRT
 ; ORGANISM: Human

US-09-801-861-7

Query Match 43.1%; Score 1000; DB 4; Length 245;
Best Local Similarity 75.9%; Pred. No. 7e-93;
Matches 186; Conservative 25; Mismatches 34; Indels 0; Gaps 0;

QY 97 FGAASSYLNLEKLGEGSYATVYKGISRINGQVAVLKVISMAEAGVPFTAIRBASLLKGL 156
DB 1 FGAADSYELKLEKLGEGSYATVYKGSKNVGLVAVLRLOEBEGTPTAIRBASLLKGL 60
QY 157 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMSQHPGGLHPHNVLLFMFOLLGLAYTH 216
DB 61 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMDKHPGGLHPHNVLLFLFOLLGLSYTH 120
QY 217 HOHVLRDLKPNQNLISHLGEKLDADFGIARAKSIPSOYSSSEVVTLMWRPDDALLGATE 276
DB 121 QRYIILHRDLKPNQNLISDTGELKLDADFGIARAKSVPSHTYSNEVVTLMWRPDDALLGSTE 180
QY 277 YSESLDIWAGCIFIEMFQGOPLFPVGSNILEQLEKIMEVLGVPTEDTWPVSKLPNNYP 336
DB 181 YSTCLDMWGVGCI FVEMIQVAAFPQMKDIQDQLERIFVLGTPTNEDTWPVSHSLPHFRP 240
QY 337 EWFPL 341
DB 241 ERFPL 245

RESULT 14

US-10-224-562-7
; Sequence 7, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-562-7

Query Match 43.1%; Score 1000; DB 4; Length 245;
Best Local Similarity 75.9%; Pred. No. 7e-93;
Matches 186; Conservative 25; Mismatches 34; Indels 0; Gaps 0;

QY 97 FGAASSYLNLEKLGEGSYATVYKGISRINGQVAVLKVISMAEAGVPFTAIRBASLLKGL 156
DB 1 FGAADSYELKLEKLGEGSYATVYKGSKNVGLVAVLRLOEBEGTPTAIRBASLLKGL 60
QY 157 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMSQHPGGLHPHNVLLFMFOLLGLAYTH 216
DB 61 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMDKHPGGLHPHNVLLFLFOLLGLSYTH 120
QY 217 HOHVLRDLKPNQNLISHLGEKLDADFGIARAKSIPSOYSSSEVVTLMWRPDDALLGATE 276
DB 121 QRYIILHRDLKPNQNLISDTGELKLDADFGIARAKSVPSHTYSNEVVTLMWRPDDALLGSTE 180
QY 277 YSESLDIWAGCIFIEMFQGOPLFPVGSNILEQLEKIMEVLGVPTEDTWPVSKLPNNYP 336
DB 181 YSTCLDMWGVGCI FVEMIQVAAFPQMKDIQDQLERIFVLGTPTNEDTWPVSHSLPHFRP 240
QY 337 EWFPL 341
DB 241 ERFPL 245

, RESULT 15

US-09-801-861-6

; Sequence 6, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-801-861-6

Query Match 42.8%; Score 993; DB 4; Length 240;
Best Local Similarity 76.7%; Pred. No. 3.5e-92;
Matches 184; Conservative 24; Mismatches 32; Indels 0; Gaps 0;

QY 97 FGAASSYLNLEKLGEGSYATVYKGISRINGQVAVLKVISMAEAGVPFTAIRBASLLKGL 156
DB 1 FGAADSYELKLEKLGEGSYATVYKGSKNVGLVAVLRLOEBEGTPTAIRBASLLKGL 60
QY 157 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMSQHPGGLHPHNVLLFMFOLLGLAYTH 216
DB 61 KHANIVLHLDIIHTKETLTFFVEYVMTDLAQYMDKHPGGLHPHNVLLFLFOLLGLSYTH 120
QY 217 HOHVLRDLKPNQNLISHLGEKLDADFGIARAKSIPSOYSSSEVVTLMWRPDDALLGATE 276
DB 121 QRYIILHRDLKPNQNLISDTGELKLDADFGIARAKSVPSHTYSNEVVTLMWRPDDALLGSTE 180
QY 277 YSESLDIWAGCIFIEMFQGOPLFPVGSNILEQLEKIMEVLGVPTEDTWPVSKLPNNYP 336
DB 181 YSTCLDMWGVGCI FVEMIQVAAFPQMKDIQDQLERIFVLGTPTNEDTWPVSHSLPHFRP 240

Search completed: December 27, 2004, 12:19:38
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 04:18:24 ; Search time 78 Seconds
(without alignments)
3208.820 Million cell updates/sec

Title: US-10-786-065-5
Predict score: 2330
Sequence: 1 MGQELCAITVPGGSCSYHCS.....CDLASYQKGMHPAQPSKCV 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2038	87.8	384	1 A2S7 HUMAN	Q96440 homo sapien
2	1844	79.5	349	2 Q81UP1	Q81UP1 homo sapien
3	1641.5	70.8	345	2 Q6ZMR9	Q6ZMR9 homo sapien
4	1641.5	70.8	345	2 BADI8656	BADI8656 homo sapi
5	1198.5	51.7	469	1 KPRT MOUSE	Q35495 mus musculu
6	1192.5	51.4	423	2 Q6NVF8	Q6NVF8 mus musculu
7	1192.5	51.4	423	2 AAB68134	AAB68134 mus muscu
8	1192.5	51.4	453	2 Q6ZQ37	Q6ZQ37 mus musculu
9	1192.5	51.4	453	2 BAC98036	BAC98036 mus muscu
10	1191	51.3	435	2 Q6DJM7	Q6DJM7 xenopus lae
11	1185.5	51.1	469	1 KPRT HUMAN	Q94921 homo sapien
12	1078.5	46.5	367	2 Q8WZ44	Q8WZ44 drosophila
13	1078.5	46.5	501	2 Q7KX04	Q7KX04 drosophila
14	1078.5	46.5	509	2 Q7KX08	Q7KX08 drosophila
15	1078.5	46.5	509	2 Q9VZN8	Q9VZN8 drosophila
16	1078.5	46.5	522	2 Q7KX03	Q7KX03 drosophila
17	1078.5	46.5	522	2 Q9XTK9	Q9XTK9 drosophila
18	1074.5	46.3	509	2 Q94888	Q94888 drosophila
19	1067.5	46.0	446	2 Q7Q6Q3	Q7Q6Q3 anopheles g
20	1024.5	44.2	339	2 Q8BN81	Q8BN81 mus musculu
21	1022.5	44.1	339	2 Q8C411	Q8C411 mus musculu
22	916	39.5	496	1 KPRT HUMAN	Q00536 homo sapien
23	916	39.5	496	2 AAB35473	AAB35473 homo sapi
24	912	39.3	496	1 KPRT MOUSE	Q04735 mus musculu
25	912	39.3	496	2 Q91WF4	Q91WF4 mus musculu
26	912	39.3	496	2 BAC34635	BAC34635 mus muscu
27	909.5	39.2	395	2 Q96GAS	Q96GAS homo sapien
28	909.5	39.2	448	2 Q9BRL4	Q9BRL4 homo sapien
29	908	39.1	496	1 KPRT RAT	Q63866 rattus norv
30	900	38.8	451	1 KPRT MOUSE	Q04899 mus musculu
31	900	38.8	451	2 BAB33732	BAB33732 mus muscu

32	897.5	38.7	504	2 Q6V3A2	Q6V3A2 homo sapien
33	897.5	38.7	504	2 AARI3066	AARI3066 homo sapi
34	897	38.7	523	2 Q8NEB8	Q8NEB8 homo sapien
35	896	38.6	451	1 KPRT RAT	Q35832 rattus norv
36	895	38.6	474	2 Q6V3A3	Q6V3A3 homo sapien
37	895	38.6	474	2 AARI3065	AARI3065 homo sapi
38	893	38.5	472	1 KPRT HUMAN	Q07002 homo sapien
39	893	38.5	472	2 AAB35963	AAB35963 homo sapi
40	893	38.5	523	1 KPRT MOUSE	Q8K0D0 mus musculu
41	891	38.4	500	2 Q7ZVJ1	Q7ZVJ1 xenopus lae
42	890	38.4	523	1 KPRT HUMAN	Q00537 homo sapien
43	885.5	38.2	523	1 KPRT RAT	Q35831 rattus norv
44	876	37.8	462	2 Q6DFZ8	Q6DFZ8 xenopus tro
45	821	35.4	551	2 Q45022	Q45022 caenorhabdi

ALIGNMENTS

RESULT 1
ID A2S7 HUMAN STANDARD; PRT; 384 AA.
AC Q96Q40;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase AHS2CR7 (EC 2.7.1.37) (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene protein 7).
GN Name=ALS2CR7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21470351; PubMed=11586298; DOI=10.1038/ng1001-166;
RA Hadano S., Hand C.K., Oeuga H., Yanagisawa Y., Otsu A., Devon R.S., Miyamoto N., Shouguuchi-Miyata J., Okada Y., Singaraia R., Figlewicz D.A., Kwiatkowski T., Hosler B.A., Sagie T., Skaug J., Nasir J., Brown R.H. Jr., Scherer S.W., Rouleau G.A., Hayden M.R., Ikeda J.-E.;
RA "A gene encoding a novel GTPase regulator is mutated in familial amyotrophic lateral sclerosis 2";
RT Nat. Genet. 29:166-173(2001).
RL -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC CDC2/CDKX subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC EMBL; AB053308; BAB69017.1; -
CC HSP; P24941; ID18.
CC Genew; HGNC:14434; ALS2CR7.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR Prodom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 52 336
FT NP_BIND 58 66 ATP (by similarity).

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FT BINDING      81      81      ATP (By similarity).
FT ACT_SITE     173      173      Proton acceptor (By similarity).
SQ SEQUENCE     384 AA; 43574 MW; 6CAD08B6E0B43BB CRC64;
Query Match      87.8%; Score 2038; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.3e-137;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 MTSFHRGLOAARAKQFKSKRPRNSDCFOEEDLRQGFQMRKSLPFGAASSTLNLEKGE 111
DB 1 MTSFHRGLOAARAKQFKSKRPRNSDCFOEEDLRQGFQMRKSLPFGAASSTLNLEKGE 60
QY 112 GSATATYKGISIRINGQVLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 171
DB 61 GSATATYKGISIRINGQVLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 120
QY 172 ETLTFVFEYMTDLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 231
DB 121 ETLTFVFEYMTDLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 180
QY 232 ISHLGELKADFGARAKSIPSGTYSSEVVTLMYRPPDALLGATYSSSLDIWGACICFI 291
DB 181 ISHLGELKADFGARAKSIPSGTYSSEVVTLMYRPPDALLGATYSSSLDIWGACICFI 240
QY 292 EMFOGQPLPFGVSNILIEOLEKIWEVLGVPTEDTPGVSKLPYNNPEWFPPLTPRSLHVVW 351
DB 241 EMFOGQPLPFGVSNILIEOLEKIWEVLGVPTEDTPGVSKLPYNNPEWFPPLTPRSLHVVW 300
QY 352 NRIGRVPEAEADLASQMLKGPPDRVSAQOALVHDYFSALPSQLYQLPDESSLTFTVSGVRL 411
DB 301 NRIGRVPEAEADLASQMLKGPPDRVSAQOALVHDYFSALPSQLYQLPDESSLTFTVSGVRL 360
QY 412 KPBMCDLLASYOKGHHPAQFSKCM 435
DB 361 KPBMCDLLASYOKGHHPAQFSKCM 384

RESULT 2
Q8UTP1 PRELIMINARY; PRT; 349 AA.
ID 08UTP1 PRELIMINARY; PRT; 349 AA.
AC 08UTP1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ALS2CR7 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Keteleman W., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- Similarity: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC038607; AF38807.1; -.
DR HSSP: P24941; ID18.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD002001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 349 AA; 39597 MW; F884A39447AaB6E CRC64;

Query Match      79.5%; Score 1844; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 8.6e-124;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 MTSFHRGLOAARAKQFKSKRPRNSDCFOEEDLRQGFQMRKSLPFGAASSTLNLEKGE 111
DB 1 MTSFHRGLOAARAKQFKSKRPRNSDCFOEEDLRQGFQMRKSLPFGAASSTLNLEKGE 60
QY 112 GSATATYKGISIRINGQVLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 171
DB 61 GSATATYKGISIRINGQVLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 120
QY 172 ETLTFVFEYMTDLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 231
DB 121 ETLTFVFEYMTDLAQVMSQHPGGLHPHNVRLFMFQLRGLAYIHQVHLRDLKQNL 180
QY 232 ISHLGELKADFGARAKSIPSGTYSSEVVTLMYRPPDALLGATYSSSLDIWGACICFI 291
DB 181 ISHLGELKADFGARAKSIPSGTYSSEVVTLMYRPPDALLGATYSSSLDIWGACICFI 240
QY 292 EMFOGQPLPFGVSNILIEOLEKIWEVLGVPTEDTPGVSKLPYNNPEWFPPLTPRSLHVVW 351
DB 241 EMFOGQPLPFGVSNILIEOLEKIWEVLGVPTEDTPGVSKLPYNNPEWFPPLTPRSLHVVW 300
QY 352 NRIGRVPEAEADLASQMLKGPPDRVSAQOALVHDYFSALPSQLYQLPDE 400
DB 301 NRIGRVPEAEADLASQMLKGPPDRVSAQOALVHDYFSALPSQLYQLPDE 349

RESULT 3
Q6ZMR9 PRELIMINARY; PRT; 345 AA.
ID 06ZMR9 PRELIMINARY; PRT; 345 AA.
AC 06ZMR9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16732.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,

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RA Yamashita H., Matsumoto K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magaruma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Suzuki Y., Sugano S., Nagahori K., Masuho Y., Nagai K., Isegaki T.,
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AK131512; BAD18656.1; -.
 DR GO: GO:0016301; F-kinase activity; IEA.
 DR InterPro: IPR011009; Kinase-like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR008271; Ser_thr_pkinase.
 DR InterPro: IPR01245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 345 AA; 38586 MW; A51640CA8C119F43 CRC64;
 SQ
 Query Match 70.8%; Score 1641.5; DB 2; Length 345;
 Best Local Similarity 93.8%; Pred. No. 2.6e-109;
 Matches 315; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
 QY 1 MGELCAKTVQPCSCYHCSEGEAHSRRSQPETTEAAFKLTDLEASCMTSPFPRGL 60
 DB 1 MGELCAKTVQPCSCYHCSEGEAHSRRSQPETTEAAFKLTDLEASCMTSPFPRGL 60
 QY 61 QAAARQKFKSKPRNSDCFOEEDLRQGWKRSLPFGAASSTYLNLEKLEGSYATVYVG 120
 DB 61 QAAARQKFKSKPRNSDCFOEEDLRQGWKRSLPFGAASSTYLNLEKLEGSYATVYVG 120
 QY 121 ISRINGQVALKLVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVPEX 180
 DB 121 ISRINGQVALKLVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVPEX 180
 QY 181 MHTDLAQVNSQHPGGLPHNVLRFMFQQLRGLAYIHQVHLRDLKPNQLLSHIGELKL 240
 DB 181 M-----LRFQQLRGLAYIHQVHLRDLKPNQLLSHIGELKL 219
 QY 241 ADPGLARAKSIPQYSSSEVTLWYRPPDALLGATYSESLDIWGAGCIFIEMFOQPLF 300
 DB 241 ADPGLARAKSIPQYSSSEVTLWYRPPDALLGATYSESLDIWGAGCIFIEMFOQPLF 279
 QY 301 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 336
 DB 301 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 315
 DB 280 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 315
 RESULT 4
 BAD18656 PRELIMINARY; PRT; 345 AA.
 AC BAD18656;
 DT 12-MAY-2004 (TRENBLrel. 27, Created)
 DT 12-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DT 12-MAY-2004 (TRENBLrel. 27, Last annotation update)
 DE CDNA FLJ16732 fig. clone BNGH42005017, moderately similar to
 DE SERINE/THREONINE-PROTEIN KINASE PCFAIRE-1 (EC 2.7.1.-).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hito Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsumoto K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magaruma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Suzuki Y., Sugano S., Nagahori K., Masuho Y., Nagai K., Isegaki T.,
 RT "NEO human cDNA sequencing project.";

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK131512; BAD18656.1; -.
 KW Kinase.
 SQ SEQUENCE 345 AA; 38586 MW; A51640CA8C119F43 CRC64;
 Query Match 70.8%; Score 1641.5; DB 2; Length 345;
 Best Local Similarity 93.8%; Pred. No. 2.6e-109;
 Matches 315; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
 QY 1 MGELCAKTVQPCSCYHCSEGEAHSRRSQPETTEAAFKLTDLEASCMTSPFPRGL 60
 DB 1 MGELCAKTVQPCSCYHCSEGEAHSRRSQPETTEAAFKLTDLEASCMTSPFPRGL 60
 QY 61 QAAARQKFKSKPRNSDCFOEEDLRQGWKRSLPFGAASSTYLNLEKLEGSYATVYVG 120
 DB 61 QAAARQKFKSKPRNSDCFOEEDLRQGWKRSLPFGAASSTYLNLEKLEGSYATVYVG 120
 QY 121 ISRINGQVALKLVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVPEX 180
 DB 121 ISRINGQVALKLVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVPEX 180
 QY 181 MHTDLAQVNSQHPGGLPHNVLRFMFQQLRGLAYIHQVHLRDLKPNQLLSHIGELKL 240
 DB 181 M-----LRFQQLRGLAYIHQVHLRDLKPNQLLSHIGELKL 219
 QY 241 ADPGLARAKSIPQYSSSEVTLWYRPPDALLGATYSESLDIWGAGCIFIEMFOQPLF 300
 DB 241 ADPGLARAKSIPQYSSSEVTLWYRPPDALLGATYSESLDIWGAGCIFIEMFOQPLF 279
 QY 301 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 336
 DB 301 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 315
 DB 280 PGVSNLEOLEKIMEVLGVPTEDTWPGVSKLPNYP 315
 RESULT 5
 PFT1_MOUSE STANDARD; PRT; 469 AA.
 ID PFT1_MOUSE
 AC O35495; O35498;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase PFTAIR-1 (EC 2.7.1.37).
 GN Name=Pftk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RC TISSUE=Testis;
 RX MEDLINE=98208722; PubMed=9547506;
 RA Besset V., Rhee K., Wolgemuth D.J.;
 RT "The identification and characterization of expression of Pftaire-1, a
 RT novel Cdk family member, suggest its function in the mouse testis and
 RT nervous system.";
 RL Mol. Reprod. Dev. 50:18-29(1998).
 RN [2]
 RP SEQUENCE OF 47-469 FROM N.A., SUBCELLULAR LOCATION, AND DEVELOPMENTAL
 RP STAGE.
 RC STRAIN=NIH Swiss; TISSUE=Brain;
 RX MEDLINE=97345837; PubMed=9202329;
 RA Lazzaro M.A., Albert P.R., Julien J.-P.;
 RT "A novel cdc2-related protein kinase expressed in the nervous
 RT system.";
 RL J. Neurochem. 69:348-364(1997).
 CC -1- FUNCTION: May play a role in meiosis as well as in neuron
 CC differentiation and/or function.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: In the adult, widely expressed at low levels
 CC except in brain, kidney and testis where expression is high. In
 CC the brain, detected in cortex, hippocampus, dentate gyrus, amgdala

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CC corex, parasubiculum and cerebellum. In the embryo, expressed
CC predominantly in the nervous system.
CC -1- DEVELOPMENTAL STAGE: In the testis, expressed at low levels in
CC Sertoli cells of 7-day-old mice, barely detected at day 17, and
CC detected at much higher levels in late pachytene/diplotene
CC spermatocytes in the adult. In the nervous system, expressed at
CC highest levels in the adult.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC CDC2/CDCX subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL: AF033655; AAB87504.1; -.
DR HSSP: P24941; 1G1I.
DR MGD: MGI:894318; Pck1.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Nuclear protein; Serine/threonine-protein kinase;
DR transferase.
KW DOMAIN 135
FT NP_BIND 141 149 ATP (By similarity).
FT BINDING 164 164 ATP (By similarity).
FT ACT_SITE 256 256 Proton acceptor (By similarity).
FT CONFLICT 222 223 EQ -> DK (in Ref. 2).
FT CONFLICT 375 375 S -> N (in Ref. 2).
SQ SEQUENCE 469 AA; 53009 MW; 7542DF46D55AC97 CRC64;

Query Match 51.7%; Score 1198.5; DB 1; Length 469;
Best Local Similarity 55.3%; Pred. No. 2e-77;
Matches 246; Conservative 55; Mismatches 103; Indels 41; Gaps 5;

QY 23 GEANSCRSQPET-TEAFKLTDLKEASCSMTSFHPRGLQA-----ARA 65
DB 14 GKKKKLRRLTSEFSRIALKEEDTTFDEICVTGSTRNCGTDSVIKHLDTIPEDKKAV 73
QY 66 QKFKS-----KRPSS-NSDCFOBEDLRQGFQWRK-----SLPFGAAS 101
DB 74 QRTQSTFDFPEKPRANQVKVHSENNACINFKSSSAGESEPKVRRHSPSPSPSKRKAD 133
QY 102 SYLNLKLEKSGSAYATVYKGISRINQOLVALKVISMAAEKGVPTPTAREASLKGKGNANI 161
DB 134 SYEKLEKLEGGSAIATYKKGSKNGKVALKVIKRLDEEBESTPTAIRKSLKGLGNANI 193
QY 162 VLLHDIITHTKETTLLVFEYVMTDLAQYMSQHPRGILPHNVRLFMFOLLRLGLAYIHQHYL 221
DB 194 VLLHDIITHTKETTLLVFEYVMTDLAQYMSQHPRGILPHNVRLFMFOLLRLGLAYIHQRYL 253
QY 222 HEDLKQNLILSHLGLKADPRGLARAKSIPSTYSSEVVTLMYRPPDALGATVSSSEL 281
DB 254 HEDLKQNLILSTGKLADPRGLARAKSVPSHTYSNEVVTLMYRPPDVLGSTEYSTCL 313
QY 282 DIMGAGCFLIEMFQGOPLFPGVSNILQLEKIEWEVGPTEDTWPVSKLPNNPMPFPL 341
DB 314 DMWGVCIVIVEMIGVAAFPKMDIODQLERIFLVLTGTRENDWPGVHSLPHKPKRFTV 373
QY 342 PTPRSILHVVVWNLGRVPEADLASQMLKGPDRDVSAGQALVHYDSALPSQLYQLPDEE 401
DB 374 YSSKSLRQAMNKLISYVNHADILASKILQSPKRLSAQALSHYEYSDLPRLMELTDMG 433

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QY 402 SLFTVSGVFLKPEKMDLASYQKH 426
DB 434 SIFTVPVNLQPEAGESMKAPGKNN 458

RESULT 6
ID 06NVF8 PRELIMINARY; PRT; 423 AA.
AC 06NVF8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pck1 protein.
GN Name=Pck1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC068134; AAB68134.1; -.
DR InterPro: IPR001199; Cyt_B5_.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 423 AA; 47684 MW; 5895A066A7C17AAB CRC64;

Query Match 51.4%; Score 1192.5; DB 2; Length 423;
Best Local Similarity 60.2%; Pred. No. 4.7e-77;
Matches 233; Conservative 56; Mismatches 83; Indels 15; Gaps 2;

QY 51 SMTSFHPRGLQAAARQKFKSKRPNSDCFOBEDLRQGFQWRK-----SLPFGA 99

```

DB 30 TOSTDPPEKPNQYKRVHSE-----NNACINFKSSAGKESPKVRRHSSPSSPTKCKX 85
 QY 100 ASSYLNEKLGEGSAATYKGISRINGOLVALKVI SMNAEEGVPTAIRASLGLKXA 159
 DB 86 ADSYKLEKLGEGSAATYKGISRINGOLVALKVI RLOEEBGTPTAIRASLGLKXA 145
 QY 160 NIVLHDIHTKETETLTPFEVYHTDLAQYMSQHPGSLHPHNRLPMFOLLRLATYHHOH 219
 DB 146 NIVLHDIHTKETETLTPFEVYHTDLCOYMDKHPGSLHPDNVKLFLFOLLRLSLYIHOXY 205
 QY 220 VLHRLDKPQNLIIISHGELKLDLADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSS 279
 DB 206 ILHRLDKPQNLIIISHGELKLDLADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYST 265
 QY 280 ELDIWGACIFIEFMQGPPLFPVGSNILEOLEKIWEVIGVPTEDTWPVSKLPNNPEWF 339
 DB 266 CLDMWGVGCIFFVEMIQVAAFPQMKDIDQLERIFLVIGTPEMDTWPVSHLPFKPERF 325
 QY 340 PLPTFRSLHVWNNRLGRVPEADLASOMLKGPFRDVSNOEALVHDYFSGALPSQYOLPD 399
 DB 326 TVSSKSLROAWNNKLSYNNHAEADLASKLQCSPPKRLSNQAALSHYFSDLPRLMELTD 385
 QY 400 EBSLFTVSGVRLKPEMCDLLASQYKQH 426
 DB 386 MSSITFVNVRLQPEAGSMRAFQKNN 412

RESULT 7

AAH68134 PRELIMINARY; PRT; 423 AA.

AC AAH68134; PRELIMINARY; PRT; 423 AA.

DT 14-APR-2004 (TREMBLrel. 27, Created)

DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)

DE pfck1 protein.

GN PFTK1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Alteschl S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stachenko M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Best Local Similarity 60.2%; Pred. No. 4,7e-77;
 Matches 233; Conservative 56; Mismatches 83; Indels 15; Gaps 2;
 QY 51 SMTSFHPRGLQAAARQKRSKRPNSNDQFOEDLRQGFQWRK-----SLPGA 99
 DB 30 TOSTDPPEKPNQYKRVHSE-----NNACINFKSSAGKESPKVRRHSSPSSPTKCKX 85
 QY 100 ASSYLNEKLGEGSAATYKGISRINGOLVALKVI SMNAEEGVPTAIRASLGLKXA 159
 DB 86 ADSYKLEKLGEGSAATYKGISRINGOLVALKVI RLOEEBGTPTAIRASLGLKXA 145
 QY 160 NIVLHDIHTKETETLTPFEVYHTDLAQYMSQHPGSLHPHNRLPMFOLLRLATYHHOH 219
 DB 146 NIVLHDIHTKETETLTPFEVYHTDLCOYMDKHPGSLHPDNVKLFLFOLLRLSLYIHOXY 205
 QY 220 VLHRLDKPQNLIIISHGELKLDLADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSS 279
 DB 206 ILHRLDKPQNLIIISHGELKLDLADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYST 265
 QY 280 ELDIWGACIFIEFMQGPPLFPVGSNILEOLEKIWEVIGVPTEDTWPVSKLPNNPEWF 339
 DB 266 CLDMWGVGCIFFVEMIQVAAFPQMKDIDQLERIFLVIGTPEMDTWPVSHLPFKPERF 325
 QY 340 PLPTFRSLHVWNNRLGRVPEADLASOMLKGPFRDVSNOEALVHDYFSGALPSQYOLPD 399
 DB 326 TVSSKSLROAWNNKLSYNNHAEADLASKLQCSPPKRLSNQAALSHYFSDLPRLMELTD 385
 QY 400 EBSLFTVSGVRLKPEMCDLLASQYKQH 426
 DB 386 MSSITFVNVRLQPEAGSMRAFQKNN 412

RESULT 8

06Z037 PRELIMINARY; PRT; 453 AA.

AC 06Z037; PRELIMINARY; PRT; 453 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE MKIA0834 protein (Fragment).

GN Name=MKIA0834;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryonic tail;

RX PubMed=14621295;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,

RA Suga Y., Nagase T., Ohara O., Koga H.,

RT "Prediction of the coding sequences of mouse homologues of KIAA gene:

RT III. the complete nucleotide sequences of 500 mouse KIAA-homologues

RT cDNAs identified by screening of terminal sequences of cDNA clones

randomly sampled from size-fractionated libraries."

RNA Reg. 10:167-180(2003).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AK129226; BAC98036.1; -

DR InterPro: IPR001199; Cyt B5.

DR InterPro: IPR001009; Kinase like.

DR InterPro: IPR000719; Prot kinase.

DR InterPro: IPR002290; Ser_thr_kinase.

DR InterPro: IPR008271; Ser_thr_kinase.

DR InterPro: IPR001245; Tyr_kinase.

DR Pfam: PF00069; Kinase; 1.

DR ProDom: PD000001; Prot kinase; 1.

DR SMART; SM00220; S_TKc_1.

DR SMART; SM00219; TYKc_1.

DR PROSITE; PS00191; CYTOCHROME B5_1; UNKNOWN_1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.

Query Match 51.4%; Score 1192.5; DB 2; Length 423;

```

FT  NON TER      1      1      4DEEE7BAAB23941D CRC64;
SQ  SEQUENCE      453 AA; 51210 MW; 4DEEE7BAAB23941D CRC64;

Query Match
Best Local Similarity 51.4%; Score 1192.5; DB 2; Length 453;
Matches 233; Conservative 56; Mismatches 83; Indels 15; Gaps 2;

QY  51 SMTSPHRLQAPARQKFKSKPRNSDCFOEEDLRQGFQMKR-----SLPFGA 99
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  60 TOSTDPPEKPKANQVRHVSE-----NNACINFKSSAGKESPKVRHSSPSSPTSPKFGK 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  100 ASSYLNLEKLGEGSVATYTKGSRINGOLVALKVISMAEBGVPTAIRBASLTKGLKKA 159
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  116 ASYKLEKLGEGSVATYTKGSKVNGKVALKVILQEBEGTPTAIRBASLTKGLKKA 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  160 NIVLHDDIHTKETLTLPFEYVHTDLAQYMSQHPGLHPHNVRLPMFOLLRLGLAYIHHQ 219
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  176 NIVLHDDIHTKETLTLPFEYVHTDLCOYMDKHPGLHPDVKLFLFOLLRLGLSYIHHQY 235
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  220 VILHRLKPNLLISHLGEIKLADFGIARAKSIPSQTYSSEVYTLTKRPPDALLGATEYSS 279
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  236 ILHRLDKPNLLISDTGELKLDLFGIARAKSVSHSTYSNEVVTLMWRPDDVLLGSTEST 295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  280 ELDINGAGCIFIEMPOGQPLPGVSNILEOLEKIMEVLGVPTEDTPGVSKLPNVNPEWF 339
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  296 CLDMNGVGCIFVEMIQGVAAPFGMKDIOQLERITLVLTGTPMEDTWPGVHSLPHKPERF 355
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  340 PLPTPRSLHVVNRLGRVPEADLASQMLKGFPRDRVSAQOALVHDYFSAALPSQLYQLPD 399
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  356 TVYSSKSILQAVNKNLSYVNHAEIDLASKLQCSPKRRLSAQALSHYFSDLPPRLMELTD 415
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  400 EESLFTVSGVRLKPEMCDLLASYOKGH 426
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  416 MSSITVFNVRILQPEAGSMRAFGKNN 442
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
BAC98036 PRELIMINARY; PRT; 453 AA.
AC BAC98036;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE MKIAA0034 protein (Fragment).
DE MKIAA0034.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=embryonic tail;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-fractionated Libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129226; BAC98036.1; -.
FT NON TER      1
SQ SEQUENCE      453 AA; 51210 MW; 4DEEE7BAAB23941D CRC64;

Query Match
Best Local Similarity 51.4%; Score 1192.5; DB 2; Length 453;
Matches 233; Conservative 56; Mismatches 83; Indels 15; Gaps 2;

QY  51 SMTSPHRLQAPARQKFKSKPRNSDCFOEEDLRQGFQMKR-----SLPFGA 99
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  60 TOSTDPPEKPKANQVRHVSE-----NNACINFKSSAGKESPKVRHSSPSSPTSPKFGK 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  100 ASSYLNLEKLGEGSVATYTKGSRINGOLVALKVISMAEBGVPTAIRBASLTKGLKKA 159
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB  116 ADYKLEKLGEGSVATYTKGSKVNGKVALKVIRLQEBEGTPTAIRBASLTKGLKKA 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  160 NIVLHDDIHTKETLTLPFEYVHTDLAQYMSQHPGLHPHNVRLPMFOLLRLGLAYIHHQ 219
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  176 NIVLHDDIHTKETLTLPFEYVHTDLCOYMDKHPGLHPDVKLFLFOLLRLGLSYIHHQY 235
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  220 VILHRLKPNLLISHLGEIKLADFGIARAKSIPSQTYSSEVYTLTKRPPDALLGATEYSS 279
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  236 ILHRLDKPNLLISDTGELKLDLFGIARAKSVSHSTYSNEVVTLMWRPDDVLLGSTEST 295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  280 ELDINGAGCIFIEMPOGQPLPGVSNILEOLEKIMEVLGVPTEDTPGVSKLPNVNPEWF 339
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  296 CLDMNGVGCIFVEMIQGVAAPFGMKDIOQLERITLVLTGTPMEDTWPGVHSLPHKPERF 355
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  340 PLPTPRSLHVVNRLGRVPEADLASQMLKGFPRDRVSAQOALVHDYFSAALPSQLYQLPD 399
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  356 TVYSSKSILQAVNKNLSYVNHAEIDLASKLQCSPKRRLSAQALSHYFSDLPPRLMELTD 415
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  400 EESLFTVSGVRLKPEMCDLLASYOKGH 426
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  416 MSSITVFNVRILQPEAGSMRAFGKNN 442
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
Q6DUM7 PRELIMINARY; PRT; 435 AA.
AC Q6DUM7;
DT 01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grove L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;

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Db 194 VLLHDIHTKETLLVFEVYHTDLCOYMDKHGGLHPDVKLFLPQLRLGSLYHQRYTL 253
Qy 222 HNDLKQNLISHGLKTLADPGLAKSPISQTVSEVVTLMYPPDALGATESSSL 281
Db 254 HNDLKQNLISHGLKTLADPGLAKSPISQTVSEVVTLMYPPDALGATESSSL 313
Qy 282 DIWGACIETEMFQGPPLFPGVSNILEQLEKIMVELVGPTEDTWPGVSKLPYNPMPFPL 341
Db 314 DMWGVCITIVEMIQVAAPFGMKDIDQLEKIFLVLTGPTNEDTWPGVSHLPFKPERFTL 373
Qy 342 PTPRSILHVWNRIGRVPEZADLASQMLKAPPRDRVSAQALVHDYPSALPQSLYQPDSE 401
Db 374 YSSKSNLRQAMNKLSTYNVHAEDLASKLLQCSPKNRLSAQALSHYFSDLPPLMELTDMS 433
Qy 402 SLFTVSGVRLKPEMCDLLASLYOKGH 426
Db 434 SLFTVSNVRLQPEAGSMAFGKN 458
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RESULT 12

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08MZ44 PRELIMINARY; PRT; 367 AA.
ID 08MZ44;
AC 08MZ44;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE L027880P.
GN Name=Elp63B;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY11367; AM29372.1; -.
DR HSBP; P24941; 1P2A.
DR FLYBase; FBgn0005640; Elp63B.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Cyt. B5.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot. kinase.
DR InterPro; IPR002290; Ser. Thr. kinase.
DR InterPro; IPR008271; Ser. Thr. pkin. AS.
DR InterPro; IPR008271; Ser. Thr. pkin. AS.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 367 AA; 42309 MW; 05EBD51133830B5 CRC64;
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Query Match 46.5%; Score 1078.5; DB 2; Length 367;
Best Local Similarity 60.2%; Pred. No. 5,7e-69;
Matches 213; Conservative 42; Mismatches 84; Indels 15; Gaps 3;
Qy 71 KRPRNSDGF---QEEDLRQGFQWRKSL-----PFGAASSYLNLEKLGSGSYATVYKG 120
Db 13 KPRPRKSEVFLNKQETHPR-----RKPRSAFGGDSFPFGQEAAYVYLPLTGBGSYATVYKG 67
```

```
Qy 121 ISRLNGQVVALKVISNNAEGVPTFAIRASLLKGLKXANIVLHDIHTKETLLVFEY 180
Db 68 FSKLTYYRVALKKEIRLOEEBAGPPTAIRASLLKGLKXANIVLHDIHTKETLLVFEY 127
Qy 181 MHTDLAQYMSQHPGGLHPHNVRLFMFOLLRLGLAYIIHQHVLHRDLKPNLISHGLKTL 240
Db 128 VNTDLSQYMEHNPGLDHRNVRFLPOLLRLGLSYCHRRVYLHRQVKNLISHGSLKTL 187
Qy 241 ADPGLARAKSPISQTVSEVVTLMYPPDALGATESSSLDIWGACIETEMFQGPPLF 300
Db 188 ADPGLARAKSPISQTVSEVVTLMYPPDALGATESSSLDIWGVCITIVEMIQVAPTF 247
Qy 301 PGVSNILEQLEKIMVELVGPTEDTWPGVSKLPYNPMPFPLPTPRSLHVWNRIGRVPEA 360
Db 248 PGIIRDTYDQDKIRFLGTPEDTWPGVTHFPYKPKHKLGYRRKRGHNPRLYDIIEG 307
Qy 361 EDLASQMLKAPPRDRVSAQALVHDYPSALPQSLYQPDSESLFTVSGVRLKPE 414
Db 308 ETIANGFLQLNPQRLGADALQHPYFAQLPKLYELPDFTSIFTVGVLQYTE 361
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RESULT 13

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07KM04 PRELIMINARY; PRT; 501 AA.
ID 07KM04;
AC 07KM04;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Serine/threonine protein kinase variant L63B3.
GN Name=L63;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stowers R.S., Garza D., Hogness D.S.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ protein kinase family.
DR EMBL; AF152403; AAD4514.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR InterPro; IPR011009; Cyt. B5.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot. kinase.
DR InterPro; IPR002290; Ser. Thr. kinase.
DR InterPro; IPR008271; Ser. Thr. pkin. AS.
DR InterPro; IPR001245; Tyr. pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot. kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 501 AA; 57741 MW; 0FB0F78DFDFA6DFD CRC64;
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Best Local Similarity 60.2%; Pred. No. 8,4e-69;
Matches 213; Conservative 42; Mismatches 84; Indels 15; Gaps 3;
Qy 71 KRPRNSDGF---QEEDLRQGFQWRKSL-----PFGAASSYLNLEKLGSGSYATVYKG 120
Db 147 KPRPRKSEVFLNKQETHPR-----RKPRSAFGGDSFPFGQEAAYVYLPLTGBGSYATVYKG 201
Qy 121 ISRLNGQVVALKVISNNAEGVPTFAIRASLLKGLKXANIVLHDIHTKETLLVFEY 180
Db 202 FSKLTYYRVALKKEIRLOEEBAGPPTAIRASLLKGLKXANIVLHDIHTKETLLVFEY 261
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QY 181 MHTDLAQVMSQHRCGLHPHNVRLFMQLRGLAYIHQVHLHRDLKRONLLISHLGEML 240
DB 262 VNTDLSQYNEKHPGGJLDHNRNRLFLFQLRGLSLCYKRRVLRHADVRCQNLISDCGLK 321
QY 241 ADFGLARAKSVSHSYSEVTLMTYRPPDALLGATEYSELIDWAGCCLFVEMVTMPF 300
DB 322 ADFGLARAKSVSHSYSEVTLMTYRPPDALLGATEYSELIDWAGCCLFVEMVTMPF 381
QY 301 PGVSNILEQLEKIWEVLGVPTEDTWPVSKLPNYPNPEWFPPLPTPSRLHYVNRNLGRVPEA 360
DB 382 PGIRDTYDQDKIFKLGLPTEDTWPVTHFPYKPHKLGFRVPRLLGNHPRLYDIIG 441
QY 361 EDLASOMLKGPRDRVSAQBALVHDYFSALPSQLYOLPDEBSLFYVSGYRLKPE 414
DB 442 ETIANGFLQINPEORLGDADLQHPYFQALPKKLYELPDETSIFVTEGVOLYTE 495
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AC 07KM08;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Serine/threonine protein kinase variant L63A2.
GN Name=L63;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RA Stowers R.S., Garza D., Hogness D.S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AF152399; AAD4510.1; -
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:004674; F:protein serine/threonine kinase activity; IEA.
DR InterPro: IPR001159; Cyt B5.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002280; Ser_Thr_kinase.
DR InterPro: IPR008271; Ser_Thr_kin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc1.
DR SMART: SM00219; TYKc1.
DR PROSITE: PS00191; CYTOCHROME B5_1; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 509 AA; 58342 MW; F99C2860C8FFA12A CRC64;
Query Match 46.5%; Score 1078.5; DB 2; Length 509;
Best local Similarity 60.2%; Pred. No. 8.5e-69;
Matches 213; Conservative 42; Mismatches 84; Indels 15; Gaps 3;
QY 71 KPRRSNSDCF---QEEDLRQGFQWRKSL-----PFGAASLYLNLEKLGEGSYATVYKG 120
DB 155 KPRPRSEVFLNKQETNPR-----RRRFGAFGDSFPFGQEAIVKLEPREGSGYATVYKG 209
QY 121 ISRINGQALALKYISNNAEGVFTAIRASILLKGLKHANIVYLHDIHTKETLTGFVPEY 180
DB 210 FSKLTQYRALKEIRIQEESGAPFTIRKESLSLKEKHSNIVYLHDIHTRETITFVPEY 269
QY 181 MHTDLAQVMSQHRCGLHPHNVRLFMQLRGLAYIHQVHLHRDLKRONLLISHLGEML 240
DB 270 VNTDLSQYNEKHPGGJLDHNRNRLFLFQLRGLSLCYKRRVLRHADVRCQNLISDCGLK 329
QY 241 ADFGLARAKSVSHSYSEVTLMTYRPPDALLGATEYSELIDWAGCCLFVEMVTMPF 300

DB 330 ADFGLARAKSVSHSYSEVTLMTYRPPDALLGATEYSELIDWAGCCLFVEMVTMPF 389
QY 301 PGVSNILEQLEKIWEVLGVPTEDTWPVSKLPNYPNPEWFPPLPTPSRLHYVNRNLGRVPEA 360
DB 390 PGIRDTYDQDKIFKLGLPTEDTWPVTHFPYKPHKLGFRVPRLLGNHPRLYDIIG 449
QY 361 EDLASOMLKGPRDRVSAQBALVHDYFSALPSQLYOLPDEBSLFYVSGYRLKPE 414
DB 450 ETIANGFLQINPEORLGDADLQHPYFQALPKKLYELPDETSIFVTEGVOLYTE 503
RESULT 15
QY 09VZN8 PRELIMINARY; PRT; 509 AA.
AC 09VZN8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CG10579-PA (CG10579-pb) (LID15250p) (Serine/threonine protein kinase variant L63B2).
GN Name=Elp63E; Synonyms=L63; ORFNames=CG10579;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabo R.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
RA Beeson K.Y., Benson P.V., Betman B.P., Bhandardi D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chervy J.M., Cawley S., Dahlke C., Davoport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.W., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusseken D.R., Paclebo J.M.,
RA Palazozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitzbaek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Waasatanan D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodgerg, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zhang X.H., Zhong F.N., Zhong X., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=24246065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svltbak R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svltbakas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Hradecky P., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beltenkourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
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 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paclet J., Paragas V., Park S.,
 RA Patel S., Pounenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Stowers R.S., Garza D., Hogness D.S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB003478; AAF47781.2; -;
 DR EMBL; BT010064; AAO22533.1; -;
 DR EMBL; AF152402; AAD45513.1; -;
 DR HSSP; P24941; 1P2A.
 DR FLYBASE; FBgn0005640; Eip63E.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 509 AA; 58517 MW; 890EFBDC04319DBA CRC64;
 Query Match 46.5%; Score 1078.5; DB 2; Length 509;
 Best Local Similarity 60.2%; Pred. No. 8,5e-69;
 Matches 213; Conservative 42; Mismatches 84; Indels 15; Gaps 3;
 QY 71 KPPRNSDCF---QEDLRQGFQWRKSL-----PFGAASSYLNLKLGEGSVATVYKG 120
 DB 155 KPPRPSSEVFLLNKQETNRR-----RKPSARFGDSPPFGKQEAIVVLEPLGEGSVATVYKG 209
 QY 121 ISRINGQVALLKVISMNAEAGVFTAIRBASILKGLKQANIVLHDIHTKETTTFVEY 180
 DB 210 PSKLTGYQVALLKEIRLQEEBGAFTAIRBASILKGLKQANIVLHDIHTKETTTFVEY 269
 QY 181 MATDIAQVMSQPPGGLHPNNVRLFMFOLLRLGLAYTHQGVHLRDLKPNQLLSHIGELKL 240
 DB 270 VNTDLSQVWEKIRPGGIDHRNVRLLFLQRLRLGLSYCHKRRVLRDVKPNQLLSIDGELKL 329
 QY 241 ADPGLARAKSIPSGTYSSEVVTLMYRPPDALLGATEYSSLDIYGAGCIFIEMFGQGPPLF 300
 DB 330 ADPGLARAKSVPSHTYSHSVVTLMTYRPPDVLGSTEYISTLDMGVGCI FVEMVTGMPTF 389
 QY 301 PGVSNILBQLEKIMVGLVPTEDTPWGVSKLPNYPNPEWFPPLTPRSLHVWNNRLGRVPEA 360
 DB 390 PGIRDTYQDLKIFLLGTPPTEDTPGVTHFGYKPKHGLGFRRPKLGHNFPRLYDIIEG 449
 QY 361 EPLASQMLKGFPRDVSQOELVHDYPSALPSQLYQLDDESLFVSGVRLKPE 414
 DB 450 EYIANGFLQINPEQRIGADDAQHYPYQLPKKLYELDETSIFVGEQVLYTE 503

Search completed: December 27, 2004, 12:18:33
 Job time : 80 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 26, 2004, 18:49:09 ; Search time 73 Seconds
(without alignment)
2137.633 Million cell updates/sec

Title: US-10-786-065-5

Perfect score: 2320
Sequence: 1 MGQELCACTVPGGSCYHCS.....CDLASYKXGHHRAQPSKCW 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneeqp19808:*
- 2: geneeqp19908:*
- 3: geneeqp20008:*
- 4: geneeqp20018:*
- 5: geneeqp20028:*
- 6: geneeqp20038:*
- 7: geneeqp20048:*
- 8: geneeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2320	100.0	435	AAOI8614	AAOI8614 Human Ptc
2	2320	100.0	435	ABR57359	ABR57359 Human ser
3	2320	100.0	435	ABR57361	ABR57361 Human ser
4	2320	100.0	435	ADJ96629	ADJ96629 Human cyc
5	2088	90.0	405	ADG31726	ADG31726 Human nov
6	2088	87.8	384	ABR57357	ABR57357 Human ser
7	1784	76.9	343	AAOI8613	AAOI8613 Human ptc
8	1659.5	71.5	321	ADG79729	ADG79729 Human kpp
9	1641.5	70.8	345	ADMI6427	ADMI6427 Human kpp
10	1432.5	61.7	296	ABP96082	ABP96082 Human pro
11	1260.5	54.3	266	AA655641	AA655641 Novel pro
12	1260.5	54.3	266	ADJ29248	ADJ29248 Human MAR
13	1198.5	51.7	469	ABR57358	ABR57358 Mouse ser
14	1198.5	51.7	469	ADJ76287	ADJ76287 Marker ge
15	1195	51.5	330	AAOI8617	AAOI8617 Human ptc
16	1194.5	51.5	423	AAO30087	AAO30087 A human c
17	1194.5	51.5	450	ADN95586	ADN95586 Human BRC
18	1194.5	51.5	451	ADN89961	ADN89961 Human can
19	1194.5	51.5	451	ADJ75554	ADJ75554 Marker ge
20	1194.5	51.5	451	ADQ17590	ADQ17590 Human sof
21	1191.5	51.4	423	AAO30088	AAO30088 A murine
22	1190	51.3	330	AAOI8618	AAOI8618 Human ptc
23	1190	51.3	330	AAOI8619	AAOI8619 Human ptc
24	1185.5	51.1	469	AAO26453	AAO26453 Human hpr
25	1185.5	51.1	469	ADJ69485	ADJ69485 Human hea

26	1044.5	45.0	509	4	ABR57849	ABR57849 Drosophila
27	1044.5	45.0	509	4	ABR67228	ABR67228 Drosophila
28	1044.5	45.0	509	4	ABR67227	ABR67227 Drosophila
29	1000	43.1	245	5	AAOI8616	AAOI8616 Human ptc
30	993	42.8	240	5	AAOI8615	AAOI8615 Human ptc
31	919.5	39.6	497	4	AAAM39021	AAAM39021 Human pol
32	916	39.5	496	4	AAOI8619	AAOI8619 Human ptc
33	916	39.5	496	6	AAOI8618	AAOI8618 Human ptc
34	916	39.5	496	7	ADN95586	ADN95586 Human BRC
35	916	39.5	496	7	ADN89961	ADN89961 Human can
36	916	39.5	496	7	ADJ75554	ADJ75554 Marker ge
37	916	39.5	496	7	ADQ17590	ADQ17590 Human sof
38	916	39.5	496	8	ADJ29248	ADJ29248 Human MAR
39	910	39.2	527	3	ABR57357	ABR57357 Human ser
40	909.5	39.2	330	7	ABR57360	ABR57360 Human ser
41	909.5	39.2	482	8	ADN87193	ADN87193 Human pro
42	908	39.1	496	4	AAU01186	AAU01186 Rat gluta
43	907.5	39.1	461	4	AAU01187	AAU01187 Rat gluta
44	907.5	39.1	462	7	ADN95586	ADN95586 Human BRC
45	907.5	39.1	462	7	ADN89961	ADN89961 Human can

ALIGNMENTS

RESULT 1	AAOI8614	standard; protein; 435 AA.
AC	AAOI8614;	
AC	AAOI8614;	
DT	24-OCT-2002	(first entry)
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DE	Human Ptfaira family kinase splice form 2.	
DE		
KW	Human, Ptfaira family kinase; kinase; enzyme; testis; brain; cytosolic;	
KW	uterus endometrium adenocarcinoma; lung fibroblast; splice form;	
KW	kidney renal cell adenocarcinoma; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200261060-A2.	
XX		
PD	08-AUG-2002.	
XX		
PF	17-JAN-2002; 2002WO-US0001106.	
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PR	31-JAN-2001; 2001US-0265151P.	
PR	09-MAR-2001; 2001US-00801861.	
PA	(PEKE) PE CORP NY.	
XX		
PI	Yan C, Ketchum K, Di Francesco V, Beasley EM;	
XX		
DR	WPI; 2002-608515/65.	
DR	N-PSDB; AAL48890, AAL48891.	
XX		
PT	New human kinase peptide with nucleic acid molecule, useful for treating disorders associated with abnormal expression of kinase protein, e.g. adenocarcinoma of uterus or lung, in drug screening assays and pharmacogenomic analysis.	
PT		
PS	Claim 1, Fig 2; 131p; English.	
XX		
CC	The present invention provides the protein, cDNA and gene sequences of two splice variants of a human Ptfaira family kinase. The sequences are specifically expressed in the human testis, brain, uterus endometrium adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and can be used to treat related diseases. The present sequence is splice variant 2 of the invention	
CC		
XX		
SQ	Sequence 435 AA;	

```

Query Match      100.0%; Score 2320; DB 5; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.4e-223;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDELCAKTVQPGSCCYHSGEGEHAHSCRRSQPETTEAFKLTDLKEASCMTSPFPRGL 60
DB 1 MGDELCAKTVQPGSCCYHSGEGEHAHSCRRSQPETTEAFKLTDLKEASCMTSPFPRGL 60
QY 61 QARAPQKFKSKPRNSNDCFOEBEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
DB 61 QARAPQKFKSKPRNSNDCFOEBEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
QY 121 ISRINGQVVALKVISMNAEAGVFTAIIRASLLKGLKHANIVLHDIHTKETLTFVFEY 180
DB 121 ISRINGQVVALKVISMNAEAGVFTAIIRASLLKGLKHANIVLHDIHTKETLTFVFEY 180
QY 181 MHTDLAQVMSQHPGGHAPHNVRLFMFQLRGLAYIHQHVLRHDLKPOULLSHLGELKL 240
DB 181 MHTDLAQVMSQHPGGHAPHNVRLFMFQLRGLAYIHQHVLRHDLKPOULLSHLGELKL 240
QY 241 ADFGLARAKSIPQSYSSSEVVTLMYRPPDALLGATEYSSSELDIWAGCIFIEMFGQPLF 300
DB 241 ADFGLARAKSIPQSYSSSEVVTLMYRPPDALLGATEYSSSELDIWAGCIFIEMFGQPLF 300
QY 301 PGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPNEMFPLPTPSRLHVVMNRLGRVPEA 360
DB 301 PGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPNEMFPLPTPSRLHVVMNRLGRVPEA 360
QY 361 EDLASQMLKGFPRDRVSAQEAALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
DB 361 EDLASQMLKGFPRDRVSAQEAALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
QY 421 STQKGHHPAQFSKCW 435
DB 421 STQKGHHPAQFSKCW 435

RESULT 2
ABR57359
ID ABR57359 standard; protein; 435 AA.
XX
AC ABR57359;
XX
DT 09-SEP-2003 (first entry)
XX
DE Human serine/threonine protein kinase SEQ ID NO:6.
XX
KW Human; serine/threonine protein kinase; kinase; enzyme; cytosolic;
KW antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
KW cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
KW gynaecological; uteropathic; dermatological; gene therapy; cancer;
KW diabetes; central nervous system disorder; CNS disorder; liver disease;
KW respiratory disorder; chronic obstructive pulmonary disease; stroke;
KW cardiovascular disorder; dermatological disorder; urological disorder;
KW gastrointestinal disease; haematological disorder; Alzheimer's disease;
KW musculoskeletal disorder; reproductive disorder; Parkinson's disease;
KW neuropathic pain.
XX
OS Homo sapiens.
XX
PN WO2003046167-A1.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-EP013268.
XX
PR 27-NOV-2001; 2001US-033131P.
XX
PA (PARR ) BAYER AG.
XX
PI Koehler RH;
XX
WPI, 2003-505196/47.

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```

DR N-PSDB; ACC79968.
XX
XX New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for diagnosing, preventing or treating diseases
PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
PT or diabetes.
XX
PS Example 3; Fig 6; 196pp; English.
XX
XX The present sequence represents a human serine/threonine protein kinase
CC (1). (1) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian,
CC nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic,
CC gastrointestinal, gynaecological, uteropathic and dermatological
CC activities, and can be used in gene therapy. Serine/threonine protein
CC kinase polynucleotide and polypeptide sequences can be used in
CC diagnosing, preventing, ameliorating or treating diseases associated with
CC serine/threonine protein kinase dysfunction. They may also be used to
CC identify test compounds that may act, for example, as activators or
CC inhibitors at the enzyme's active site. The human serine/threonine
CC protein kinase and its fragments are also useful in raising specific
CC antibodies that can block the enzyme and effectively reduce its activity.
CC Human serine/threonine protein kinase sequences can be used in the
CC preparation of a medicament for modulating the activity of a serine/
CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
CC nervous system (CNS) disorder, a respiratory disorder (including chronic
CC obstructive pulmonary disease), a cardiovascular disorder, a
CC dermatological disorder, a gastrointestinal or liver disease, a
CC haematological disorder, a musculoskeletal disorder, a reproductive
CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
CC disease, Parkinson's disease, stroke or neuropathic pain
XX
SQ Sequence 435 AA;
Query Match      100.0%; Score 2320; DB 7; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.4e-223;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDELCAKTVQPGSCCYHSGEGEHAHSCRRSQPETTEAFKLTDLKEASCMTSPFPRGL 60
DB 1 MGDELCAKTVQPGSCCYHSGEGEHAHSCRRSQPETTEAFKLTDLKEASCMTSPFPRGL 60
QY 61 QARAPQKFKSKPRNSNDCFOEBEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
DB 61 QARAPQKFKSKPRNSNDCFOEBEDLRQGFQWRKSLPFGAASLYLNLEKLGEGSYATVYKG 120
QY 121 ISRINGQVVALKVISMNAEAGVFTAIIRASLLKGLKHANIVLHDIHTKETLTFVFEY 180
DB 121 ISRINGQVVALKVISMNAEAGVFTAIIRASLLKGLKHANIVLHDIHTKETLTFVFEY 180
QY 181 MHTDLAQVMSQHPGGHAPHNVRLFMFQLRGLAYIHQHVLRHDLKPOULLSHLGELKL 240
DB 181 MHTDLAQVMSQHPGGHAPHNVRLFMFQLRGLAYIHQHVLRHDLKPOULLSHLGELKL 240
QY 241 ADFGLARAKSIPQSYSSSEVVTLMYRPPDALLGATEYSSSELDIWAGCIFIEMFGQPLF 300
DB 241 ADFGLARAKSIPQSYSSSEVVTLMYRPPDALLGATEYSSSELDIWAGCIFIEMFGQPLF 300
QY 301 PGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPNEMFPLPTPSRLHVVMNRLGRVPEA 360
DB 301 PGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPNEMFPLPTPSRLHVVMNRLGRVPEA 360
QY 361 EDLASQMLKGFPRDRVSAQEAALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
DB 361 EDLASQMLKGFPRDRVSAQEAALVHDYFSALPSQLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
QY 421 STQKGHHPAQFSKCW 435
DB 421 STQKGHHPAQFSKCW 435

RESULT 3
ABR57361
ID ABR57361 standard; protein; 435 AA.

```

```

XX  ABR57361;
AC  09-SEP-2003 (first entry)
DT
XX
XX  Human serine/threonine protein kinase SEQ ID NO:10.
DE
XX
XX  Human; serine/threonine protein kinase; kinase; enzyme; cytosolic;
KW  antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
KW  cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
KW  gynaecological; uropathic; dermatological; gene therapy; cancer;
KW  diabetes; central nervous system disorder; CNS disorder; liver disease;
KW  respiratory disorder; chronic obstructive pulmonary disease; stroke;
KW  cardiovascular disorder; dermatological disorder; urological disorder;
KW  gastrointestinal disease; haematological disorder; Alzheimer's disease;
KW  musculoskeletal disorder; reproductive disorder; Parkinson's disease;
KW  neuropathic pain.
XX
XX  Homo sapiens.
OS
XX  WO2003046167-A1.
PN
XX
XX  05-JUN-2003.
PD
XX
XX  26-NOV-2002; 2002WO-EP013268.
PF
XX
XX  27-NOV-2001; 2001US-033131P.
PR
XX
XX  (FARB ) BAYER AG.
PA
XX  Koehler RH;
PI
XX  WPI; 2003-505196/47.
DR  N-PSDB; ACC79970, ACC79971.
XX
XX  New polynucleotide encoding a serine/threonine protein kinase
PT  polypeptide, useful for diagnosing, preventing or treating diseases
PT  associated with serine/threonine protein kinase dysfunction, e.g. cancer
PT  or diabetes.
XX
XX  Disclosure; Page 188-190; 196pp; English.
XX
XX  The present sequence represents a human serine/threonine protein kinase
CC  (1). (1) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian,
CC  nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic,
CC  gastrointestinal, gynaecological, uropathic and dermatological
CC  activities, and can be used in gene therapy. Serine/threonine protein
CC  kinase polynucleotide and polypeptide sequences can be used in
CC  diagnosing, preventing, ameliorating or treating diseases associated with
CC  serine/threonine protein kinase dysfunction. They may also be used to
CC  identify test compounds that may act, for example, as activators or
CC  inhibitors at the enzyme's active site. The human serine/threonine
CC  protein kinase and its fragments are also useful in raising specific
CC  antibodies that can block the enzyme and effectively reduce its activity.
CC  Human serine/threonine protein kinase sequences can be used in the
CC  preparation of a medicament for modulating the activity of a serine/
CC  threonine protein kinase in a disease, e.g. cancer, diabetes, a central
CC  nervous system (CNS) disorder, a respiratory disorder (including chronic
CC  obstructive pulmonary disease), a cardiovascular disorder, a
CC  dermatological disorder, a gastrointestinal or liver disease, a
CC  haematological disorder, a musculoskeletal disorder, a reproductive
CC  disorder, or a urological disorder. CNS disorders may include Alzheimer's
CC  disease, Parkinson's disease, stroke or neuropathic pain
XX
XX
XX  Sequence 435 AA:
SQ
XX
XX  Query Match 100.0%; Score 2320; DB 7; Length 435;
XX  Best Local Similarity 100.0%; Pred. No. 3.4e-223;
XX  Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MGEELCAKTVVQPCSCYHSGEGEASHCRSOPETTEAAFKLTDLEASCSMTSPFPRGL 60
XX  1 MGEELCAKTVVQPCSCYHSGEGEASHCRSOPETTEAAFKLTDLEASCSMTSPFPRGL 60

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```

QY  61 QAAAPQKFKSKRPRNSDGFQEDLRQGFQMRKSLPFGAASSTLNLEKLGEGSYATVYKG 120
DB  61 QAAAPQKFKSKRPRNSDGFQEDLRQGFQMRKSLPFGAASSTLNLEKLGEGSYATVYKG 120
QY  121 ISRINGQVALVAVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVFEY 180
DB  121 ISRINGQVALVAVISNNAEEGVPFTAIRASLLKGLKHNIVLHDIHTKETLTFVFEY 180
QY  181 MHTDLAQVNSQHPGGLHPNNVLFMFQLRGLAYIHQHVLRDLKPQMLLSHLGELKL 240
DB  181 MHTDLAQVNSQHPGGLHPNNVLFMFQLRGLAYIHQHVLRDLKPQMLLSHLGELKL 240
QY  241 ADPGLARAKSISQYSSSVTLWTRPPALLGATRYSELDLWAGCIFIEMFQOQLP 300
DB  241 ADPGLARAKSISQYSSSVTLWTRPPALLGATRYSELDLWAGCIFIEMFQOQLP 300
QY  301 PGVSNLEQLEKIMEVLGVPTEDTPGVSKLPNNYPMWPLPTPSLHVVMRLGRVPEA 360
DB  301 PGVSNLEQLEKIMEVLGVPTEDTPGVSKLPNNYPMWPLPTPSLHVVMRLGRVPEA 360
QY  361 EDLASQMLKGFPRDRVSAQEALVHDYFSALPQOLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
DB  361 EDLASQMLKGFPRDRVSAQEALVHDYFSALPQOLYQLPDEBSLFTVSGVRLKPEMCDLLA 420
QY  421 SYQKGHHHPAQFSKCW 435
DB  421 SYQKGHHHPAQFSKCW 435

RESULT 4
ADJ96629
ID  ADJ96629 standard; protein; 435 AA.
XX
XX  ADJ96629;
AC
XX
XX  06-MAY-2004 (first entry)
DT
XX
XX  Human cyclin dependent kinase PFTAIRB2 protein Seqid 86.
DE
XX
XX  kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW  PTK; gene therapy; cancer; immune-related disease; metabolic;
KW  cardiovascular disease; brain; neuronal associated disease;
KW  inflammatory disorder; cytosolic; neuroprotective; immunomodulator;
XX  antiinflammatory; enzyme; cyclin dependent kinase; PFTAIRB2.
XX
XX  Homo sapiens.
OS  55.
XX
XX  WO2004006838-A2.
PN
XX
XX  22-JAN-2004.
PD
XX
XX  15-UTL-2003; 2003WO-US021730.
PF
XX
XX  15-UTL-2002; 2002US-0395632P.
PR
XX
XX  (SUGB-) SUGEN INC.
PA
XX
XX  whyte D, Manning G, Caenepeel S;
PI  WPI; 2004-122753/12.
XX  N-PSDB; ADJ96563.
DR
XX
XX  New nucleic acid molecule encoding a kinase polypeptide, useful for
PT  preparing a composition for treating diseases or disorders, e.g., cancer,
PT  or neurological, immunological or inflammatory disorders.
XX
XX  Claim 1, SEQ ID NO 86; 366pp; English.
PS
XX
XX  This invention relates to a novel isolated, enriched or purified nucleic
CC  acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC  to human tyrosine and serine/threonine protein kinases (PTK's and STK's),

```

CC as well as protein kinase-like enzymes. The present invention describes
 CC screening methods to identify agonists, antagonists and antibodies that
 CC can be used to modulate the activity or function of the mammalian kinase
 CC enzymes. As such, these compositions can be used for gene therapy
 CC purposes to treat diseases or disorders including cancer, immune-related
 CC diseases, cardiovascular disease, brain or neuronal associated disease,
 CC metabolic and inflammatory disorders. Accordingly, they exhibit
 CC cytoprotective, neuroprotective, immunomodulator and anti-inflammatory
 CC activities. This polypeptide sequence is a human kinase protein sequence
 CC of the invention.

XX Sequence 435 AA;

XX Query Match 100.0%; Score 2320; DB 8; Length 435;

XX Best Local Similarity 100.0%; Pred. No. 3.4e-223;

XX Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDELCAKTYOPCSCYHSGEGEAAHSCRRSOPETTEAAFKLTDLKEASCSMTSPFRGL 60
 Db 1 MGDELCAKTYOPCSCYHSGEGEAAHSCRRSOPETTEAAFKLTDLKEASCSMTSPFRGL 60

QY 61 QAARAKFKSKRRNSDCFOEBDLRQGFQWRKSLPFGAASLYINLEKLGEGSYATVYKG 120
 Db 61 QAARAKFKSKRRNSDCFOEBDLRQGFQWRKSLPFGAASLYINLEKLGEGSYATVYKG 120

QY 121 ISRINGQLVALKTI SMNAEEGVPTAIRASLLKGLKHANIVLHDI IHTKETLTVEFY 180
 Db 121 ISRINGQLVALKTI SMNAEEGVPTAIRASLLKGLKHANIVLHDI IHTKETLTVEFY 180

QY 181 MHRTDLQVMSQHGGHAPHNVRLFMFQOLRGLAYIHQHVLHNDLPQNLISHLELKY 240
 Db 181 MHRTDLQVMSQHGGHAPHNVRLFMFQOLRGLAYIHQHVLHNDLPQNLISHLELKY 240

QY 241 ADGGLARAKSIPSOQYTSSEVVTLMYRPPDALGATEYSBELDWAGCIFIEMFOGQPLF 300
 Db 241 ADGGLARAKSIPSOQYTSSEVVTLMYRPPDALGATEYSBELDWAGCIFIEMFOGQPLF 300

QY 301 PGVSNILEQLEKIEWVLGVPTEDTWGVSCLPNYNBEMFPLTPRSLHVTYNNFLGRVPER 360
 Db 301 PGVSNILEQLEKIEWVLGVPTEDTWGVSCLPNYNBEMFPLTPRSLHVTYNNFLGRVPER 360

QY 361 EDLASQMLKGFPRDRVSAOELVHDYFSALPSQLYQLPDESLFTVSGVRLKPEMCDLLA 420
 Db 361 EDLASQMLKGFPRDRVSAOELVHDYFSALPSQLYQLPDESLFTVSGVRLKPEMCDLLA 420

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

QY 421 SYQGHHPAQFSKCM 435
 Db 421 SYQGHHPAQFSKCM 435

PD 10-APR-2003.

XX 24-SEP-2002; 2002WO-US030474.

XX 24-SEP-2001; 2001US-0324631P.

XX (HYSE-) HYSEQ INC.

XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;

XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Wang G;

XX Haley-Vicente D, Drmanac RT;

XX WPI: 2003-371981/35.

XX N-PSDB; AD30755.

XX New polynucleotide and polypeptide useful for diagnosing, preventing or

XX treating conditions such as neurodegenerative diseases, anemias, platelet

XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

XX cancer.

XX Claim 20; SEQ ID NO 1808; 1185pp; English.

XX The invention relates to 971 novel human cDNA sequences (AD329919-

XX AD330889) and the polypeptides they encode (AD330890-AD331860). The

XX invention also relates to nucleic acid sequences over 99% identical with

XX the novel human cDNAs. The invention additionally encompasses expression

XX vectors and host cells comprising a nucleic acid of the invention; the

XX recombinant production of a polypeptide of the invention; an antibody

XX against a polypeptide of the invention; a method of detecting

XX polynucleotides or polypeptides of the invention; and methods of

XX identifying a compound which binds to a polypeptide of the invention. The

XX invention further discloses methods of preventing, treating or

XX ameliorating a medical condition; kits comprising polynucleotide probes

XX and/or monoclonal antibodies for carrying out the methods of the

XX invention; method for the identification of compounds that modulate the

XX expression or activity of the polynucleotide and/or polypeptide; and 767

XX config sequences corresponding to the cDNA sequences of the invention

XX (AD331861-AD332627) and the polypeptides encoded by the configs (AD332628

XX -AD333394). The nucleic acids and polypeptides of the invention are

XX useful in diagnostics, drug screening, forensics, gene mapping, in the

XX identification of mutations responsible for genetic disorders or other

XX traits, for assessing biodiversity, and in producing many other types of

XX data and products dependent on DNA and amino acid sequences. They are

XX also used for treating diseases such as Parkinson's disease, Alzheimer's

XX disease and other neurodegenerative diseases, anaemia, platelet

XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

XX cancer. The nucleic acids may also be used as hybridisation probes or

XX primers, and in the recombinant production of a protein. The polypeptides

XX are also useful in generating antibodies, as molecular weight markers,

XX and as food supplements. The present sequence represents a specifically

XX claimed human polypeptide sequence of the invention. Note: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 405 AA;

XX Query Match 90.0%; Score 2088; DB 7; Length 405;

XX Best Local Similarity 100.0%; Pred. No. 5.7e-200;

XX Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 LNDLKEASCSMTSPFRPGIQAARAKFKSKRRNSDCFOEBDLRQGFQWRKSLPFGAAS 101

Db 12 LNDLKEASCSMTSPFRPGIQAARAKFKSKRRNSDCFOEBDLRQGFQWRKSLPFGAAS 71

QY 102 SYLNLEKLGEGSYATVYKGISRINGQLVALKTI SMNAEEGVPTAIRASLLKGLKHANI 161

Db 72 SYLNLEKLGEGSYATVYKGISRINGQLVALKTI SMNAEEGVPTAIRASLLKGLKHANI 131

QY 162 VLLHDI IHTKETLTVEFYMHRTDLAQVMSQHGGHAPHNVRLFMFQOLRGLAYIHQHVL 221

Db 132 VLLHDI IHTKETLTVEFYMHRTDLAQVMSQHGGHAPHNVRLFMFQOLRGLAYIHQHVL 191

PI Van C, Ketchum K, Di Francesco V, Beasley EM;
 XX WPI; 2002-608515/65.
 DR N-PSDB; AAL48889, AAL48890.
 XX
 PT New human kinase peptide and nucleic acid molecule, useful for treating
 PT disorders associated with abnormal expression of kinase protein, e.g.
 PT adenocarcinoma of uterus or lung, in drug screening assays and
 PT pharmacogenomic analysis.
 XX
 PS Claim 1; Fig 2; 131pp; English.
 XX
 CC The present invention provides the protein, cDNA and gene sequences of
 CC two splice variants of a human pftaire family kinase. The sequences are
 CC specifically expressed in the human testis, brain, uterus endometrium
 CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinoma, and
 CC can be used to treat related diseases. The present sequence is splice
 CC variant 1 of the invention
 CC
 XX Sequence 343 AA;
 SQ
 Query Match 76.3%; Score 1784; DB 5; Length 343;
 Best Local Similarity 100.0%; Pred. No. 1,3e-169;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGQELAKTVQPCSCYCHGSEGEAHSRCRSQPEETBAARKLTDLEASGSMTSFPRGL 60
 Db 1 MGQELAKTVQPCSCYCHGSEGEAHSRCRSQPEETBAARKLTDLEASGSMTSFPRGL 60
 QY 61 QAAARAQFKFSKRPNSNDCEQBEDLRQGFQWRKSLPFGAASLYLNTLEKLGESGATVYKG 120
 Db 61 QAAARAQFKFSKRPNSNDCEQBEDLRQGFQWRKSLPFGAASLYLNTLEKLGESGATVYKG 120
 QY 121 ISRLNGQLVALKVIYSMNAEEGVPTAIRESALLKGLKHNIVLLHDIHTKETLTFFVFX 180
 Db 121 ISRLNGQLVALKVIYSMNAEEGVPTAIRESALLKGLKHNIVLLHDIHTKETLTFFVFX 180
 QY 181 MHTDLAOWMSQHGGLHPHNVRLFMQOLRGLAYIHQVYLDLDPQNLISHLEBLKL 240
 Db 181 MHTDLAOWMSQHGGLHPHNVRLFMQOLRGLAYIHQVYLDLDPQNLISHLEBLKL 240
 QY 241 ADPGLARAKSIPESQTSSEVVTLMYRPPDALLGATEVSESLDIMGAGCTFIEMFOGQPLF 300
 Db 241 ADPGLARAKSIPESQTSSEVVTLMYRPPDALLGATEVSESLDIMGAGCTFIEMFOGQPLF 300
 QY 301 PGVSNILBQLEKTIWEVLGVPTEDTPGVSKLPYNNP 336
 Db 301 PGVSNILBQLEKTIWEVLGVPTEDTPGVSKLPYNNP 336
 RESULT 8
 AAG79729
 ID AAG79729 standard; protein; 321 AA.
 XX
 AC AAG79729;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human KPP-7, Incyte ID No. 7494145D01.
 XX
 KW Kinase; phosphatase; KPP; cell proliferation; arteriosclerosis;
 KW atherosclerosis; cirrhosis; hepatitis; reproduction; infertility;
 KW paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;
 KW primary chromocytopenia; cancer; development; renal tubular acidosis;
 KW anaemia; mental retardation; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; epilepsy; Sjogren's syndrome; uveitis; asthma;
 KW menstrual cycle; autoimmune; inflammation; rheumatoid arthritis; AIDS;
 KW autoimmune thyroiditis; contact dermatitis; Crohn's disease; allergy;
 KW diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout;
 KW Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;
 KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
 KW Reiter's syndrome; mouse; PFTAIR kinase; enzyme.
 XX

OS Homo sapiens.
 XX
 FH Key
 FT Modified-site
 FT Modified-site
 FT Modified-site
 FT Domain
 FT Domain
 FT Binding-site
 FT Modified-site
 FT Peptide
 FT Active-site
 FT Protein
 FT Modified-site
 FT Domain
 FT Domain
 FT WO200290530-A2.
 FT 14-NOV-2002.
 FT 16-JAN-2002; 2002WO-US001369.
 FT 18-JAN-2001; 2001US-0263083P.
 FT 23-FEB-2001; 2001US-0271117P.
 FT 23-FEB-2001; 2001US-0271205P.
 FT 16-MAR-2001; 2001US-0276859P.
 FT 23-MAR-2001; 2001US-02768504P.
 FT 23-MAR-2001; 2001US-02768522P.
 FT 29-MAR-2001; 2001US-0280266P.
 FT 29-MAR-2001; 2001US-0280510P.
 PA (INCYTE GENOMICS INC.
 XX
 XX Lee EA, Wallia NK, Baughn MR, Ison CH, Gurrurajan R, Arvizu C;
 PI Yao MG, Jackson JL, Tang TY, Yue H, Tran B, Ding L, Lu DM;
 PI Lal PG, Warren BA;
 XX
 DR WPI; 2003-111972/10.
 DR N-PSDB; ABA00722.
 XX
 PT New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX
 PS Claim 1; Page 135-36; 144pp; English.
 XX
 CC The sequences given in AAG79723-30 show human kinases and phosphatases
 CC (KPP). The KPP polypeptides, polynucleotides, and agonists and
 CC antagonists to them, are useful for diagnosing, treating or preventing
 CC disorders associated with aberrant expression of KPP, particularly cell
 CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
 CC cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia
 CC vera, psoriasis, primary chromocytopenia or cancer), developmental
 CC disorders (e.g. renal tubular acidosis, anaemia or mental retardation),
 CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or

CC epilepsy), reproductive disorders (e.g. infertility or a disruption in
 CC the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. They
 CC are also useful in the assessment of the effects of exogenous compounds
 CC on the expression of nucleic acid and amino acid sequences of proteins
 CC associated with KRP. This protein is homologous to mouse PFTAIRK kinase
 XX
 XX Sequence 321 AA:

Query Match 71.5%; Score 1659.5; DB 6; Length 321;
 Best Local Similarity 83.6%; Pred. No. 3.7e-157;
 Matches 321; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

QY 52 MTSFPRGQARARQKFKSKPRNSDCFOEBDLRGCFQWRKSLPFGAASSTYLNLEKGE 111
 DB 1 MTSFPRGQARARQKFKSKPRNSDCFOEBDLRGCFQWRKSLPFGAASSTYLNLEKGE 60
 QY 112 GSATATYKGISIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTK 171
 DB 61 GSATATYKGISIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTK 120
 QY 172 ETLTFVFEYMTDLAQYMSQHFGGLHPHNVRLFMFOLLRLGLAYIHQVHLHDLKPNLL 231
 DB 121 ETLTFVFEYMTDLAQYMSQHFGGLHPHNVRLFMFOLLRLGLAYIHQVHLHDLKPNLL 180
 QY 232 ISHLGELKADGRLARAKSIPSCYTSSSVVTLWYRPPDALLGATEYSSSLDIWGACITF 291
 DB 181 ISHLGELKADGRLARAKSIPSCYTSSSVVTLWYRPPDALLGATEYSSSLDIWGACITF 240
 QY 292 EMFGQGPLPFGVSNILEQLEKIMEVLAGVPTEDTWPGVSKLPNNYPFPLPRSLHYVW 351
 DB 241 EMFGQGPLPFGVSNILEQLEKIMEVLAGVPTEDTWPGVSKLPNNYPFPLPRSLHYVW 285
 QY 352 NRLGVRPEADLASQMLKGPDRVSAQBALVHYPSALPSQLYQLPDESLFTVSGVRL 411
 DB 286 -----ESLFTVSGVRL 297
 QY 412 KPEMCDLASXQKSHHPAQFSKCW 435
 DB 298 KPEMCDLASXQKSHHPAQFSKCW 321

RESULT 9

ID ADM16427 standard; protein; 345 AA.

AC ADM16427;

DT 17-JUN-2004 (first entry)

DE Human kinase protein, seq id 6.

KM Cytostatic; cardiant; neuroprotective; nootropic; antiinfertility;

KM vulnery; antidiabetic; kinase; cancer; heart disease;

KM Alzheimer's disease; infertility; wound; diabetes; neurological disease.

OS Homo sapiens.

PN WO2004024913-A1.

PD 25-MAR-2004.

PF 10-SEP-2003; 2003WO-JP011552.

PR 10-SEP-2002; 2002JP-00264345.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX (ZOEGB-) ZOEGNE CORP.

XX Kondo J, Kawai K, Miyama N, Nakajima M, Isogai T, Sugiyama T;
 PI Wakamatsu A, Irie R, Ishii S;
 XX WPI; 2004-270042/25.
 DR N-PsDB; ADM16422.
 XX
 XX Proteins of human origin having kinase activity, useful for prevention
 PT and treatment of kinase-associated diseases including cancer, heart
 PT disease and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 6; 105pp; Japanese.

CC The invention relates to four proteins of human origin (1) having kinase
 CC activity, and to proteins derived from these by addition, deletion and/or
 CC substitution of one or more amino acid residues, and having similar
 CC activity. The proteins and other aspects of the invention are useful for
 CC the prevention and treatment of kinase-associated diseases including
 CC cancer, heart disease, Alzheimer's disease, infertility, wounds, diabetes
 CC and neurological diseases. The current sequence represents a human
 CC protein having kinase activity.

XX Sequence 345 AA;

Query Match 70.8%; Score 1641.5; DB 8; Length 345;
 Best Local Similarity 93.8%; Pred. No. 2.6e-155;
 Matches 315; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 MGOELCAKTVQRCGSCYHSEGEBAHSCRRSQPETTEBAFKLTDKEASCMTSPHPRGL 60
 DB 1 MGOELCAKTVQRCGSCYHSEGEBAHSCRRSQPETTEBAFKLTDKEASCMTSPHPRGL 60
 QY 61 QARAQKFKSKPRNSDCFOEBDLRGCFQWRKSLPFGAASSTYLNLEKGBSVATVYKG 120
 DB 61 QARAQKFKSKPRNSDCFOEBDLRGCFQWRKSLPFGAASSTYLNLEKGBSVATVYKG 120
 QY 121 ISIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTKTLTFVFEY 180
 DB 121 ISIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTKTLTFVFEY 180
 QY 181 IIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTKTLTFVFEY 180
 DB 181 IIRINGQLVALKVIYSMNAEGVPFTAIRASLLKGLKHANIVLLHDIHTKTLTFVFEY 180
 QY 181 M-----LPMFOLLRLGLAYIHQVHLHDLKPNLL 240
 DB 181 M-----LPMFOLLRLGLAYIHQVHLHDLKPNLL 219
 QY 241 ADFGLARAKSIPSCYTSSSVVTLWYRPPDALLGATEYSSSLDIWGACITFEMFGQPLF 300
 DB 220 ADFGLARAKSIPSCYTSSSVVTLWYRPPDALLGATEYSSSLDIWGACITFEMFGQPLF 279
 QY 301 PGVSNILEQLEKIMEVLAGVPTEDTWPGVSKLPNNY 336
 DB 280 PGVSNILEQLEKIMEVLAGVPTEDTWPGVSKLPNNY 315

RESULT 10

ID ABP96082 standard; protein; 296 AA.

AC ABP96082;

DT 07-MAY-2003 (first entry)

DE Human protein kinase SEQ ID NO:70.

KM Human; protein kinase; enzyme; antiaesthetic; antiinflammatory;

KM antidiabetic; antiparkinsonian; antigravine; cardiant; cytostatic;

KM immunosuppressive; vulnery; gene therapy; COPD; asthma; migraine;

KM chronic obstructive pulmonary disease; non-insulin dependent diabetes;

KM Parkinson's disease; myocardial infarction; inflammatory bowel disease;

KM autoimmune disorder; allograft rejection; graft versus host disease;

OS cancer; leukaemia; wound granulation.

PN WO2003000901-A2.
 XX 03-JAN-2003.
 PD
 XX
 PF 24-JUN-2002; 2002WO-IB002358.
 XX
 XX 26-JUN-2001; 2001US-0301098P.
 PR 06-NOV-2001; 2001US-0332870P.
 XX
 PA (DECO-) DECODE GENETICS EHF.
 XX
 PI Martinez RAM, Sigurdson GT;
 XX
 DR WPI; 2003-201429/19.
 DR N-PSDB; AB277160.
 XX
 XX New protein kinase genes and polypeptides, useful for diagnosing diseases
 PT associated with a protein kinase, or in gene therapy for treating e.g.
 PT Parkinson's disease, migraine, myocardial infarction, allograft rejection
 PT or cancers.
 PS
 PS Claim 9; Page 85; 258pp; English.
 XX
 XX AB277126 to AB277165 encode the human protein kinases given in ABP96048
 CC to ABP96087. The protein kinases have antidiabetic, antiinflammatory,
 CC antidiabetic, antiparkinsonian, antimigraine, cardiant, cyostatic,
 CC immunosuppressive and vulnerary activities, and can be used in gene
 CC therapy. A protein kinase therapeutic agent from the present invention,
 CC particularly a protein kinase gene agonist or antagonist, can be used for
 CC treating a disease or condition associated with a protein kinase in an
 CC individual. These diseases include chronic obstructive pulmonary diseases
 CC (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,
 CC migraine, myocardial infarction, inflammatory bowel disease, autoimmune
 CC disorders (e.g. allograft rejection or graft vs. host disease), cancers
 CC (e.g. leukaemia) or wound granulation
 CC
 XX Sequence 296 AA;
 SQ
 Query Match 61.7%; Score 1432.5; DB 6; Length 296;
 Best Local Similarity 93.7%; Pred. No. 1.9e-134;
 Matches 282; Conservative 5; Mismatches 7; Indels 7; Gaps 3;
 QY 100 ASSYLNLEKLGEGSYATYKGISRINQVLAQVSNABRGVFTAIRASLLKGLKHA 159
 DB 1 ASSYLNLEKLGEGSYATYKGISRINQVLAQVSNABRGVFTAIRASLLKGLKHA 60
 QY 160 NIVLHDIHTRKETLTFVEFYMHDLAQYMSOHGGLHPHVRLFMFQLRGALAYIHQH 219
 DB 61 NIVLHDIHTRKETLTFVEFYMHDLAQYMSOHGGLHPHVRLFMFQLRGALAYIHQH 120
 QY 220 VLHRLDKPQNTLLISHLGELKLDLFGALRAKSIPOQYSSSEVVTLMYRPPDALLGATEYSS 279
 DB 121 VLHRLDKPQNTLLISHLGELKLDLFGALRAKSIPOQYSSSEVVTLMYRPPDALLGATEYSS 180
 QY 280 ELDIYGACIPIEMNGOQPLPPGVSNILIEOLEKIMVTLGVPTEDTWGVSGLPNVYNPE-W 338
 DB 181 ELDIYGACIPIEMNGOQPLPPGVSNILIEOLEKIMVTLGVPTEDTWGVSGLPNVYNPE-W 240
 QY 339 FFLPFRSLHYV-VNRLGRVPEAEADLASOMLKGPRDRVSAQELVHDFYFALPSQLYQL 397
 DB 241 -----RNSIFLSHFRSLGRVPEAEADLASOMLKGPRDRVSAQELVHDFYFALPSQLYQL 295
 QY 398 P 398
 DB 296 P 296
 RESULT 11
 AAB65641
 ID AAB65641 standard; protein; 266 AA.
 XX
 AC AAB65641;
 XX

DT 27-MAR-2001 (first entry)
 XX
 DB Novel protein kinase, SEQ ID NO: 168.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antidiabetic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 XX 26-MAY-2000; 2000WO-US014842.
 PF
 XX 28-MAY-1999; 99US-0136503P.
 PR
 XX (SUGEN-) SUGEN INC.
 PA
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 DR WPI; 2001-032161/04.
 DR N-PSDB; AAF44668.
 XX
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 PS
 PS Claim 10; Fig 1; 310pp; English.
 XX
 XX The present sequence is a novel protein kinase. The novel protein kinases
 CC and the nucleic acids that encode them may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomypathies, strokes, renal failure, oxidative-
 CC stress related disorder, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 CC disorders
 CC
 XX Sequence 266 AA;
 SQ
 Query Match 54.3%; Score 1260.5; DB 4; Length 266;
 Best Local Similarity 90.6%; Pred. No. 2.8e-117;
 Matches 241; Conservative 4; Mismatches 18; Indels 3; Gaps 1;
 QY 173 TLTFFVEYHNTDLAQYMSOHGGLHPHVN---RLFMFQLRGALAYIHQHVLHRLDKQN 229
 DB 1 TLTFFVEYHNTDLAQYMSOHGGLHPHVN---RLFMFQLRGALAYIHQHVLHRLDKQN 60
 QY 230 LILSHLGELKLDLFGALRAKSIPOQYSSSEVVTLMYRPPDALLGATEYSSSELDIYGACI 289
 DB 61 LILSHLGELKLDLFGALRAKSIPOQYSSSEVVTLMYRPPDALLGATEYSSSELDIYGACI 120
 QY 290 FIEMFOGQPLPPGVSNILIEOLEKIMVTLGVPTEDTWGVSGLPNVYNPEFPLPTRSLHY 349
 DB 121 FIEMFOGQPLPPGVSNILIEOLEKIMVTLGVPTEDTWGVSGLPNVYNPEFPLPTRSLHY 180
 QY 350 VVNRRLGRVPEAEADLASOMLKGPRDRVSAQELVHDFYFALPSQLYQLPDESSLFTVSGV 409
 DB 181 VVNRRLGRVPEAEADLASOMLKGPRDRVSAQELVHDFYFALPSQLYQLPDESSLFTVSGV 240

QY 410 RLKPEMCDLLASYOKGHHPAQPSKCM 435
 DB 241 RLKPEMCDLLASYOKGHHPAQPSKCM 266

RESULT 12

AD129248
 ID AD129248 standard; protein; 266 AA.
 XX
 AC AD129248;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human MARK3-associated protein #36.
 XX
 KW Human; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003232771-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 17-JUN-2002; 2002US-00174319.
 XX
 PR 17-JUN-2002; 2002US-00174319.
 XX
 PA (ISTS-) ISTS PHARM INC.
 XX
 PI Ward DT, Freier SM, Dobie KW;
 XX
 DR WPI: 2004-052188/05.
 DR N-PSDB; AD129366.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 168; 233bp; English.

The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the specification.

Sequence 266 AA:

Query Match 54.3%; Score 1260.5; DB 8; Length 266;
 Best Local Similarity 90.6%; Pred. No. 2.8e-117;
 Matches 241; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

QY 173 TLTFVEYHWTDLAQMSQHPCGHLPHNV---RLFMFOLLRGALYHHQVHVRDLPKN 229
 DB 1 TLTTFEYHWTDLAQMSQHPCGHLPHNV---RLFMFOLLRGALYHHQVHVRDLPKN 60

QY 230 LLTSHLGEKLADFGFLARAKSIPQTYSEFVTLWYRPPDALGATEYSSSELDIMGAGCT 289
 DB 61 LLTSHLGEKLADFGFLARAKSIPQTYSEFVTLWYRPPDALGATEYSSSELDIMGAGCT 120

QY 290 FIEMFOGOLFPFGVSNILLEOLEKIEWELGVPTEDTPMGVSKLPNNYPMWFPLPTPSLHV 349
 DB 121 FIEMFOGOLFPFGVSNILLEOLEKIEWELGVPTEDTPMGVSKLPNNYPMWFPLPTPSLHV 180

QY 350 VVNRRLGRVPEADLASQMLKGFPRDRVSAQELVHDYFSAIPDSQYQLPDEESLFTVSGV 409
 DB 181 VVNRRLGRVPEADLASQMLKGFPRDRVSAQELVHDYFSAIPDSQYQLPDEESLFTVSGV 240

QY 410 RLKPEMCDLLASYOKGHHPAQPSKCM 435
 DB 241 RLKPEMCDLLASYOKGHHPAQPSKCM 266

RESULT 13

ABR57358
 ID ABR57358 standard; protein; 469 AA.
 XX
 AC ABR57358;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Mouse serine/threonine protein kinase SEQ ID NO:3.
 XX
 KW Mouse; serine/threonine protein kinase; kinase; enzyme; cytostatic;
 KW antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
 KW cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
 KW gynaecological; uropathic; dermatological; gene therapy; cancer;
 KW diabetes; central nervous system disorder; CNS disorder; liver disease;
 KW respiratory disorder; chronic obstructive pulmonary disease; stroke;
 KW cardiovascular disorder; dermatological disorder; urological disorder;
 KW gastrointestinal disease; haematological disorder; Alzheimer's disease;
 KW musculoskeletal disorder; reproductive disorder; Parkinson's disease;
 KW neuropathic pain.
 XX
 OS Mus musculus.
 XX
 PN WO2003046167-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-EP013268.
 XX
 PR 27-NOV-2001; 2001US-0333131P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI: 2003-505196/47.
 XX
 PT New polynucleotide encoding a serine/threonine protein kinase
 PT polypeptide, useful for diagnosing, preventing or treating diseases
 PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
 PT or diabetes.
 XX
 PS Disclosure; Fig 3; 166bp; English.

The present sequence represents a mouse serine/threonine protein kinase (I). (I) has cytostatic, antidiabetic, neuroprotective, antiparkinsonian, nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic, gastrointestinal, gynaecological, uropathic and dermatological activities, and can be used in gene therapy. Serine/threonine protein kinase polynucleotide and polypeptide sequences can be used in diagnosing, preventing, ameliorating or treating diseases associated with serine/threonine protein kinase dysfunction. They may also be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. The human serine/threonine protein kinase and its fragments are also useful in raising specific antibodies that can block the enzyme and effectively reduce its activity. Human serine/threonine protein kinase sequences can be used in the preparation of a medicament for modulating the activity of a serine/threonine protein kinase in a disease, e.g. cancer, diabetes, a central nervous system (CNS) disorder, a respiratory disorder (including chronic

CC obstructive pulmonary disease), a cardiovascular disorder, a
 CC dermatological disorder, a gastrointestinal or liver disease, a
 CC haematological disorder, a musculoskeletal disorder, a reproductive
 CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
 CC disease, Parkinson's disease, stroke or neuropathic pain
 XX
 SQ Sequence 469 AA;

Query Match 51.7%; Score 1198.5; DB 7; Length 469;
 Best Local Similarity 55.3%; Pred. No. 1,1e-110;
 Matches 246; Conservative 55; Mismatches 103; Indels 41; Gaps 5;

QY 23 GEANSCRSQPER-TEAATLTLTLKASCSMTSPHRLQA-----ARA 65
 DB 14 GKMKKLRLTSSFSRIALKKEDTTFDELCTVMSTRNCGTDSVIKHLDTIPEDKKVRV 73
 QY 66 QKPKS-----KRPRS-NSDCFQEBEDLRQGFQWRK-----SLPPGAAS 101
 DB 74 QRTOSTFPDFPEKPRANQVKRVHSENNACINFKSSAGKSPKVRHSSPSPSPKFGKAD 133
 QY 102 SYLNLEKLGEGSYATVYKGISRINGOLVALKVISMNAEBCVPTAIRBASLKLKXKANI 161
 DB 134 SYEKLEKLGEGSYATVYKGISRINGOLVALKVISMNAEBCVPTAIRBASLKLKXKANI 193
 QY 162 VLLHDIHTKETLTVEFVMTDLAQYMSOHGGLPHNVRLFMFOLRLGLAYIHQHYL 221
 DB 194 VLLHDIHTKETLTVEFVMTDLAQYMSOHGGLPHNVRLFMFOLRLGLAYIHQHYL 253
 QY 222 HRDLKQNTLLISHGELKADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSSSL 281
 DB 254 HRDLKQNTLLISHGELKADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSSSL 313
 QY 282 DIMGAGCIFIEMFQOGOPRLPGVSNILBOLEKIWEVLTGPTEDTWPGVSKLPYNPEWEP 341
 DB 314 DIMGAGCIFIEMFQOGVAAFPKMDIODLERILVLTGPTEDTWPGVSHLPFKPERFTV 373
 QY 342 PTPRSILHVVNRLGRVPEAEDLASOMLKGPBRDVSQOELVVDYSALPSQYLQYLPDEE 401
 DB 374 YSSKSLRQAWNKLSYVNHAEEDLASKLQCSFKNRLSAQALSHYFSDLPRLMELTDWS 433
 QY 402 SLFTVSGVRLKPEMCDLASQYQKH 426
 DB 434 SFTVSNVRLQPEAGSMRAFGKNN 458

RESULT 14

ADJ76287
 ID ADJ76287 standard; protein; 469 AA.

AC ADJ76287;

DT 20-MAY-2004 (first entry)

XX Marker gene related amino acid sequence SEQ ID NO:1539.

XX bronchial asthma; chronic obstructive pulmonary disease;
 XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 XX gene therapy; marker.

OS Mus musculus.

PN EP1394274-A2.

PD 03-MAR-2004.

PF 04-AUG-2003; 2003BP-00254857.

PR 06-AUG-2002; 2002JP-00229312.

PR 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhabara K;

XX MPI; 2004-193155/19.
 XX
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX Example 11; SEQ ID NO 1539; 241p; English.

XX The present invention describes a method of testing for bronchial asthma
 XX or chronic obstructive pulmonary disease. The method comprises
 XX determining the expression level of a marker gene in a biological sample
 XX from a subject, comparing the expression level determined with the
 XX expression level of the marker gene in a biological sample from a healthy
 XX subject, and judging whether the subject has bronchial asthma or chronic
 XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
 XX genes (81) whose expression levels increase when respiratory epithelial
 XX cells are stimulated with interleukin-13; or (b) a group of genes (82)
 XX whose expression levels decrease when respiratory epithelial cells are
 XX stimulated with interleukin-13. Also described: (1) a reagent (1) for
 XX testing for bronchial asthma or chronic obstructive pulmonary disease;
 XX (2) a kit for screening for a candidate compound for a therapeutic agent
 XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 XX an animal model for bronchial asthma or chronic obstructive pulmonary
 XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 XX method for producing an animal model for bronchial asthma or chronic
 XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 XX asthma or chronic obstructive pulmonary disease, comprising the compound,
 XX a marker gene or an antisense nucleic acid corresponding to a portion of
 XX the marker gene, a ribozyme, a polynucleotide that suppresses the
 XX expression of the gene through an RNA effect or an antibody recognising
 XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
 XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
 XX probe has been immobilised to assay a marker gene. (1) has respiratory
 XX and antiasthmatic activities, and can be used in gene therapy. The method
 XX is useful for testing for or screening for a therapeutic agent for
 XX bronchial asthma or chronic obstructive pulmonary disease. The present
 XX sequence is used in the exemplification of the present invention.

XX Sequence 469 AA;

Query Match 51.7%; Score 1198.5; DB 8; Length 469;
 Best Local Similarity 55.3%; Pred. No. 1,1e-110;
 Matches 246; Conservative 55; Mismatches 103; Indels 41; Gaps 5;

QY 23 GEANSCRSQPER-TEAATLTLTLKASCSMTSPHRLQA-----ARA 65
 DB 14 GKMKKLRLTSSFSRIALKKEDTTFDELCTVMSTRNCGTDSVIKHLDTIPEDKKVRV 73
 QY 66 QKPKS-----KRPRS-NSDCFQEBEDLRQGFQWRK-----SLPPGAAS 101
 DB 74 QRTOSTFPDFPEKPRANQVKRVHSENNACINFKSSAGKSPKVRHSSPSPSPKFGKAD 133
 QY 102 SYLNLEKLGEGSYATVYKGISRINGOLVALKVISMNAEBCVPTAIRBASLKLKXKANI 161
 DB 134 SYEKLEKLGEGSYATVYKGISRINGOLVALKVISMNAEBCVPTAIRBASLKLKXKANI 193
 QY 162 VLLHDIHTKETLTVEFVMTDLAQYMSOHGGLPHNVRLFMFOLRLGLAYIHQHYL 221
 DB 194 VLLHDIHTKETLTVEFVMTDLAQYMSOHGGLPHNVRLFMFOLRLGLAYIHQHYL 253
 QY 222 HRDLKQNTLLISHGELKADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSSSL 281
 DB 254 HRDLKQNTLLISHGELKADFGIARAKSIPSTYSSEVTLWYRPDALLGATEYSSSL 313
 QY 282 DIMGAGCIFIEMFQOGOPRLPGVSNILBOLEKIWEVLTGPTEDTWPGVSKLPYNPEWEP 341
 DB 314 DIMGAGCIFIEMFQOGVAAFPKMDIODLERILVLTGPTEDTWPGVSHLPFKPERFTV 373
 QY 342 PTPRSILHVVNRLGRVPEAEDLASOMLKGPBRDVSQOELVVDYSALPSQYLQYLPDEE 401
 DB 374 YSSKSLRQAWNKLSYVNHAEEDLASKLQCSFKNRLSAQALSHYFSDLPRLMELTDWS 433

QY 402 SLFTVSGVRLKPEKCDLLASYOKH 426
 DB 434 SIFTVPNVRLQPEAGESMRAFGKNN 458

RESULT 15

AA018617
 ID AAO18617 standard; protein; 330 AA.

AC AAO18617;
 XX

DT 24-OCT-2002 (first entry)

DE Human pftaire family kinase related murine protein SEQ ID NO: 8.

KW Human; pftaire family kinase; kinase; enzyme; testis; brain; cytotatic;
 uterus endometrium adenocarcinoma; lung fibroblast; splice form;

KW kidney renal cell adenocarcinoma; gene therapy; mouse.

OS Mus musculus.

PN WO200261060-A2.

PD 08-AUG-2002.

PF 17-JAN-2002; 2002WO-US001106.

PR 31-JAN-2001; 2001US-0265151P.

PR 09-MAR-2001; 2001US-00801861.

PA (PEKE) PE CORP NY.

PI Yan C, Ketchum K, Di Francesco V, Beasley EM;

DR WPI; 2002-608515/65.

XX New human kinase peptide and nucleic acid molecule, useful for treating

PT disorders associated with abnormal expression of kinase protein, e.g.

PT adenocarcinoma of uterus or lung, in drug screening assays and

XX pharmacogenomic analysis.

XX Disclosure; Page 129-130; 131pp; English.

CC The present invention provides the protein, cDNA and gene sequences of

CC two splice variants of a human pftaire family kinase. The sequences are

CC specifically expressed in the human testis, brain, uterus endometrium

CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and

CC can be used to treat related diseases. The present sequence is a murine

CC protein shown in the invention. Note: The present sequence is not

XX described further in the specification

XX Sequence 330 AA;

QY Query Match 51.5%; Score 1195; DB 5; Length 330;

DB Best Local Similarity 68.2%; Pred. No. 1.4e-110; Mismatches 60; Indels 0; Gaps 0;

QY 97 FGAAASYLLEKLEGGSVATYVKGISRINGOLVALKVISMNAEEGVPTAIRASLLKGL 156

DB 1 FGKADSYELKLEGGSVATYVKGISKVGKVALKIRIQEEGGTPTAIRASLLKGL 60

QY 157 KHANIVLADHDIIHTKETLTTFVEFYMTDLAQYMSQHPGGLHPHNVLFMFOLLRLGLAYIH 216

DB 61 KHANIVLADHDIIHTKETLTTFVEFYMTDLAQYMSQHPGGLHPHNVLFMFOLLRLGLAYIH 120

QY 217 HQHVLHRLDKPQNLISHLGEKLADFGALAKASIPQYSSSVTLWYRPPDALLGATE 276

DB 121 ORYIHLHRLDKPQNLISHLGEKLADFGALAKASIPQYSSSVTLWYRPPDALLGATE 180

QY 337 EWFPLPTFRSLHVVNNRLGRVPEADLASOMLKGFPRDRVSNQOALVHDFSAFSLQLYQ 396
 DB 241 ERFTVSSKSLRQAVNNKLSYVNHADLASKLQCSPPKRLSAQALSHYFSDLPRLME 300
 QY 397 LPDESLFTVSGVRLKPEKCDLLASYOKH 426
 DB 301 LTDMSIFTVPNVRLQPEAGESMRAFGKNN 330

Search completed: December 27, 2004, 12:16:10
 Job time : 76 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 17:48:22 ; Search time 421.082 Seconds
(without alignments)
17296.376 Million cell updates/sec

Title: US-10-786-065-4

Perfect score: 1308

Sequence: 1 acgggtcaagagcgtgctgc.....agttacgaatcgtgctgta 1308

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues 8210666

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1308	100.0	1308	9	US-09-801-861-4
2	1308	100.0	1308	14	US-10-224-562-4
3	1308	100.0	2250	18	US-10-618-941-20
4	1009	77.1	2203	9	US-09-801-861-1
5	1009	77.1	2203	14	US-10-224-562-1
6	887.6	67.9	1376	16	US-10-466-759-15
7	851.8	65.1	3210	16	US-10-425-114-26244
8	481	36.8	481	9	US-09-948-802-14
9	481	36.8	481	15	US-10-121-925-14
10	438	33.5	2467	15	US-10-153-242-3
11	437.8	33.5	1372	15	US-10-153-242-1
12	436.2	33.3	1549	15	US-10-153-242-13

13	436.2	33.3	4957	18	US-10-723-860-406	Sequence 406, App
14	436.2	33.3	5161	18	US-10-723-860-5096	Sequence 5096, App
15	299.8	22.9	3024	16	US-10-296-115-483	Sequence 483, App
16	297.8	22.8	1745	15	US-10-017-621-3	Sequence 3, App1
17	297.8	22.8	1745	15	US-10-354-358-63	Sequence 63, App1
18	297.8	22.8	1745	15	US-10-172-118-1254	Sequence 1254, App
19	297.8	22.8	1745	16	US-10-342-887-1254	Sequence 1254, App
20	297.8	22.8	2382	15	US-10-112-944-42	Sequence 42, App
21	297.8	22.8	2987	15	US-10-017-621-89	Sequence 89, App1
22	297.8	22.8	3131	18	US-10-723-860-2262	Sequence 2262, App
23	297.8	22.8	3182	15	US-10-017-621-88	Sequence 88, App1
24	297.4	22.7	2825	9	US-09-925-298-72	Sequence 72, App1
25	297.4	22.7	2825	13	US-10-102-806-72	Sequence 324, App
26	296.6	22.7	2580	13	US-10-098-861-324	Sequence 31, App1
27	296.6	22.7	2858	16	US-10-258-106-31	Sequence 31, App1
28	296.6	22.7	3094	18	US-10-851-921-7	Sequence 7, App1
29	296.6	22.7	3229	18	US-10-618-941-19	Sequence 19, App1
30	296.6	22.7	3243	13	US-10-087-192-1301	Sequence 1301, App
31	296.2	22.6	2868	15	US-10-037-270-53	Sequence 53, App1
32	296.2	22.6	2868	15	US-10-117-722-53	Sequence 53, App1
33	291.8	22.3	1125	15	US-10-325-430-5	Sequence 5, App1
34	291.8	22.3	1242	15	US-10-325-430-4	Sequence 4, App1
35	291.8	22.3	1242	16	US-10-305-720-1283	Sequence 1283, App
36	291.8	22.3	1242	18	US-10-757-262-49	Sequence 49, App1
37	290.8	22.2	2653	13	US-10-087-192-1298	Sequence 1298, App
38	285.2	21.8	3605	18	US-10-723-860-6480	Sequence 6480, App
39	269.2	20.6	1738	15	US-10-354-358-85	Sequence 85, App1
40	269.2	20.6	1738	15	US-10-160-787-4	Sequence 4, App1
41	244	18.7	2785	13	US-10-087-192-1505	Sequence 1505, App
42	231.2	17.7	667	9	US-09-764-868-183	Sequence 183, App
43	231.2	17.7	667	11	US-09-764-875-195	Sequence 395, App
44	227	17.4	1287	11	US-09-764-875-78	Sequence 78, App
45	221.4	16.9	918	9	US-09-801-368-261	Sequence 261, App

ALIGNMENTS

US-09-801-861-4	Application US/09801861
Sequence 4, App1	
Patent No. US0020119544A1	
GENERAL INFORMATION:	
APPLICANT: YAN, Chunhua et al.	
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC	
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES	
TITLE OF INVENTION: THEREOF	
FILE REFERENCE: CLO01098	
CURRENT APPLICATION NUMBER: US/09/801,861	
CURRENT FILING DATE: 2001-03-09	
NUMBER OF SEQ ID NOS: 10	
SOFTWARE: FASTSEQ for Windows Version 4.0	
SEQ ID NO: 4	
LENGTH: 1308	
TYPE: DNA	
ORGANISM: Human	
US-09-801-861-4	
Query Match	100.0%; Score 1308; DB 9; Length 1308;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1308; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGTCAAGAGCTGTGTCAGAAAGCTGTACAGCTGTGATGAGCTGTACATTTGTTCA	60
DB	1	ATGGGTCAAGAGCTGTGTCAGAAAGCTGTACAGCTGTGATGAGCTGTACATTTGTTCA	60
QY	61	GAGGAGGCGGAGGACACACAGCTGTGAGGAGATGACCTGAGACCAAGGAGGCTGCTTC	120
DB	61	GAGGAGGCGGAGGACACACAGCTGTGAGGAGATGACCTGAGACCAAGGAGGCTGCTTC	120
QY	121	AAGCTTACAGAGCTTAAAGAGCATCATGTTCCATGACTTTCATCCAGGGGACTTT	180
DB	121	AAGCTTACAGAGCTTAAAGAGCATCATGTTCCATGACTTTCATCCAGGGGACTTT	180

QY 181 CAAGTCCCCGTCGAGAGTTCAAGATTAAGGAGGAGTAACTGATGTTT 240
DB 181 CAAGTCCCCGTCGAGAGTTCAAGATTAAGGAGGAGTAACTGATGTTT 240
QY 241 CAGGAAGAGATCTGAGGAGGTTTCACTGAGGAGAGAGCTCCCTTTTGGGAGGCC 300
DB 241 CAGGAAGAGATCTGAGGAGGTTTCACTGAGGAGAGAGCTCCCTTTTGGGAGGCC 300
QY 301 TCATCTTACTTGAACCTTGAGAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAAGGG 360
DB 301 TCATCTTACTTGAACCTTGAGAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAAGGG 360
QY 361 ATTAGAGAAATAATGAGCAACTAGTGGCTTTAAAGTATCGATCGATGATGAGAGAA 420
DB 361 ATTAGAGAAATAATGAGCAACTAGTGGCTTTAAAGTATCGATGATGAGAGAA 420
QY 421 GGAGTCCATTTACAGCTATCCGAGAGAGCTTCTCTGAGAGGTTTGAACATGCAAT 480
DB 421 GGAGTCCATTTACAGCTATCCGAGAGAGCTTCTCTGAGAGGTTTGAACATGCAAT 480
QY 481 ATTGTCCTCTGATGATGATATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTGTCCTCTGATGATGATATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 ATGACACAG 600
DB 541 ATGACACAG 600
QY 601 GTGAGACTTTTCACTGTTCACTTTGCGGGGCTGGGAGTCACTCCACCAAGAGAGT 660
DB 601 GTGAGACTTTTCACTGTTCACTTTGCGGGGCTGGGAGTCACTCCACCAAGAGAGT 660
QY 661 CTTCACAGGAG 720
DB 661 CTTCACAGGAG 720
QY 721 GCGATTTTGTCTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 GCGATTTTGTCTTGGCCGGGAG 780
QY 781 GTGAGCCCTGTGATCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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QY 841 CTGAGATATGGGGTGAAG 900
DB 841 CTGAGATATGGGGTGAAG 900
QY 901 CCGGGGTTTCCAACTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CCGGGGTTTCCAACTCTTGAAG 960
QY 961 ACAGAGAGATCTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 ACAGAGAGATCTTGGCCGGGAG 1020
QY 1021 CTGCTTACCTTGAAG 1080
DB 1021 CTGCTTACCTTGAAG 1080
QY 1081 GAG 1140
DB 1081 GAG 1140
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QY 1261 TCCTACAG 1308
DB 1261 TCCTACAG 1308

RESULT 2
US-10-224-562-4
; Sequence 4, Application US/10224562
; Publication No. US20030022229A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-10-224-562-4

Query Match 100.0%; Score 1308; DB 14; Length 1308;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTCAAGAGCTGTGTCAG 60
DB 1 ATGGGTCAAGAGCTGTGTCAG 60
QY 61 GAGGAGGAG 120
DB 61 GAGGAGGAG 120
QY 121 AAGCTTAACAGAGCTTAAAG 180
DB 121 AAGCTTAACAGAGCTTAAAG 180
QY 181 CAAGTCCCCGTCGAG 240
DB 181 CAAGTCCCCGTCGAG 240
QY 241 CAGGAAGAGATCTGAGGAGGTTTCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CAGGAAGAGATCTGAGGAGGTTTCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TCATCTTACTTGAACCTTGAGAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAAGGG 360
DB 301 TCATCTTACTTGAACCTTGAGAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAAGGG 360
QY 361 ATTAGAGAAATAATGAGCAACTAGTGGCTTTAAAGTATCGATCGATGATGAGAGAA 420
DB 361 ATTAGAGAAATAATGAGCAACTAGTGGCTTTAAAGTATCGATCGATGATGAGAGAA 420
QY 421 GGAGTCCATTTACAGCTATCCGAGAGAGCTTCTCTGAGAGGTTTGAACATGCAAT 480
DB 421 GGAGTCCATTTACAGCTATCCGAGAGAGCTTCTCTGAGAGGTTTGAACATGCAAT 480
QY 481 ATTGTCCTCTGATGATGATATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTGTCCTCTGATGATGATATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 ATGACACAG 600
DB 541 ATGACACAG 600
QY 601 GTGAGACTTTTCACTGTTCACTTTGCGGGGCTGGGAGTCACTCCACCAAGAGAGT 660
DB 601 GTGAGACTTTTCACTGTTCACTTTGCGGGGCTGGGAGTCACTCCACCAAGAGAGT 660

QY 661 CTTCAAGGAGCTGTAAGACCTGAGAACTTACTCATGTCACCTGGAGAGGCTCAAACTG 720
DB 661 CTTCAAGGAGCTGTAAGACCTGAGAACTTACTCATGTCACCTGGAGAGGCTCAAACTG 720
QY 721 GCTGATTTTGGTCTTGCCCGGGGCAAGTCATTTCCAGCAGACATATCTTTCAGAAATC 780
DB 721 GCTGATTTTGGTCTTGCCCGGGGCAAGTCATTTCCAGCAGACATATCTTTCAGAAATC 780
QY 781 GTGACCCCTCTGTGATCCGCGCCCTGTATGCTTTGCTGGAGCCATGTAAATTTCTGTAG 840
DB 781 GTGACCCCTCTGTGATCCGCGCCCTGTATGCTTTGCTGGAGCCATGTAAATTTCTGTAG 840
QY 841 CTGACATATGGGGGTGAGAGCTGACCTTATTTGAAATGTCAGAGGCTCAACCTTTGTTT 900
DB 841 CTGACATATGGGGGTGAGAGCTGACCTTATTTGAAATGTCAGAGGCTCAACCTTTGTTT 900
QY 901 CCTGGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCT 960
DB 901 CCTGGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCT 960
QY 961 ACAGAGATATCTTGGCCGGGAGTCTTCAGAGCTAACCTAACATCAGAAATGTTCCCA 1020
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QY 1081 GAAGACTGGCTTCCAGATGCTAAAGGCTTTCAGAGAGCCGCTCTCCGCCAGAA 1140
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QY 1141 GCATTTGTTCAATGATTTATTCAGCGCCCTGTCATCTCAGCTGTACCAAGTTCTGTAG 1200
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QY 1261 TCTTACAGAAAGGTCACCAAGCCAGCTTATGCAATGCTGTGGA 1308
DB 1261 TCTTACAGAAAGGTCACCAAGCCAGCTTATGCAATGCTGTGGA 1308

RESULT 3
US-10-618-941-20
; Sequence 20, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 2250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-20

Query Match 100.0%; Score 1308; DB 18; Length 2250;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGTCAAGAGCTGTGTGCAAAAGACTGTACAGCTGTAGTGCAGCTTACCATTTGTCA 60

DB 45 ATGGGTCAAGAGCTGTGTGCAAAAGACTGTACAGCTGTAGTGCAGCTTACCATTTGTCA 104
QY 61 GAGGAGGCGAGGCAACAGCTGTGTGAGAGATCAGCTGTAGAACCAACGAGGCTGTGCTC 120
DB 105 GAGGAGGCGAGGCAACAGCTGTGTGAGAGATCAGCTGTAGAACCAACGAGGCTGTGCTC 164
QY 121 AAGCTAACAGACCTTAAAGAAACATCATGTTCCATGACTTTCATTTCAACCCAGGGAATT 180
DB 165 AAGCTAACAGACCTTAAAGAAACATCATGTTCCATGACTTTCATTTCAACCCAGGGAATT 224
QY 181 CAGCTGCCGCGTCCAGAAAGTTCAGAGTAAAGGCAACGAGTAAAGATTTGTTT 240
DB 225 CAGCTGCCGCGTCCAGAAAGTTCAGAGTAAAGGCAACGAGTAAAGATTTGTTT 284
QY 241 CAGGAAAGAGATCTGAGGCAAGGTTTTCAGTGAAGAAAGGCTCCCTTTTGGGCAAGC 300
DB 285 CAGGAAAGAGATCTGAGGCAAGGTTTTCAGTGAAGAAAGGCTCCCTTTTGGGCAAGC 344
QY 301 TCATCTTACTTGAACCTGGAGAAAGCTGGGTGAAGGCTCTTATGCGACAGTTTACAGGGG 360
DB 345 TCATCTTACTTGAACCTGGAGAAAGCTGGGTGAAGGCTCTTATGCGACAGTTTACAGGGG 404
QY 361 ATTACAGAAATTAATGGAACAATACTAGCTTTTAAAGTCAATCAGATGATGAGAGAA 420
DB 405 ATTACAGAAATTAATGGAACAATACTAGCTTTTAAAGTCAATCAGATGATGAGAGAA 464
QY 421 GAGTCCCATTTACAGCTATCCGAGAGCTTCTCTGAAAGGTTTGAACATGCAAT 480
DB 465 GAGTCCCATTTACAGCTATCCGAGAGCTTCTCTGAAAGGTTTGAACATGCAAT 524
QY 481 ATTGCTCTCCGACAGACATTAATCCACCAAGAGACATGACATTCGTTTGAATAC 540
DB 525 ATTGCTCTCCGACAGACATTAATCCACCAAGAGACATGACATTCGTTTGAATAC 584
QY 541 ATGCAACAGACCTGCGCCAGATATATGCTCAGATTCAGAGAGGCTTATCTATAT 600
DB 585 ATGCAACAGACCTGCGCCAGATATATGCTCAGATTCAGAGAGGCTTATCTATAT 644
QY 601 GTCAAGCTTTGATGTTTCAATTTTGGGGGCTGTGGGTATATCAACCAACACGTT 660
DB 645 GTCAAGCTTTGATGTTTCAATTTTGGGGGCTGTGGGTATATCAACCAACACGTT 704
QY 661 CTTCAAGGAGCTGTAAGACCTGAGAACTTACTCATGTCACCTGGAGAGGCTCAAACTG 720
DB 705 CTTCAAGGAGCTGTAAGACCTGAGAACTTACTCATGTCACCTGGAGAGGCTCAAACTG 764
QY 721 GCTGATTTTGGTCTTGCCCGGGGCAAGTCATTTCCAGCAGACATATCTTTCAGAAATC 780
DB 765 GCTGATTTTGGTCTTGCCCGGGGCAAGTCATTTCCAGCAGACATATCTTTCAGAAATC 824
QY 781 GTGACCCCTCTGTGATCCGCGCCCTGTATGCTTTGCTGGAGCCATGTAAATTTCTGTAG 840
DB 825 GTGACCCCTCTGTGATCCGCGCCCTGTATGCTTTGCTGGAGCCATGTAAATTTCTGTAG 884
QY 841 CTGACATATGGGGGTGAGAGCTGACCTTATTTGAAATGTCAGAGGCTCAACCTTTGTTT 900
DB 885 CTGACATATGGGGGTGAGAGCTGACCTTATTTGAAATGTCAGAGGCTCAACCTTTGTTT 944
QY 901 CCTGGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCT 960
DB 945 CCTGGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCT 1004
QY 961 ACAGAGATATCTTGGCCGGGAGTCTTCAGAGCTAACCTAACATCAGAAATGTTCCCA 1020
DB 1005 ACAGAGATATCTTGGCCGGGAGTCTTCAGAGCTAACCTAACATCAGAAATGTTCCCA 1064
QY 1021 CTGCTTAAGCTTGAAGCTTATGTTCTGGAACAGGCTGGGAGGTTCTGAAAGT 1080
DB 1065 CTGCTTAAGCTTGAAGCTTATGTTCTGGAACAGGCTGGGAGGTTCTGAAAGT 1124
QY 1081 GAAGACTGGCTTCCAGATGCTAAAGGCTTTTCCAGAGACCGGCTCTCCGCCAGAA 1140
DB 1125 GAAGACTGGCTTCCAGATGCTAAAGGCTTTTCCAGAGACCGGCTCTCCGCCAGAA 1184

QY 1141 GCACTGTTTCATGATATTATTTGAGCCCTGCGCATCTGAGTGAACAAGCTTCTCTATGAG 1200
DB 1185 GCACTGTTTCATGATATTATTTGAGCCCTGCGCATCTGAGTGAACAAGCTTCTCTATGAG 1244
QY 1201 GAGCTCTTTGTTTACAGTTTCAGAGTGAAGCTAAAGCCAGAAATGTGTGACTTTTGAGCC 1260
DB 1245 GAGCTCTTTGTTTACAGTTTCAGAGTGAAGCTAAAGCCAGAAATGTGTGACTTTTGAGCC 1304
QY 1261 TCCCTACAGAAAGGTGACCAACCCAGCCAGTTTAAAGATGCTGTGA 1308
DB 1305 TCCCTACAGAAAGGTGACCAACCCAGCCAGTTTAAAGATGCTGTGA 1352

RESULT 4
US-09-801-861-1
; Sequence 1, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01098
; CURRENT APPLICATION NUMBER: US/09/801,861
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2203
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-1

Query Match 77.1%; Score 1009; DB 9; Length 2203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1009; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTCAGAGCTGTGTGCAAGAGCTGTAACAGCTTGATGACGCTGCTAACCATTGTTCA 60
DB 118 ATGGGTCAGAGCTGTGTGCAAGAGCTGTAACAGCTTGATGACGCTGCTAACCATTGTTCA 177
QY 61 GAGGAGGCGAGGCAACAGCTGTCGAGAGAGTCAAGCTGAGACACGAGAGCTGAGTTC 120
DB 178 GAGGAGGCGAGGCAACAGCTGTCGAGAGAGTCAAGCTGAGACACGAGAGCTGAGTTC 237
QY 121 AAGCTAACAGACCTTAAAGAGCATGTTCCATGACTTCAATTTCAACCCAGAGGACTT 180
DB 238 AAGCTAACAGACCTTAAAGAGCATGTTCCATGACTTCAATTTCAACCCAGAGGACTT 297
QY 181 CAAGCTGCCCCGTCGCAAGAGTTCAGAGTGAAGAGCCACGAGTAAACAGTATTTGTTT 240
DB 298 CAAGCTGCCCCGTCGCAAGAGTTCAGAGTGAAGAGCCACGAGTAAACAGTATTTGTTT 357
QY 241 CAGGAGAGGATGAGGAGGTTTTCAGTGAAGAGAGCTCCCTTTTGGGAGAGCC 300
DB 358 CAGGAGAGGATGAGGAGGTTTTCAGTGAAGAGAGCTCCCTTTTGGGAGAGCC 417
QY 301 TCATCTTACTTGAAGCTGGAAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAGAGGG 360
DB 418 TCATCTTACTTGAAGCTGGAAGAGCTGGGTGAAGGCTTTATGCAACAGTTTCAAGAGGG 477
QY 361 ATTAGAGAAATTAATGAGCAACATGAGCTTTAAAGTCAATGAGTGAATGAGAGAA 420
DB 478 ATTAGAGAAATTAATGAGCAACATGAGCTTTAAAGTCAATGAGTGAATGAGAGAA 537
QY 421 GAGATCCCATTTTACAGCTATCCGAAAGCTTCTCTGTAAGGGTTTGAACAATGCAAT 480
DB 538 GAGATCCCATTTTACAGCTATCCGAAAGCTTCTCTGTAAGGGTTTGAACAATGCAAT 597
QY 481 ATTGCTCTCTGATGACATTAATCAACCAAGAGAGACATGACTTGTGTTTGAATAC 540
DB 598 ATTGCTCTCTGATGACATTAATCAACCAAGAGAGACATGACTTGTGTTTGAATAC 657

QY 541 ATGCACACAGACCTGGGCCAGATATATGTTCAGCATCCAGAGAGGCTTATCTCTATANT 600
DB 658 ATGCACACAGACCTGGGCCAGATATATGTTCAGCATCCAGAGAGGCTTATCTCTATANT 717
QY 601 GTACAGCTTTATGATTTTCAATTTTGGGGGCTGGAGCTAATCATCACCAGCAACAGTT 660
DB 718 GTACAGCTTTATGATTTTCAATTTTGGGGGCTGGAGCTAATCATCACCAGCAACAGTT 777
QY 661 CTTCACAGGAGCTGAAACCTTCAGAACTTATCATCATGCTACCTGGAGAGCTCAAACTG 720
DB 778 CTTCACAGGAGCTGAAACCTTCAGAACTTATCATCATGCTACCTGGAGAGCTCAAACTG 837
QY 721 GCTGATTTTGGTCTTGCCCGGGGCAAGTCCATTTCCAGCAGACATCTTCAAGAGTC 780
DB 838 GCTGATTTTGGTCTTGCCCGGGGCAAGTCCATTTCCAGCAGACATCTTCAAGAGTC 897
QY 781 GTGACCCCTGGTACCGGCCCCCTGATGCTTGTGAGAGCAGCATGATATTTCTGTAG 840
DB 898 GTGACCCCTGGTACCGGCCCCCTGATGCTTGTGAGAGCAGCATGATATTTCTGTAG 957
QY 841 CTGACATATGAGGAGTGCAGAGCTGCATCTTATTTAAATGTTCCAGGCTCAACCTTTGTT 900
DB 958 CTGACATATGAGGAGTGCAGAGCTGCATCTTATTTAAATGTTCCAGGCTCAACCTTTGTT 1017
QY 901 CTTGGGCTTTCCAAACATCTTTGAACAGCTGAGAAATTTGGAGAGTGTGGAGTCCCT 960
DB 1018 CTTGGGCTTTCCAAACATCTTTGAACAGCTGAGAAATTTGGAGAGTGTGGAGTCCCT 1077
QY 961 ACAGAGATATCTTGGCCGGAGTCTCAAGCTACCTAATCAATTCAG 1009
DB 1078 ACAGAGATATCTTGGCCGGAGTCTCAAGCTACCTAATCAATTCAG 1126

RESULT 5
US-10-224-562-1
; Sequence 1, Application US/10224562
; Publication No. US20030022229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-562-1

Query Match 77.1%; Score 1009; DB 14; Length 2203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1009; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTCAGAGCTGTGTGCAAGAGCTGTAACAGCTTGATGACGCTGCTAACCATTGTTCA 60
DB 118 ATGGGTCAGAGCTGTGTGCAAGAGCTGTAACAGCTTGATGACGCTGCTAACCATTGTTCA 177
QY 61 GAGGAGGCGAGGCAACAGCTGTCGAGAGAGTCAAGCTGAGACACGAGAGCTGAGTTC 120
DB 178 GAGGAGGCGAGGCAACAGCTGTCGAGAGAGTCAAGCTGAGACACGAGAGCTGAGTTC 237
QY 121 AAGCTAACAGACCTTAAAGAGCATGTTCCATGACTTCAATTTCAACCCAGAGGACTT 180
DB 238 AAGCTAACAGACCTTAAAGAGCATGTTCCATGACTTCAATTTCAACCCAGAGGACTT 297
QY 181 CAAGCTGCCCCGTCGCAAGAGTTCAGAGTGAAGAGCCACGAGTAAACAGTATTTGTTT 240
DB 298 CAAGCTGCCCCGTCGCAAGAGTTCAGAGTGAAGAGCCACGAGTAAACAGTATTTGTTT 357

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QY 241 CAGGAAGAGATCTGAGGCGGTTTCACTGAGAGAAAGCCTCCCTTTGGGGGAGCC 300
DB 358 CAGGAAGAGATCTGAGGCGGTTTCACTGAGAGAAAGCCTCCCTTTGGGGGAGCC 417
QY 301 TCATCTTACTTGAACCTGGAGAGCTGGGGAAGGCTTTAATGCGACAGTTTCAAGGGG 360
DB 418 TCATCTTACTTGAACCTGGAGAGCTGGGGAAGGCTTTAATGCGACAGTTTCAAGGGG 477
QY 361 ATTAGCAGAAATAATGAGCAACTAGTGGCTTTAAAAGTCATGAGATGATGAGAGAA 420
DB 478 ATTAGCAGAAATAATGAGCAACTAGTGGCTTTAAAAGTCATGAGATGATGAGAGAA 537
QY 421 GAGATCCCTTTACAGCTATCCGAGAAAGCTTCTCTGAGAGGTTTGAACATGCCAAT 480
DB 538 GAGATCCCTTTACAGCTATCCGAGAAAGCTTCTCTGAGAGGTTTGAACATGCCAAT 597
QY 481 ATTGCTCTCTGAGATGAGCACTAATCCAGCAAGAGAGACATGACATTCGTTTGAATAC 540
DB 598 ATTGCTCTCTGAGATGAGCACTAATCCAGCAAGAGAGACATGACATTCGTTTGAATAC 657
QY 541 ATGACACAGAGACTGGCCCGAGATATATGCTCAGCATCCAGAGGGCTTGCATCTCAAT 600
DB 658 ATGACACAGAGACTGGCCCGAGATATATGCTCAGCATCCAGAGGGCTTGCATCTCAAT 717
QY 601 GTGACACTTTTCACTGTTTCACTTTGGCGGGGCTGGCGTACATCCACCAACACGTT 660
DB 718 GTGACACTTTTCACTGTTTCACTTTGGCGGGGCTGGCGTACATCCACCAACACGTT 777
QY 661 CTTACAGGAGACTGAAACCTCAGAACTTACTCATGATCAGCTGGGAGAGCTCAAACTG 720
DB 778 CTTACAGGAGACTGAAACCTCAGAACTTACTCATGATCAGCTGGGAGAGCTCAAACTG 837
QY 721 GCTGATTTTGTCTTGGCCCGGCGCAAGTCATTTCCAGCAGACATATCTTCAGAAATC 780
DB 838 GCTGATTTTGTCTTGGCCCGGCGCAAGTCATTTCCAGCAGACATATCTTCAGAAATC 897
QY 781 GTGACCTCTTGTGATCCGCGCCCTGATGCTTTGCTGGAGCCCACTGAAATATCTCTGAG 840
DB 898 GTGACCTCTTGTGATCCGCGCCCTGATGCTTTGCTGGAGCCCACTGAAATATCTCTGAG 957
QY 841 CTGACATATGGGGTGCAGAGCTGCATCTTATTTGAATGTTCCAGGGTCAACCTTGTGTT 900
DB 958 CTGACATATGGGGTGCAGAGCTGCATCTTATTTGAATGTTCCAGGGTCAACCTTGTGTT 1017
QY 901 CTTGGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGAGGCTGCTGGAGTCCCT 960
DB 1018 CTTGGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGAGGCTGCTGGAGTCCCT 1077
QY 961 ACAGAGATATCTTGGCCGGGAGTCTTCAAGCTTACTTAACTTCAATCCAG 1009
DB 1078 ACAGAGATATCTTGGCCGGGAGTCTTCAAGCTTACTTAACTTCAATCCAG 1126
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RESULT 6
US-10-466-759-15
Sequence 15, Application US/10466759
Publication No. US20040081983A1

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION
APPLICANT: LEE, Ernestine A.
APPLICANT: CHAMLA, Narinder K.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: ISON, Craig H.
APPLICANT: GURUBAJAN, Rajagopal
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, Monique G.
APPLICANT: JACKSON, Jennifer L.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: TRAN, Bao
APPLICANT: DING, Li
APPLICANT: LU, Dying Aina M.

```
APPLICANT: LAL, Preeti G.  
APPLICANT: WARREN, Bridget A.  
FILE OF INVENTION: KINASES AND PHOSPHATASES  
FILE REFERENCE: PI-0344 USN  
CURRENT APPLICATION NUMBER: US/10/466,759  
PRIOR FILING DATE: 2003-07-17  
PRIOR APPLICATION NUMBER: PCT/US02/01369  
PRIOR FILING DATE: 2002-01-16  
PRIOR APPLICATION NUMBER: US 60/263,083  
PRIOR FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/271,205  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: US 60/271,117  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: US 60/276,859  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: US 60/278,504  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: US 60/278,522  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: US 60/280,510  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: US 60/280,266  
PRIOR FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PERL Program  
SEQ ID NO 15  
LENGTH: 1376  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: 7494145CB1  
US-10-466-759-15  
Query Match 67.9%; Score 887.6; DB 16; Length 1376;  
Best Local Similarity 99.6%; Pred. No. 7.2e-288;  
Matches 890; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 122 ACCTAAGAGAGCTTAAAGAGATATGTTCCATGATCTTCAATTTCAACCCAGGGGACTTC 181  
DB 266 ACTTAAGAGAGCTTAAAGAGATATGTTCCATGATCTTCAATTTCAACCCAGGGGACTTC 325  
QY 182 AAGCTGCCCTGCCAGAAAGTTCAAGAGTAAAGGCGACGAGATACAGTATGTTTTC 241  
DB 326 AAGCTGCCCTGCCAGAAAGTTCAAGAGTAAAGGCGACGAGATACAGTATGTTTTC 385  
QY 242 AGGAAGAGATCTGAGGCGGCTTTTCACTGAGAGAGAGGCTCCCTTTGGGGGAGCCCT 301  
DB 386 AGGAAGAGATCTGAGGCGGCTTTTCACTGAGAGAGAGGCTCCCTTTGGGGGAGCCCT 445  
QY 302 CATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGGGGA 361  
DB 446 CATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGGGGA 505  
QY 362 TTAGCAGAAATAATGAGCAACTAGTGGCTTTAAAAGTCATGAGATGAGAGGAAG 421  
DB 506 TTAGCAGAAATAATGAGCAACTAGTGGCTTTAAAAGTCATGAGATGAGAGGAAG 565  
QY 422 GAGTCCCATTTACAGCTATCCGAGAAAGCTTCTCTGAGAGGTTTGAACAATGCCAATA 481  
DB 566 GAGTCCCATTTACAGCTATCCGAGAAAGCTTCTCTGAGAGGTTTGAACAATGCCAATA 625  
QY 482 TTGTGCTCTGATGAGATATTCACACCAAGAGACATGATTCGTTTGAATACA 541  
DB 626 TTGTGCTCTGATGAGATATTCACACCAAGAGACATGATTCGTTTGAATACA 685  
QY 542 TGCACACAGAGCTGGCCCGAGATATATGCTCAGCATCCAGAGGGCTTCAATCTCATATG 601  
DB 686 TGCACACAGAGCTGGCCCGAGATATATGCTCAGCATCCAGAGGGCTTCAATCTCATATG 745  
QY 602 TCAGACTTTTCACTGTTTCACTTTGGCGGGGCTGGCGTACATCCACCAACACGTTTC 661
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Db 746 TCAGACTTTTCATGTTTCAACTTTTGGGGGCGCTGGCTACATCCACCAACCAAGCTTC 805
Qy 662 TTCACAGGAGCTGAAAACCTCAGAACTTACTCATCATGTCACCTGGAGAGCTCAAACTGG 721
Db 806 TTCACAGGAGCTGAAAACCTCAGAACTTACTCATCATGTCACCTGGAGAGCTCAAACTGG 865
Qy 722 CTGATTTTGGTCTTGGCCCCGGGCGAAGTCCATTCCACGCGCAAGATCTCTTCAGAAAGTCG 781
Db 866 CTGATTTTGGTCTTGGCCCCGGGCGAAGTCCATTCCACGCGCAAGATCTCTTCAGAAAGTCG 925
Qy 782 TGACCTCTGTATCGGCGCCCTGATGCTTTGCTGGAGGACCTGAATATTTCCTGAGC 841
Db 926 TGACCTCTGTATCGGCGCCCTGATGCTTTGCTGGAGGACCTGAATATTTCCTGAGC 985
Qy 842 TGACATATGAGGCTGACGCTGCATCTTTATTTGAAATGTTTCAAGGCTCAACCTTTGTTTC 901
Db 986 TGACATATGAGGCTGACGCTGCATCTTTATTTGAAATGTTTCAAGGCTCAACCTTTGTTTC 1045
Qy 902 CTGGGGGTTTCCAACTCTCTTGAACAGCTGGAGAAATCTGGAGAGTGTGGGAGTCCCTA 961
Db 1046 CTGGGGGTTTCCAACTCTCTTGAACAGCTGGAGAAATCTGGAGAGTGTGGGAGTCCCTA 1105
Qy 962 CAGAGGATATCTTGGCGGAGTCTCCAGCTACTACTAATCAATCCAGATGCT 1015
Db 1106 CAGAGGATATCTTGGCGGAGTCTCCAGCTACTACTAATCAATCCAGAGAGT 1159

RESULT 7
US-10-425-114-26244
; Sequence 26244, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26244
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-079-cl_FLI
US-10-425-114-26244

Query Match 65.1%; Score 851.8; DB 16; Length 3210;
Best Local Similarity 99.7%; Pred. No. 1.4e-275;
Matches 864; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 443 GAGAACTCTCTCCCTGGAAGGTTGAACATGCCAATTTGTCTCCCTGCATGACATTA 502
Db 59 GATTAAGCTTCTCTCCCTGGAAGGTTGAACATGCCAATTTGTCTCCCTGCATGACATTA 118
Qy 503 TCCACACCAAGAGACACTGACATTTGTTTGAATATACGACACAGACCTGGGCCAGT 562
Db 119 TCCACACCAAGAGAGACACTGACATTTGTTTGAATATACGACACAGACCTGGGCCAGT 178
Qy 563 ATATGCTCAGATCCAGAGAGGCTTCATCTCATATATGTCAGACTTTTCATGTTTCAAC 622
Db 179 ATATGCTCAGATCCAGAGAGGCTTCATCTCATATATGTCAGACTTTTCATGTTTCAAC 238
Qy 623 TTTTGGGGGCTCGGGTACATCCACCAACACAGCTTTCTTCACAGGAGCTGAAACCTTC 682
Db 239 TTTTGGGGGCTCGGGTACATCCACCAACACAGCTTTCTTCACAGGAGCTGAAACCTTC 298
Qy 683 AGAACTTACTCATGTCACCTGGAGAGCTCAAACTGCTGATTTTGGTCTTGGCCGGG 742
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Db 299 AGAACTTACTCATGTCACCTGGAGAGCTCAAACTGCTGATTTTGGTCTTGGCCGGG 358
Qy 743 CCAGTCCATTTCCAGCCAGACATATCTTTGAGAAAGTGTCAGCCCTGCTGACCGGCC 802
Db 359 CCAGTCCATTTCCAGCCAGACATATCTTTGAGAAAGTGTCAGCCCTGCTGACCGGCC 418
Qy 803 CTGATGCTTTGCTGGAGGCACTGAATATTCCTGAGCTGACATATGAGGCTGACAGCT 862
Db 419 CTGATGCTTTGCTGGAGGCACTGAATATTCCTGAGCTGACATATGAGGCTGACAGCT 478
Qy 863 GCATCTTTATGAAATGTTTCCAGGCTCAACCTTTGTTTCTGGGTTTCCAACTTCCTG 922
Db 479 GCATCTTTATGAAATGTTTCCAGGCTCAACCTTTGTTTCTGGGTTTCCAACTTCCTG 538
Qy 923 AACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCTACAGAGATATTTGGCCGGAG 982
Db 539 AACAGCTGAGAAATCTGGAGAGTGTGGAGTCCCTACAGAGATATTTGGCCGGAG 598
Qy 983 TCTCCAGCTACTTAATCAATCCAGAAATGCTTCCACTGCTACGCTCGAAGCTTTC 1042
Db 599 TCTCCAGCTACTTAATCAATCCAGAAATGCTTCCACTGCTACGCTCGAAGCTTTC 658
Qy 1043 ATGTTGCTGGAACAGGCTGGGCGAGGTTCTGAGCTGGAAGACCTGGCTCCAGATGC 1102
Db 659 ATGTTGCTGGAACAGGCTGGGCGAGGTTCTGGAAGCTGGAAGACCTGGCTCCAGATGC 718
Qy 1103 TAAAGGCTTTTCCAGAGCCGCTCTCCGCCAGAGACATTTGTCATGATTTTCA 1162
Db 719 TAAAGGCTTTTCCAGAGCCGCTCTCCGCCAGAGACATTTGTCATGATTTTCA 778
Qy 1163 GCGCCCTGCTCATCTGAGCTGTACAGCTTCTGATGAGAGTCTTTGTTTACAGTTTCA 1222
Db 779 GCGCCCTGCTCATCTGAGCTGTACAGCTTCTGATGAGAGTCTTTGTTTACAGTTTCA 838
Qy 1223 GAGTAGAGCTAAAGCAG-AAATGTTGACCTTTGGCTCTTACAGAAAGGTACACAC 1281
Db 839 GAGTAGAGCTAAAGCAGAAATGTTGACCTTTGGCTCTTACAGAAAGGTACACAC 898
Qy 1282 CCAGCCAGTTTATGCAAAATGCTGTGA 1308
Db 899 CCAGCCAGTTTATGCAAAATGCTGTGA 925

RESULT 8
US-09-948-802-14
; Sequence 14, Application US/09948802
; Publication No. US20020172981A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MN1-090
; CURRENT APPLICATION NUMBER: US/09/948, 802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387, 212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-802-14

Query Match 36.8%; Score 481; DB 9; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.1e-151;
Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 720 GGCTGATTTGCTTGTGCGCGGCGCAAGTCCATTTCCAGCCAGACATATCTTGAAGT 779
Db 1 GGCTGATTTGCTTGTGCGCGGCGCAAGTCCATTTCCAGCCAGACATATCTTGAAGT 60
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QY 780 CGTGAACCTCTGTAACCGGCCCCCTGATGCTTGTGGAAGCACTGAATATTCCTCTGA 839
DB 61 CGTGACCTCTGTGACCGGCCCCCTGATGCTTGTGGAAGCACTGAATATTCCTCTGA 120
QY 840 GCTGACATATGAGGCTGACGAGCTGATCTTTATGAAATGTTCCAGGGTCAACCTTTGTT 899
DB 121 GCTGACATATGAGGCTGACGAGCTGATCTTTATGAAATGTTCCAGGGTCAACCTTTGTT 180
QY 900 TCTGTGGGTTTCCAACTCTTGAACAGCTGGAAGAAATCTGGAGGTTCTGGAGTCCC 959
DB 181 TCTGTGGGTTTCCAACTCTTGAACAGCTGGAAGAAATCTGGAGGTTCTGGAGTCCC 240
QY 960 TACAGAGATTAATGAGGCTGAGGAGTCTCCAGAGTAATACTAATCCAGAAATGTTTCCC 1019
DB 241 TACAGAGATTAATGAGGCTGAGGAGTCTCCAGAGTAATACTAATCCAGAAATGTTTCCC 300
QY 1020 ACTGCTACGCTCGAAGGCTTCAATGTTGTCTGAAACAGGCTGGGAGGTTCTGTAAC 1079
DB 301 ACTGCTACGCTCGAAGGCTTCAATGTTGTCTGAAACAGGCTGGGAGGTTCTGTAAC 360
QY 1080 TGAAGACCTGAGCTCCAGAGTCTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGGA 1139
DB 361 TGAAGACCTGAGCTCCAGAGTCTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGGA 420
QY 1140 AGCACTTGTTCATGATTAATTTAGAGGCTCTGCAATCTGAGTGTACAGCTTCTGATGA 1199
DB 421 AGCACTTGTTCATGATTAATTTAGAGGCTCTGCAATCTGAGTGTACAGCTTCTGATGA 480
QY 1200 G 1200
DB 481 G 481

RESULT 9
US-10-121-925-14

Sequence 14, Application US/10121925
Publication No. US20030104505A1
GENERAL INFORMATION:
APPLICANT: ROBINSON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
FILE REFERENCE: MNT-090
CURRENT APPLICATION NUMBER: US/10/121,925
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/09/948,802
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 481
TYPE: DNA
ORGANISM: Homo sapiens
US-10-121-925-14

Query Match 36.8%; Score 481; DB 15; Length 481;
Best Local Similarity 100.0%; Pred. No. 6,1e-151;

Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 GGCTGATTTTGTCTTTCCTCCGAGCCAAATTCATTCACAGCCAGACATCTTTCAGAGT 779
DB 1 GGCTGATTTTGTCTTTCCTCCGAGCCAAATTCATTCACAGCCAGACATCTTTCAGAGT 60
QY 780 CGTGAACCTCTGTGACCGGCCCCCTGATGCTTGTGGAAGCACTGAATATTCCTCTGA 839
DB 61 CGTGACCTCTGTGACCGGCCCCCTGATGCTTGTGGAAGCACTGAATATTCCTCTGA 120
QY 840 GCTGACATATGAGGCTGACGAGCTGATCTTTATGAAATGTTCCAGGGTCAACCTTTGTT 899
DB 121 GCTGACATATGAGGCTGACGAGCTGATCTTTATGAAATGTTCCAGGGTCAACCTTTGTT 180
QY 900 TCTGTGGGTTTCCAACTCTTGAACAGCTGGAAGAAATCTGGAGGTTCTGGAGTCCC 959

DB 181 TCTGTGGGTTTCCAACTCTTGAACAGCTGGAAGAAATCTGGAGGTTCTGGAGTCCC 240
QY 960 TACAGAGATTAATGAGGCTGAGGAGTCTCCAGAGTAATACTAATCCAGAAATGTTTCCC 1019
DB 241 TACAGAGATTAATGAGGCTGAGGAGTCTCCAGAGTAATACTAATCCAGAAATGTTTCCC 300
QY 1020 ACTGCTACGCTCGAAGGCTTCAATGTTGTCTGAAACAGGCTGGGAGGTTCTGTAAC 1079
DB 301 ACTGCTACGCTCGAAGGCTTCAATGTTGTCTGAAACAGGCTGGGAGGTTCTGTAAC 360
QY 1080 TGAAGACCTGAGCTCCAGAGTCTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGGA 1139
DB 361 TGAAGACCTGAGCTCCAGAGTCTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGGA 420
QY 1140 AGCACTTGTTCATGATTAATTTAGAGGCTCTGCAATCTGAGTGTACAGCTTCTGATGA 1199
DB 421 AGCACTTGTTCATGATTAATTTAGAGGCTCTGCAATCTGAGTGTACAGCTTCTGATGA 480
QY 1200 G 1200
DB 481 G 481

RESULT 10
US-10-153-242-3

Sequence 3, Application US/10153242
Publication No. US20030166217A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Pot, David
APPLICANT: Kassam, Alcafe
APPLICANT: Marenbach, Taisha
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPFTAIR)
FILE REFERENCE: PP-01429, 103/200130, 445D1
CURRENT APPLICATION NUMBER: US/10/153,242
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2467
TYPE: DNA
ORGANISM: mouse
US-10-153-242-3

Query Match 33.5%; Score 438; DB 15; Length 2467;
Best Local Similarity 65.8%; Pred. No. 4,9e-136;

Matches 636; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 277 AAGAGCTCTCTTTTGGGAGCCTCATCTTAATTTGAATTTGGAAGAGCTGGGTGAAGC 336
DB 353 AAGAGCTCTCTTTTGGGAGCCTCATCTTAATTTGAATTTGGAAGAGCTGGGTGAAGC 412
QY 337 TCTTATGCAACGTTTACAGGAGTTAGCAGAAATTAATGCAACACTAGTCTTTAAAG 396
DB 413 TCTTATGCAACGTTTACAGGAGTTAGCAGAAATTAATGCAACACTAGTCTTTAAAG 472
QY 397 GTCATCAGCATGAATGAGAGAGAGTCCATTTAACAGTATCCAGAACTTCTCTC 456
DB 473 GTCATCAGCATGAATGAGAGAGAGTCCATTTAACAGTATCCAGAACTTCTCTC 532
QY 457 CTGAAGGTTTGAACATGCCAATATGTTGCTCTGCAATGATATTCACCAACCAAGAG 516
DB 533 TTGAAGAGCTTAAGCAGGCCAATCGTGTGTTTCAAGCATATCCACACTAAGGA 592
QY 517 AACTGACATTTGTTTGAATATACATGACAGACAGCTGGCCAGTATATGCTCAGCT 576
DB 593 ACCCTGACCTTTGTTTGAATATACATGACAGACAGCTGGCCAGTATATGCTCAGCT 652
QY 577 CCAGAGAGGCTTCAATCCATATATGTCAGACTTTCAATTTGCGGGGCTG 636
DB 653 CTTGAGAGACTCAATCCAGATTAATGTAAGTTGTTTATTTTCACTGCTGAGAGACTG 712

QY 637 GCCTACATCCACCACCAAGCTTCTTACAGGAGCTGAACCTCAGAACTTAATCTATC 696
DB 713 TCTTACATCCACGAGCTTATATTTTGACAGAGACTGAACCGCAGAACTTCTATC 772
QY 697 AGTCACTGGAGAGCTCAACCTGGATTTTGTGCTTTCGCCGGGCAAGCTCATTTCC 756
DB 773 AGGATACGGGGAGTTGAAGCTGGAGATTTGGTTGGACAGAAATCCGCTCT 832
QY 757 AGCCAGACATATCTTTCAGAAAGTCGTACCCCTGTGATCCGGCCCCCTGATGCTTTC 816
DB 833 AGCCAGACATATCTTTCAGAAAGTCGTACCCCTGTGATCCGGCCCCCTGATGCTTTC 892
QY 817 GAGAGCACTGAATATTTCTTCTGAGCTGACATATGGGCTGCAAGCTGCACTTTATTGA 876
DB 893 GGGCTTACAGAAATTTTCACTGCTGACATGTGGGAGTTGGCTGTATCTTCTGTAG 952
QY 877 ATGTTCCAGGGTCAACCTTTGTTTCTTGGGGTTTCCAACTCTTGAACAGCTGAGAA 936
DB 953 ATGATCCAGAGAGTTGCTGCGTTTCCAGGATGAAGACATTCAGGATCACTTGAACGG 1012
QY 937 ATCTGGAGGTGTGGAGTCCCTACAGAGATCTTGGCCGGAGTCTTCAAGTAACT 996
DB 1013 ATATTTCTGTTCTTGGACACCGAATGAGACACGTGGCTGAGTTCACTTTTACCA 1072
QY 997 AACTCAATCCAGAAATGTTCCTCACTGCTTACCGCTTCAAGCTTCACTGTTCTGGAAC 1056
DB 1073 CATTTTAAGCAAAAGCTTTTACCGTGTACACTTAAAGCCCTTGAACAAAGATGGAAT 1132
QY 1057 AGGCTGGAGGCTGCTTCTTGAAGCTGAAGACTGGAGCTCCAGATGTCTAAAGCTTTCC 1116
DB 1133 AACTCACTATGTAAATATATCTGAAGACTTGGCTTCAAGCTTCTTCCAGTTCCTCCA 1192
QY 1117 AGAGACCGCTCTCCGCCAGAGACACTTGTTCATGATATTTTCAAGCCCTGCCATCT 1176
DB 1193 AAGAAAGGCTATCAGACAGAGCCGCTTGAACATGATTTTCAAGCATCTGCTCCA 1252
QY 1177 CAGCTGACAGCTTCTGATGAGAGCTCTTGTTTTACAGTTTCAGAGTGAAGCTAAAG 1236
DB 1253 CGGCTATGGAGCTGACTGATATGCTTCTTATTTTACCGTCCAAATGATGAGATTGCA 1312
QY 1237 CCAGAA 1242
DB 1313 CCAGAA 1318

RESULT 11
US-10-153-242-1
; Sequence 1, Application US/10153242
; Publication No. US20030166217A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Pot, David
; APPLICANT: Kassam, Aliaf
; APPLICANT: Marenbach, Tasha
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRE)
; FILE REFERENCE: PP-01429.103/200130.445D1
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: human
US-10-153-242-1

Query Match 33.5%; Score 437.8; DB 15; Length 1272;
Best Local Similarity 65.1%; Pred. No. 3.9e-136;
Matches 646; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

QY 280 AGCTTCCTTTTGGGAGCTCATCTTACTTGAACCTTGAAGAGCTGGGTGAAGGCTCT 339

DB 238 AGTCCCAATTTTGAAGAAAGCTGATCTATTTGAAGAAAGCTGAAAGAACTTAGGGAGATCT 297
QY 340 TATGCAAGATTTTACAAAGGAGATTAGCAGATTAATATGACAACTAGTGGCTTTAAAGTC 399
DB 298 TATGCTACGATATACAAAGGAGAAAGAGGATTAATGGAAGTTGTAGCTTGAAGGTG 357
QY 400 ATCAGATGAATGACAGAGAGAGAGTCCCATTTTACAGTATCCGAGAACTTCTCTCG 459
DB 358 ATCAGGCTCAG 417
QY 460 AAGGTTTGAACATGAG 519
DB 418 AAGGCTTGAACATGAG 477
QY 520 CTGACATTTGTTTGAATATACATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
DB 478 CTGACATTTGTTTGAATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
QY 580 GAGAGGCTTCACTCTCATATATGTCAAGACTTTTCAATGTTTCAACTTTTGGGGCTGG 639
DB 538 GGGGGGCTGATCCAGATATGTGAAGTTGTTTATTTTCAAGTGTGAGAGGCTGTCT 597
QY 640 TACATCCACCAACACAGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
DB 598 TACATCCACCAACAGCTTATATTTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
QY 700 CACTGGAGAGCTCAAACTGCTGATATTTTGTCTTGTCCCGGAGAGAGAGAGAGAGAG 759
DB 658 GACAGGGGAGATTTAAAGCTGACAGATTTTGGTCTTTGCAAGAGAGAGAGAGAGAGAG 717
QY 760 CAGACATCTTTCAG 819
DB 718 CACACATCTCCAG 777
QY 820 GCACTGAATATTTCTGAGCTGACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
DB 778 TCAAGAGATATTTTCAAGCTGCTTGAACATGTGGAGAGAGAGAGAGAGAGAGAGAG 837
QY 880 TTCCAGAGCTCAACTTGTGTTTCTGGGGTTTCCAACTATCTTGAACAGCTGAGAGAAATC 939
DB 838 ATCCAAAG 897
QY 940 TGGAGAGTCTGGAGAGTCCCTTACAGAGATATTTGGCCGGAGAGTCTCAAGCTTACTAAC 999
DB 898 TTTCTGTTCTTGAACACCAATGAGAGACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
QY 1000 TACAATCCAGAAATGGTCCCACTGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
DB 958 TTTTAAGCCAG 1017
QY 1060 CTGGGCAAGGTTCTTGAAG 1119
DB 1018 CTGAGCTATGTGAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
QY 1120 GACCGGCTCTCCGCCAG 1179
DB 1078 AACCAACTGTGGACAG 1137
QY 1180 CTGTACCAAGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
DB 1138 CTATGGAAGTCAACAG 1197
QY 1240 GAATGTGTGACCTTTTGGCTCTTACAGAGAA 1272
DB 1198 GAACTGAGAGAAAGCATGCGGCTTTGGGAAA 1230

RESULT 12
US-10-153-242-13
; Sequence 13, Application US/10153242
; Publication No. US20030166217A1
; GENERAL INFORMATION:

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; APPLICANT: Reinhard, Christoph
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Marensbach, Tasha
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRE)
; FILE REFERENCE: PP-01429.103/200130.44501
; CURRENT APPLICATION NUMBER: US/10/153,242
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-153-242-13

Query Match      33.3%; Score 436.2; DB 15; Length 1549;
Best Local Similarity 65.0%; Pred. No. 1.5e-135;
Matches 645; Conservative 0; Mismatches 348; Indels 0; Gaps 0;

280 ACCCTCCCTTTGGGAGAGCTTCATCTTGAACCTTGAGAGAGCTGGAGAGCTCT 339
451 AGTCCCAATTTGGAAAAGCTGACTCATATGAAAAGCTGGAAAAGCTAGGAGATCT 510
340 TATGGACAGTTTACAAAGGAGTTAGCAGATTAATGACAACTAGTGCCTTTAAAGTC 399
511 TATGCTACAGTATACAAAGGAGAAAGCAGGTTAAAGGAAAGTTGAGTCTGAAAGTG 570
400 ATCAGATTAATGACAGAGAGAGAGCTCCATTTACAGCTATCCGAGAACCTTCTCCG 459
571 ATCAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
460 AAGGTTTGAACATSCCATATATGCTCTCTGATGATATATCCACAAAGAGAGA 519
631 AAGAGCTAAACATCTCTACATAGTCTATCTTCACTGATCATCTCATACAAAGAGAG 690
520 CTGACATTCGTTTGAATATACATGACACAGAGAGAGAGAGAGAGAGAGAGAGAG 579
691 CTGACATTCGTTTGAATATGACACATGATTTATGTCAGTACATGACAAAGAGAG 750
580 GAGAGCTTCATCTCTATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
751 GAGAGCTTCATCTCTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
640 TACATCCACACCAACAGCTCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
811 TACATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
700 CACCTGGAGAGAGCTCAAACTGCTGATTTGCTTTCGCCGGGCAAGTCCATTCACG 759
871 GACAGGGGAGAGTTAAAGCTGGGAGATTCGGTCTTGCAAGAGCAAAATCCGCTAG 930
760 CAGACATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
931 CACACATCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
820 GGCATGAAATATCTCTGAGCTGAGACATATGAGGAGAGAGAGAGAGAGAGAGAG 879
991 TCAACAGAAATATCTCTGAGCTGAGACATATGAGGAGAGAGAGAGAGAGAGAG 1050
880 TTCCAGAGAGAGCTTCTTGTCTTCTGGGAGTTTCCAACTCTTGAAGAGAGAGAG 939
1051 ATCCAAAGAGAGAGCTCTTCTTCTTCCAGAAATGAAAGATTCAGAGATCAACTTGA 1110
940 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
1111 TTTCTGAGTCTTGGAAACACCAATATGAGAGACATGAGCTGAGAGATTCATCTT 1170
1000 TACATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
1171 TTTAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230

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1060 CTGGAGAGAGAGTCTCTGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119
1231 CTGAGCTATGTAACCATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
1120 GACCCGCTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1179
1291 AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
1180 CTGATACAGCTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
1351 CTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
1240 GAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
1411 GAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443

RESULT 13
US-10-723-860-406
; Sequence 406, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; APPLICANT: Gineburg, Wendy M.
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882, 0193, NPLS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 406
; LENGTH: 4957
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-723-860-406

Query Match      33.3%; Score 436.2; DB 18; Length 4957;
Best Local Similarity 65.0%; Pred. No. 2.9e-135;
Matches 645; Conservative 0; Mismatches 348; Indels 0; Gaps 0;

280 ACCCTCCCTTTGGGAGAGCTTCATCTTGAACCTTGAGAGAGAGAGAGAGAGCTCT 339
466 AGTCCCAATTTGGAAAAGCTGACTCATATGAAAAGCTGAGAAAAGAGAGATCT 525
340 TATGGACAGTTTACAAAGGAGTTAGCAGATTAATGACAACTAGTGCCTTTAAAGTC 399
526 TATGCTACAGTATACAAAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
400 ATCAGATTAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
586 ATCAGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
460 AAGGTTTGAACATSCCATATATGCTCTCTGATGATATATCCACAAAGAGAGA 519
646 AAGAGCTAAACATGCTAAATGAGTACTTCAATGATCATCATCAATCAAGAGAGAG 705
520 CTGACATTCGTTTGAATATACATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
706 CTGACATTCGTTTGAATATGACACATGATTTATGTCAGTATACATGAGAGAGAG 765
580 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
766 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
640 TACATCCACACCAACAGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
826 TACATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
700 CACCTGGAGAGAGCTCAAACTGCTGATTTTGTCTTTCGCCGGGCAAGTCCATTC 759

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Db 886 GACACGGGGAGTTAAAGCTGCGAGATTTGAGTCTTTCAGAGCAAGCAAAATCGTCCCTAGC 945
Qy 760 CAGACATCTCTTCAAGAGTGTGACCTCTGGTACCGGCCCTGATGCTTGTCTGGGA 819
Db 946 CACACATCTCTCAACGAAAGTGTACCTTGTGGTACAGACTTCAGATGTCTTCTAGGC 1005
Qy 820 GCCACTGAATATCTCTGAGCTGACATATGGGGTGGCAGGCTGCATCTTTATTTGAATG 879
Db 1006 TCACAAGAAATATTCACCTGCTTGAATGTGGGAGTAGGTGCAATCTTTGTGAAATG 1065
Qy 880 TTCCAGGGTCAACCTTTGTTCTCTGGGGTTTCCAACTCTTGAACAGCTGAGAAATC 939
Db 1066 ATCCAGAGATGCTGCTTTTCCAGGAATAAAGACATTTAGATCACTTGAACGAAT 1125
Qy 940 TGGAGGTGCTGGAGTCCCTACAGAGATCTTGGCCGGAGTCTTCAAGCTACCTAAC 999
Db 1126 TTTCTGGTCTTGGAAACACCAATGAGGACACATGGCCTGGAGTTCACTTACCAT 1185
Qy 1000 TACAATCCAGAAATGTCTCCATGCTCAGCCTTCGAAGCCTTCATGTGTCTGGAACAG 1059
Db 1186 TTTAAGCGAAGACGCTTTTACCTGTACAGCTTAAACCTTAGACAGCATGAAATAG 1245
Qy 1060 CTGGGAGGGTCTCTGAAGCTGAAGACTGGCTCCAGATGCTTAAAGGCTTTCCAGA 1119
Db 1246 CTGAGCTATGTGAACATGAGAGAGACTGGCTCCAGCTCCTACATGTTCCTCAAG 1305
Qy 1120 GACCGGTCTCCGCCAGAGAGACTTGTTCATGATTTATTCAGCCCTGCAATCTCAG 1179
Db 1306 AACAGACTGTGGCAGACAGGCTGCTTGAGCCAGAGATTTTGTAGTACCTGCGCCAG 1365
Qy 1180 CTGTACAGCTCTCTGATGAGAGTCTTTGTTCAGTTTCAGAGTTCAGAGCTTAAAGCA 1239
Db 1366 CTATGGAACTCACCGACATGCTTCTATTTTATCTGCTCCAAATGAGATTGCAACA 1425
Qy 1240 GAAATGTGTACCTTTTGGCTCTTACAGAAA 1272
Db 1426 GAACTGTGAGAAAGCATGGGGCTTTGGGAAA 1458

RESULT 14
US-10-723-860-5096
; Sequence 5096, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5096
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4985)..(5005)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5096

Query Match 33.3%; Score 436.2; DB 18; Length 5161;
Best Local Similarity 65.0%; Pred. No. 36-135;
Matches 645; Conservative 0; Mismatches 348; Indels 0; Gaps 0;
Qy 280 AGCTTCCTTTGGGAGCTTCATCTTACCTTGAAGTGGAGAGCTGGAGAGCTCT 339

Db 466 AGTCCCAATTTTGAAAAGCTGACTCATATGAAAAGCTGGAAAACTAGGGAGAGATCT 525
Qy 340 TATGCGACATTTTACAGGGGATTTAGCAGAAATPAAATGACAACTAGTGGCTTTAAAGTC 399
Db 526 TATGCTACAGTATTAACAAGGAGAAAAGCAAGTAAATGGAAAGTTGTAGCTCTGAAGT 585
Qy 400 ATCAGATGAATGCAAGGAGAAAGAGTCCATTTACAGCTATCCGGAACCTCTCCCG 459
Db 586 ATCAGGCTGAGAGAAAGAAAGAGACCTTTCACAGCTATCAGGAGACCTTCTTTTA 645
Qy 460 AAGGTTTGAACATGCCAATATTTGTCTCTGCATGACATATCCACCAAGAGACA 519
Db 646 AAGGACTAAACATGCTAATGATGCTACTTCAATGATCATCATATCCAAAGAGAG 705
Qy 520 CTGACATTCGTTTTGAAATACATGACACACAGACTGGCCAGATATATGCTCAGATCCA 579
Db 706 CTGACACTTGTGTTGAATATGTGACACTGTATTTATGTCAATACATGACAAGACCT 765
Qy 580 GGAAGGCTTCATCCATATATGTCAGACTTTTCATGTTTCACTTTTGGGGGGCTGGG 639
Db 766 GGGGGCTGCTCAGATATATGTGAAGTGTGTTTATTTTCACTTGTGAGAGTCTGT 825
Qy 640 TACATCCACCAACACAGCTTCTTCAAGAGACTGAAACCTCAGAACTTACTCATAGT 699
Db 826 TATATCCACAGGTTATATTTTGCACAGAGACTGAAACACAGAACTTCTGATCAGT 885
Qy 700 CACTGGGAGAGCTCAACTGGCTGATTTTGTCTTGGCCGGGCCAAGTCCATTCCAGC 759
Db 886 GACAGGGGAGATTAAGCTGGCAGATTTGGTCTTTCAGAGCAAAATCCCTCTAGC 945
Qy 760 CAGACATCTCTTGAAGATGTGACCCCTGCTGTCGGGCCCTGATGCTTTGCTGGGA 819
Db 946 CACACATCTCAAGAAATGTGTACCTTGTGTACAGACTTCCAGATGCTCTTACAGC 1005
Qy 820 GCCACTGAATATCTCTGAGCTGACATATGGGATGACAGCTGACATCTTTATTTGAATG 879
Db 1006 TCACAGAAATATTTCCACCTGCTTGAATGTGGGAGTATGATCTTTGTGAAATG 1065
Qy 880 TTCCAGGGTCAACCTTTGTTCTCTGGGGTTTCCAACTCTTGAACAGTGGAGAAAATC 939
Db 1066 ATCCAGAGATGCTGCTTTTTCAGAAATGAAAAGCATTCAGATCACTTGAAGCAATA 1125
Qy 940 TGGGAGGTGCTGGAGATCCCTTCAAGAGATCTTGGCGGAGTCTCCAAAGCTACTAAC 999
Db 1126 TTTCTGTCTTGTGAACACAAATAGAGACATAGCTCTGAGTTCATTTTACACAT 1185
Qy 1000 TACAATCCAGAAATGTCTCCACTGCTACGCTTCGAAGCTTCATGTGTCTGGAACAG 1059
Db 1186 TTTAAGCCAGAACGCTTTTACCTGTACAGCTCTAATAAACCTTAGACAAGCATGGAATAAG 1245
Qy 1060 CTGGGAGAGGTCTCTGAAGCTGAAGACTGGCTCCAGATGCTTAAAGCTTTCCAGA 1119
Db 1246 CTGACCTATGTGAACCATGACAGAGACCTGGCTTCAAGCTCTTCAATGTTCCTCAAG 1305
Qy 1120 GACCGGTCTCCGCCAGAGAGACTGTTCATGATTTTTCAGGCGCTGCAATCTCAG 1179
Db 1306 AACAGACTGTGCGACAGAGCTGCTTGAAGCCAGAGATTTTATAGTACTGCGCCAGCG 1365
Qy 1180 CTGTACAGCTCTCTGATGAGAGTCTTTGTTTACAGTTTCAGAGTGAAGCTTAAAGCCA 1239
Db 1366 CTATGGAACTCACCGACATGCTTCTATTTTATCTGCTCCAAATGATGAGATTGCAACA 1425
Qy 1240 GAAATGTGTACCTTTTGGCTCTTACAGAAA 1272
Db 1426 GAACTGTGAGAAAGCATGGGGCTTTGGGAAA 1458

RESULT 15
US-10-296-115-483
; Sequence 483, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc

TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 784ACT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO: 483
LENGTH: 3024
TYPE: DNA
ORGANISM: Homo sapiens
US-10-296-115-483

Query Match 22.9%; Score 299.8; DB 16; Length 3024;
Best Local Similarity 58.7%; Pred. No. 2.3e-89;
Matches 577; Conservative 0; Mismatches 397; Indels 9; Gaps 3;

QY 289 TTTGGGCGAGCTCATCTTACTTGAACCTTGAGAGCTGGGTGAAGGCTTTATGCGACA 348
DB 301 TTTGGGAACTGAAACATACGTAACCTGAACTGGAGAGGCACTATGCGACA 360
QY 349 GTTTCAGAGGAGTTTACAGAAATGAACAAGTGTGCTTTAAAGTCATCAGCATG 408
DB 361 GTCTTCAAGGGGCGAGCAAACTGACGAGAACCTTGTGCGCTGAAAGATCCGGCTG 420
QY 409 AATGACAGAGAGAGTCCCATTTACAGTATCCGAGAGCTTCTCTGAAAGGTTTG 468
DB 421 GAGCAGAGAGAGGAGCGCGCTGCACTGCAATCCGAGAGGTGCTTGCTGAAGACCTG 480
QY 469 AAACATGCCAATATTTGTCTCTGCTGATGACATATCCACACCAAGAGACCTGACATTG 528
DB 481 AAGCAGCGCAATATGTGACCTCGCATGACCTCATCACAAGATGATCCCTCACCTG 540
QY 529 GTTTTGAATATGATGACACAGACCTGGCGCCAGTATATGCTCAGATCCAGAGGCTT 588
DB 541 GTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 589 CATCTCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 648
DB 601 AGCATGACACAGTCAAGATTTTCAATGTTCAAGTCTCCGGGCTCCGCTATCTGTAC 660
QY 649 CACCAACAGCTTCTTACAGGAGCTGAAACCTCAGAACTTACTCATCATCTGGA 708
DB 661 CACCGAAGATCTGACCGGAGCTGAAAGCCCAAGAACCTGCTCATCAACGAGAGGG 720
QY 709 GAGCTCAACCTGCTGATTTTGTCTTGGCCGGGCGCAATCCATTCGCCAGCAGACATAC 768
DB 721 GAGCTGAAGCTGCGCTGATTTGATGCGCGGCGCAAGTCAAGTGCACAAAGACTTAC 780
QY 769 TCTTCAGAGTGTGAGCTCTGTGTACCGGCGCCCTGATGCTTTGCTGGAGCCACTGAA 828
DB 781 TCCATGAGGTGTGACCTGTGTGTACAGGCGCCCGGATGTGTGTGTGTGTGTGTGTGT 840
QY 829 TATTCCTGAGCTGACATATGAGGTGACAGCTGATCTTTAATGAAATGTTTCAGGGT 888
DB 841 TACTCCAGCCCATGATATGTGGGGCGTGGGCTGATCACAAGATGAGCAGAGG 900
QY 889 CAACCTTTGTTTCTGGGGTTTCCACATCTTTGAAACAGCTGGAAGAAATCTGGAGGTG 948
DB 901 AGGCGCCCTCTTCCC--GGGCTCCACAGTCAAGAGAGAGCTGCACAAATCAATGCGCTC 957
QY 949 CTGGAGTCTCTACAGAGATATTTGGCGGAGTCTCCAGAGTACTTAATCAATCA 1008
DB 958 CTCGGGACCCCAAGAGAGAGAGTGTGCGCGGTGACCGCTTCTGTGAGTTCCGCAAC 1017
QY 1009 GAATGTTTCCAGCTGCTACGCTTCAGAGCTTCAATGTTGTGAAACAGGCTGGCAGG 1068
DB 1018 TACAGCTTCC--CTGTCTACCTCCCGCAGC---GCTCATCAACACGCGCCAGGTTG 1071
QY 1069 GTTCTGAAGTGAAGACCTGCGCTCCAGATGCTAAAGGCTTTCCAGAGACCGCGCTC 1128

DB 1072 GATACGATGGATCAGCTCCTGAGCAGCTGCTCTGTATGAATCCAAAGATGCGCATG 1131
QY 1129 TCCGCCAGAGAGCACTTGTATATTTACAGCGCCCTGCACTTCAAGCTGTAACAG 1188
DB 1132 TCAGCAGAGGCTGCGCTGAGTCACTTCCGCTCTGTGGAGAGGTTGTGACACAG 1191
QY 1189 CTTCGTATGAGAGTCTTTGTTTACAGTTTCAGAGTGAAGCTAAAGCAGAAATGTGT 1248
DB 1192 CTTGAAGACACTGCTTCCATCTTCTCCTGAAGAGATTCAGACTCCAGAGACCCAGGC 1251
QY 1249 GACCTTTGGCGCTCTTACAGAA 1271
DB 1252 TACGAGGCTTGGCTTCCAGCA 1274

Search completed: December 27, 2004, 12:15:31
Job time : 424.082 secs

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QY	901	CTGGGGGTTTCCAAATCCTCTTGAACAGCTGGAGAAAATCTGGAGAGTCTGGAGTCCCT	960
Db	901	CTGGGGGTTTCCAAATCCTCTTGAACAGCTGGAGAAAATCTGGAGAGTCTGGAGTCCCT	960
QY	961	ACAGAGGATATCTTGGCGGGAGTCTCCAGTACTTAATACTCAATTCAGAAATGGTTCCCA	1020
Db	961	ACAGAGGATATCTTGGCGGGAGTCTCCAGTACTTAATACTCAATTCAGAAATGGTTCCCA	1020
QY	1021	CTGGCTTACGCTCGAAGCTTCAATGTGTCTTGGAAACAGGCTGGGCAAGGTTCTGAAAGCT	1080
Db	1021	CTGGCTTACGCTCGAAGCTTCAATGTGTCTTGGAAACAGGCTGGGCAAGGTTCTGAAAGCT	1080
QY	1081	GAAGACCTGGGCTGCCAGATGTCTAAAGAGCTTTCCACAGAGACCGGCTTCCGCCCAAGSAA	1140
Db	1081	GAAGACCTGGGCTGCCAGATGTCTAAAGAGCTTTCCACAGAGACCGGCTTCCGCCCAAGSAA	1140
QY	1141	GCACCTTGTTCATGATTAATTTCCAGCGCCCTGCGCATCTCAGCTGTACACAGCTTCTGATGAG	1200
Db	1141	GCACCTTGTTCATGATTAATTTCCAGCGCCCTGCGCATCTCAGCTGTACACAGCTTCTGATGAG	1200
QY	1201	GAGTCTTTGTTTACAGTTTACAGAGTGAAGGCTAAAGCCAGAAATGTGTGACCTTTTGCC	1260
Db	1201	GAGTCTTTGTTTACAGTTTACAGAGTGAAGGCTAAAGCCAGAAATGTGTGACCTTTTGCC	1260
QY	1261	TTCCTACAGAAAGGTCAACACCCAGGCCAGTTTGGCAAAATGTCTGTGA	1308
Db	1261	TTCCTACAGAAAGGTCAACACCCAGGCCAGTTTGGCAAAATGTCTGTGA	1308

RESULT 3
US-09-801-861-1
; Sequence 1, Application US/09801861

```

; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2203
; TYPE: DNA
; ORGANISM: Human
; US-09-801-861-1

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Query Match	77.1%	Score 1009	DB 4	Length 2203
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1009	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	ATGGGTCAAGAGCTGTGTGCAAAAGCTGTACAGCTGGATCAGCTGTCATCATTTGCA	60
QY	118	ATGGGTCAAGAGCTGTGTGTGCAAAAGCTGTACAGCTGGATCAGCTGTCATCATTTGCA <td>177</td>	177
QY	61	GAGGGAGGCGGAGGCAACAGCTGTGTGGAGAGTCAAGCTTGAGACCAAGGAGCTGTGCTTC <td>120</td>	120
Db	178	GAGGGAGGCGGAGGCAACAGCTGTGTGGAGAGTCAAGCTTGAGACCAAGGAGCTGTGCTTC	237
QY	121	AAGCTTAACAGACCTTAAGAAAGAGCATCATGTCATGATTTACATTTACCCAGGGAGATT <td>180</td>	180
Db	238	AAGCTTAACAGACCTTAAGAAAGAGCATCATGTCATGATTTACATTTACCCAGGGAGATT	297
QY	181	CAAGCTGCCCTGTGCCAAGAGTTCAAGAGTAAAGGCCACGAGTAAACAGTGAATTTGTTT <td>240</td>	240
Db	298	CAAGCTGCCCTGTGCCAAGAGTTCAAGAGTAAAGGCCACGAGTAAACAGTGAATTTGTTT <td>357</td>	357
QY	241	CAGGAAGAAGATCTGAGGCAAGGTTTTACGTGAGGAAGAACCTTCCCTTTTGGGGCAGCC <td>300</td>	300
Db	358	CAGGAAGAAGATCTGAGGCAAGGTTTTACGTGAGGAAGAACCTTCCCTTTTGGGGCAGCC <td>417</td>	417

Qy	30.	TCATCTTACTTGAACTTGAGAAAGCTGGAGTAAAGCTCTTATGGAACAGTTTACAAGGGG	360
Db	418	TCATCTTACTTGAACTTGAGAAAGCTGGAGTAAAGCTCTTATGGAACAGTTTACAAGGGG	477
Qy	361	ATTAGCAGAAATAAATGACAACTAGTGGCTTTTAAAGTCATCAGCATGATGACAGAGAA	420
Db	478	ATTAGCAGAAATAAATGACAACTAGTGGCTTTTAAAGTCATCAGCATGATGACAGAGAA	537
Qy	421	GGAGTCCCATTTACAGTATCCGGAAGCTTCTCCTGSAAGGGTTTGAACATGCCAAT	480
Db	538	GGAGTCCCATTTACAGTATCCGGAAGCTTCTCCTGSAAGGGTTTGAACATGCCAAT	597
Qy	481	ATTGTGCTCTGTGACATATATCCACACCMAAGACACTGACATTCGTTTTGAATAC	540
Db	598	ATTGTGCTCTGTGACATATATCCACACCMAAGACACTGACATTCGTTTTGAATAC	657
Qy	541	ATGACACAAACCTGGGCGCCAGTAAATATGTCAGATCCAGAGGGGCTTCAATCCATAT	600
Db	658	ATGACACAAACCTGGGCGCCAGTAAATATGTCAGATCCAGAGGGGCTTCAATCCATAT	717
Qy	601	GTCAGACTTTTCATATGTTTCAACTTTTGGGGGGCTGGCGTATCCACACCAACAGTT	660
Db	718	GTCAGACTTTTCATATGTTTCAACTTTTGGGGGGCTGGCGTATCCACACCAACAGTT	777
Qy	661	CTTTCACAGGGACCTGAAACCTCAGAACCTTACTCATGTCACCTGGGAGAGCTCAACTG	720
Db	778	CTTTCACAGGGACCTGAAACCTCAGAACCTTACTCATGTCACCTGGGAGAGCTCAACTG	837
Qy	721	GCTGATTTTGGTCTTGGCCGGGGCCAGTCCATTCCTCCAGCAGACATATCTTTCAAGAGTC	780
Db	838	GCTGATTTTGGTCTTGGCCGGGGCCAGTCCATTCCTCCAGCAGACATATCTTTCAAGAGTC	897
Qy	781	GTCACCTCTGATACGGGCCCTCTGATGCTTGTGCTGGAAGCACTGAATATTCCTGTGAG	840
Db	898	GTCACCTCTGATACGGGCCCTCTGATGCTTGTGCTGGAAGCACTGAATATTCCTGTGAG	957
Qy	841	CTGGACATATGGGGGTGAGGCTGATCTTTATTTGAATATGTTCCAGGGGTCAACCTTTGTTT	900
Db	958	CTGGACATATGGGGGTGAGGCTGATCTTTATTTGAATATGTTCCAGGGGTCAACCTTTGTTT	1017
Qy	901	CTTGGGGTTTTCCACATCTTTGAAACAAGCTGGAGAAAAATCTGGAGAGTGTGGGAGTCCCT	960
Db	1018	CTTGGGGTTTTCCACATCTTTGAAACAAGCTGGAGAAAAATCTGGAGAGTGTGGGAGTCCCT	1077
Qy	961	ACAGAGATATCTTGGCCGGGAGTCTCCAAAGTACTTAATCAATCCAG 1009	
Db	1078	ACAGAGATATCTTGGCCGGGAGTCTCCAAAGTACTTAATCAATCCAG 1126	

RESULT 4
US-10-224-562-1
; Sequence 1, Application US/10224562

```

1  APPLICANT: YAN, Chunhua et al.
2  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIC
3  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
4  TITLE OF INVENTION: THEREOF
5  FILE REFERENCE: CL001098DIV
6  CURRENT APPLICATION NUMBER: US/10/224,562
7  CURRENT FILING DATE: 2002-08-21
8  NUMBER OF SEQ ID NOS: 10
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 1
11 LENGTH: 2203
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 US-10-224-562-1

```

Query Match	77.1%	Score 1009;	DB 4;	Length 2203;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 1009;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY 1 ATGGGTCAAGAGCTGTGTGCAAGACTGTACAGCTTGATGACGCTGTAACCAATGTTCA 60
DB 118 ATGGGTCAAGAGCTGTGTGCAAGACTGTACAGCTTGATGACGCTGTAACCAATGTTCA 177
QY 61 GAGGAGGCGGAGGACACAGCTGTGCGAGAGAGTCAAGCTGACCAACGAGGCGGCTTC 120
DB 178 GAGGAGGCGGAGGACACAGCTGTGCGAGAGAGTCAAGCTGACCAACGAGGCGGCTTC 237
QY 121 AAGCTAACAGACCTTAAAGAGCATCATGTTCATGATTCATTCACCCAGGGGACTT 180
DB 238 AAGCTAACAGACCTTAAAGAGCATCATGTTCATGATTCATTCACCCAGGGGACTT 297
QY 181 CAAGCTGCCCCGTCGCCAGAGTTCAAGATTAAGGCGACAGAGTAAACAGTATGTTT 240
DB 298 CAAGCTGCCCCGTCGCCAGAGTTCAAGATTAAGGCGACAGAGTAAACAGTATGTTT 357
QY 241 CAGGAAGAGATCTGAGGCGAGGTTTCACTGAGAGAGAGCCTCCCTTTTGGGGGAGCC 300
DB 358 CAGGAAGAGATCTGAGGCGAGGTTTCACTGAGAGAGAGCCTCCCTTTTGGGGGAGCC 417
QY 301 TCATCTTACTTGAACCTTGAGAAAGCTGGTGAAGGCTTTATGCGACAGTTTCAAAGGG 360
DB 418 TCATCTTACTTGAACCTTGAGAAAGCTGGTGAAGGCTTTATGCGACAGTTTCAAAGGG 477
QY 361 ATTAGAGATTAATAGCAACATAGTGGCTTTAAAGTCAATGACATGATGACAGAGAA 420
DB 478 ATTAGAGATTAATAGCAACATAGTGGCTTTAAAGTCAATGATGATGACAGAGAA 537
QY 421 GAGATCCATTTACAGCTATCCGAGAGGCTTCTCTCTGAAAGGTTTGAACATGCGCAT 480
DB 538 GAGATCCATTTACAGCTATCCGAGAGGCTTCTCTCTGAAAGGTTTGAACATGCGCAT 597
QY 481 ATGTGCTCTGATGACATATTCACACCAAGAGACACTGACATTCGTTTGAATAC 540
DB 598 ATGTGCTCTGATGACATATTCACACCAAGAGACACTGACATTCGTTTGAATAC 657
QY 541 ATGCACACAGACCTGGGCGGAGTATATGTCTCAGCATCCAGAGGCTTCACTCTCAAT 600
DB 658 ATGCACACAGACCTGGGCGGAGTATATGTCTCAGCATCCAGAGGCTTCACTCTCAAT 717
QY 601 GTGAGACTTTTCAATGTTTCACTTTTGCAGGAGCTGACATCCACCAACCAAGCTT 660
DB 718 GTGAGACTTTTCAATGTTTCACTTTTGCAGGAGCTGACATCCACCAACCAAGCTT 777
QY 661 CTTCACAGGAGCTGAACTCTGAACTTACTATGATGACCTGGAGAGCTCAAACTG 720
DB 778 CTTCACAGGAGCTGAACTCTGAACTTACTATGATGACCTGGAGAGCTCAAACTG 837
QY 721 GCTGATTTTGTCTGTCGCCGAGGCAAGTCAATCCAGAGCAGACATACCTTCAGAAATC 780
DB 838 GCTGATTTTGTCTGTCGCCGAGGCAAGTCAATCCAGAGCAGACATACCTTCAGAAATC 897
QY 781 GTGACCTCTGTGATCCGAGGCGGCTGTGATGCTTGTGCGAGCACTGAAATATTCCTGAG 840
DB 898 GTGACCTCTGTGATCCGAGGCGGCTGTGATGCTTGTGCGAGCACTGAAATATTCCTGAG 957
QY 841 CTGGAATATAGGGGTGAGAGCTGACATCTTTATTTGAATGTTCCAGGCTCAACTTTGTTT 900
DB 958 CTGGAATATAGGGGTGAGAGCTGACATCTTTATTTGAATGTTCCAGGCTCAACTTTGTTT 1017
QY 901 CCGTGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGGTGCGGGAGTCCCT 960
DB 1018 CCGTGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGGTGCGGGAGTCCCT 1077
QY 961 ACAGAGAGATCTTGGCGGGAGTCTTCAAGCTACCTTACATCAATCCAG 1009
DB 1078 ACAGAGAGATCTTGGCGGGAGTCTTCAAGCTACCTTACATCAATCCAG 1126
```

RESULT 5
US-09-387-212-14
; Sequence 14, Application US/09387212A

```
Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/387, 212A
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-387-212-14

Query Match 36.8%; Score 481; DB 3; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.6e-149; Mismatches 0; Gaps 0;
Matches 481; Conservative 0; Indels 0;

QY 720 GGCTGATTTTGTGTTGCCCCGAGCAAGTCAATCCAGCAGACATACCTTTCAGAACT 779
DB 1 GGCTGATTTTGTGTTGCCCCGAGCAAGTCAATCCAGCAGACATACCTTTCAGAACT 60
QY 780 CGTGACCTCTGTACCGGCCCCCTGATGCTTTGCTGGAGGCACTGAATATTCCTTGA 839
DB 61 CGTGACCTCTGTACCGGCCCCCTGATGCTTTGCTGGAGGCACTGAATATTCCTTGA 120
QY 840 GCTGACATATGAGGGTGCAGGCTGATCTTTATGAAATGTTCCAGGGTCAACTTTGTT 899
DB 121 GCTGACATATGAGGGTGCAGGCTGATCTTTATGAAATGTTCCAGGGTCAACTTTGTT 180
QY 900 TCTTGAGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGAGAGTCC 959
DB 181 TCTTGAGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGTGTGAGAGTCC 240
QY 960 TACAGAGATTAATAGGCGGAGTCTCAAGTACTCAATCAATCCAGAAATGAGTCCC 1019
DB 241 TACAGAGATTAATAGGCGGAGTCTCAAGTACTCAATCAATCCAGAAATGAGTCCC 300
QY 1020 ACTGCTACGCTCTCAAGCTTCAATGTTGTCTGAAACAGGCTGGCAGGGTTCTGAAGC 1079
DB 301 ACTGCTACGCTCTCAAGCTTCAATGTTGTCTGAAACAGGCTGGCAGGGTTCTGAAGC 360
QY 1080 TGAAGACTGCGCTCTCCAGAGTCTTAAAGGCTTTCCAGAGACCGGCTCTCCGACAGA 1139
DB 361 TGAAGACTGCGCTCTCCAGAGTCTTAAAGGCTTTCCAGAGACCGGCTCTCCGACAGA 420
QY 1140 AGCACTGTGATGATTAATTTTCAAGGCGCTGCATCTGAGCTGACAGCTTCCGATGA 1199
DB 421 AGCACTGTGATGATTAATTTTCAAGGCGCTGCATCTGAGCTGACAGCTTCCGATGA 480
QY 1200 G 1200
DB 481 G 481
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RESULT 6
US-09-948-802-14
; Sequence 14, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/948, 802
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387, 212
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14

LENGTH: 481
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-948-802-14

Query Match 36.8%; Score 481; DB 4; Length 481;
 Best Local Similarity 100.0%; Pred. No. 2.6e-149;
 Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 GGCTGATTTTGGCTCTTCCCGGCGCAAGTCCATTCCAGCAGACATCTTCCAGAAAGT 779
 DB 1 GGCTGATTTTGGCTCTTCCCGGCGCAAGTCCATTCCAGCAGACATCTTCCAGAAAGT 60
 QY 780 CGTGACCTCTGCTGATCCGCGCCCTCTGATGCTTGGTGGAGCACTGAAATATCTCTGA 839
 DB 61 CGTGACCTCTGCTGATCCGCGCCCTCTGATGCTTGGTGGAGCACTGAAATATCTCTGA 120
 QY 840 GCTGACATATGGGGTGGAGGCTGATCTTATTGAATGTTCCAGGGTCAACTTGT 899
 DB 121 GCTGACATATGGGGTGGAGGCTGATCTTATTGAATGTTCCAGGGTCAACTTGT 180
 QY 900 TCCCTGGGGTTTCCAGATCTCTTGAAGAGTGAAGAAATCTGGAGGCTGCGAGTCC 959
 DB 181 TCCCTGGGGTTTCCAGATCTCTTGAAGAGTGAAGAAATCTGGAGGCTGCGAGTCC 240
 QY 960 TACAGAGATATCTTGGCGCGGAGTCTCCAGAGTACCTAATCAATCCAGATGTTCC 1019
 DB 241 TACAGAGATATCTTGGCGCGGAGTCTCCAGAGTACCTAATCAATCCAGATGTTCC 300
 QY 1020 ACTGACCTAGGCGCTCGAAGCCTTATGTTCTGGAACAGGCTGGGAGGTTCTGAAG 1079
 DB 301 ACTGACCTAGGCGCTCGAAGCCTTATGTTCTGGAACAGGCTGGGAGGTTCTGAAG 360
 QY 1080 TGAAGACTGCTGCCCTCCAGATGCTAAAGGCTTCCAGAGACCGGCTCTCCGCCAGGA 1139
 DB 361 TGAAGACTGCTGCCCTCCAGATGCTAAAGGCTTCCAGAGACCGGCTCTCCGCCAGGA 420
 QY 1140 AGCATTGTTTCATGATTATTTACGCGCCCTGCACTCAGCTTACAGCTTCTGATGA 1199
 DB 421 AGCATTGTTTCATGATTATTTACGCGCCCTGCACTCAGCTTACAGCTTCTGATGA 480
 QY 1200 G 1200
 DB 481 G 481

RESULT 7

US-09-206-344A-3
 Sequence 3, Application US/09206344A
 Patent No. 6432668
 GENERAL INFORMATION:
 APPLICANT: Christoph Reinhard
 APPLICANT: David Pot
 APPLICANT: Aliaf Kassam
 APPLICANT: Tasha Marenbach
 APPLICANT: Lewis T. Williams
 TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRB)
 FILE REFERENCE: 200103.445 / 1429.002
 CURRENT APPLICATION NUMBER: US/09/206,344A
 CURRENT FILING DATE: 1998-12-17
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 2467
 TYPE: DNA
 ORGANISM: mouse
 US-09-206-344A-3

Query Match 33.5%; Score 438; DB 4; Length 2467;
 Best Local Similarity 65.8%; Pred. No. 1.5e-134;
 Matches 636; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 277 AAGAGCTCCCTTTGGGCGCAGCTCATCTTACTTGAACCTTGAGAGAGCTGGGTGAAGC 336

DB 353 ACGAGTCCCAAAATTTGGAAAAGCTGACTCATACGAAAACTGGAAAACTGGGGAGGA 412
 QY 337 TCTTATGCGACAGTTTACAAAGGAGATTACAGAAATTAATGACAACTAGTGGCTTTAAA 396
 DB 413 TCTTATGCGACAGTTTACAAAGGAGATTACAGAAATTAATGAGAGTGGTGGCTTTAAA 472
 QY 397 GTCATGACATGAATGACAGAGAGAGAGATGCCATTTTACAGCTATCCGAGAGCTTCTC 456
 DB 473 GTGATCCGCTCAGAGAAAGAGAGGACACCTTTTACAGCCATCGGGAAGCTTCCG 532
 QY 457 CTGAAGGGTTTGAACATGCCAATATGTCCTCCGTCATGACATATTCACACCAAGAG 516
 DB 533 TTGAAGAGACTAAGACCCACATCGTTGCTTACAGACATATCCACTTAAGAA 592
 QY 517 ACACTGACATTTGGTTTGAATATGACACAGACCTGCGCCAGTATATGTTCTGCAT 576
 DB 593 ACCCTGACCTTGTCTTTAATATACGTGACACATGATTTATGTCAGTACATGACAAAG 652
 QY 577 CCAGAGGGCTTCATCTCATATATGTCAGACTTTTCACTTTTCACTTTTGGGGGCTG 636
 DB 653 CCGAGAGACTCATCCATCCAGATATGTAAGTTTATTTTCACTGCTGGAGAGACTG 712
 QY 637 GGGTACATCCACCAACCAACAGCTTCTCAAGGAGCTGAACCTCAGAACTTACTCATC 696
 DB 713 TCTTATATCCACAGGCTTATATTTTGAACAGACCTTAAACCGAGAACCTTCTCATC 772
 QY 697 ACTCACCTGGAGAGCTCAAACTGCTGATTTTGTCTTCCCGGCGCAAGTCCATTC 756
 DB 773 ACGAATAGGGGAGAGTTGAAGCTGGAGATTTCCGTCTGGCAAGCAAAATCCGTCCT 832
 QY 757 AGCCAGACATCTTTCAGAAAGTCTGACCTCTGATCCGCGCCCTGATGCTTGTCTG 816
 DB 833 AGCCAGACATCTTTCAGAAAGTCTGATCCGCTGATCCGCGCCCTGATGCTTGTCTG 892
 QY 817 GGAAGCAGATATTTCCCTGAGCTGACATATGGGGTGGAGGCTGACCTTATTAAG 876
 DB 893 GGCTTACAGAAATATTCACCTGCTTGAACATGTTGGAGGTTGGCTGATCTTCGTTAG 952
 QY 877 ATGTTCCAGGCTCAACCTTGTGTTCTCTGGGTTTCCACATCTTGAACAGCTGAGAA 936
 DB 953 ATGATCCAAAGAGTTGCTGCTGTTCCAGAAATGAAGAACTTCAAGATCACTGAACGG 1012
 QY 937 ATCTGGAGCTGCTGGAGTCCCTACAGAGATCTTGGCCGGAGTCTTCAAGCTACCT 996
 DB 1013 ATATTTCTGTTCTTGGAAACACCGAATGAGGACAGCTGCTGAGTTCTTATACCA 1072
 QY 997 AACTCAATCCAGAAATGTTCCCACTGCTAGCGCTCGAAGGCTTCATGTTCTGGAG 1056
 DB 1073 CATTTTAAAGCCAGAAAGCTTTTACCGTTTACAACTTAAAGGCTTGAACAGATGGAAT 1132
 QY 1057 AGGCTGGGAGAGGTTCTGTAAGCTGTAAGACTGAGCTCCAGATGCTAAAGGCTTCCC 1116
 DB 1133 AAGCTAGCTATGTAATATATCTGAAGCTTGGCTCCAAAGCTTCTCAAGTGTCCCA 1192
 QY 1117 AAGAACCGGCTCTCGCCCGAGAGACATTTGTCATGATTAATTTAGCGCCCTGCATCT 1176
 DB 1193 AAGAACAGGCTATACAGACAGCGCCCTGAGCCATGATTAATTTAGCATATGCTTCA 1252
 QY 1177 CAGCTGTACAGCTTCCGTAAGAGAGAGTCTTTTACAGTTTCAAGAGTGAAGGCTTAA 1236
 DB 1253 CGGCTATGGAGCTGATATGTTCTTATTTTACCGTCCCAAAATGTAAGATTGCA 1312
 QY 1237 CCAGAA 1242
 DB 1313 CCAGAA 1318

RESULT 8

US-09-206-344A-1
 Sequence 1, Application US/09206344A
 Patent No. 6432668
 GENERAL INFORMATION:

```

; APPLICANT: Christoph Reinhard
; APPLICANT: David Pot
; APPLICANT: Alfat Kassem
; APPLICANT: Tasha Marendach
; APPLICANT: Lewis T. Williams
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRE)
; FILE REFERENCE: 200103.445 / 1429.002
; CURRENT APPLICATION NUMBER: US/09/206,344A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: human
US-09-206-344A-1

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Query Match          33.5%; Score 437.8; DB 4; Length 1272;
Best Local Similarity 65.1%; Pred. No. 1,1e-134;
Matches 646; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

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QY 280 AGCTCCCTTTGGGCGAGCTCATCTTGAAGTTGAGAGAGCTGGAGGCTCT 339
DB 238 AGTCCCAATTGGAAAAGCTGACTATGAAAAGCTGAGAAAAGCTAGGGAGGATCT 297
QY 340 TATGCCAGATTTCAGAGGATTAGAGAAATTAATGACACACTAGGCTTTAAAAGTC 399
DB 298 TATGCTACATATACAAAGGAAAAGGATAATGGAAAGTTGTAAGCTCGAAGGTG 357
QY 400 ATCAGCATGATCAGAGAGAGAGTCCATTATACAGTATCCGAGAGCTTCTCTCTG 459
DB 358 ATCAGGCTGAGAGAAAGAGAGGACACCTTTCAGAGCTATCAGGAGGCTTCTTTTA 417
QY 460 AAGGTTTGAACATGCGCAATATTGCTCTCTGATGACATTAATCCACCAAGAGACA 519
DB 418 AAGAGCTAAACATGCTAATCATATGCTCTTATGATGACATCATCAACCAAGAGACG 477
QY 520 CTGACATGCTTTTGAATATCATGACACAGAGCTGGCCCAAGATATGCTCAGACCTCA 579
DB 478 CTGACATGCTTTGTAATATGTCACACTGATTTATGTCAGTACATGACAAAGACCTT 537
QY 580 GAGAGGCTTCATCTCATTAATGTCAGACTTTTCATGTTTCACCTTTGCGGGGCTGCG 639
DB 538 GGGGGCTGCTCATCAGATATATGTAAGTGTTTTATTTCAAGTTGCTGAGAGTCTGTCT 597
QY 640 TACATCCACCAACCAACGCTTTCACAGGAGCTGAAACCTCAAACTTACTCATAGT 699
DB 598 TACATCCACCAACGCTTATATTTGACACAGAGACTGAAACCAAGAACTTCTGATCAGT 657
QY 700 CACCTGGAGAGCTCAAACTGGCTGATTTGCTTGGCCCGGGCCCAAGTCCATTCACAG 759
DB 658 GACACGGGGAGTTAAAGCTGGCAATTTGGCTTTCAGAGCAAAATTCGCTCCAGT 717
QY 760 CAGACATCTCTTCAGAAAGTGTGACCTCTGCTGACCGGCCCTGATGCTTTGCTGGA 819
DB 718 CACACATCTCTCAACAGAAAGTGTGACCTCTGCTGACAGCTCCATATGCTCTTACAGC 777
QY 820 GCCACTGATATTTCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAATG 879
DB 778 TCACAGGAATATTCACCTGCTTGACATGTGGGGAGTGGTTGCACTTTTGTGAAAAG 837
QY 880 TTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAAATCCTTGAACAGGCTGGAGAAATC 939
DB 838 ATCCAGAGAGTCTGCTTTTCCAGAAATGAAAGAAATTCAGAGTAACTTGAAGCAATA 997
QY 940 TGGAGAGTGTGGAGTCTCTTCAAGAGATTACTTGGCCGGAGTCTTCAAGTCACTTAAC 999
DB 898 TTCTCTGTTCTTGGACACCAAAATGAGGACATGGCTGAGGTTCAATCTTTACACAT 957
QY 1000 TACAATCCAGAAATGTTCCCATGCTCAGGCTCAGAGCTTATGTTGTGAAACAGG 1059
DB 958 TTTAAGCCAGAAAGCTTTTACCTCTGTAACAGCTTAAAAAAGCTTGAACAGACATGAAATAG 1017

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QY 1060 CTGGGCGAGGTTCTGAAGCTGAACCTGGCTCTCCAGATGCTAAAGGCTTTCCAGA 1119
DB 1018 CTCAGCTATGTGAACCATGACAGAGGACCTGGCTCCAGAGCTCTCAAAATGTTCCCAAG 1077
QY 1120 GACCGGCTCCGCGCCAGAGAGCACTGTTCAATGATATTTTCAAGGGCCCTGCATCTGAG 1179
DB 1078 AACAGCTGTCCGACAGAGCTGCTTGAAGCACAGATATTTTATGATACCTGCGCCAGG 1137
QY 1180 CTGTACAGCTTCTGATGAGAGTCTTTGTTTACAGTTTCAAGTTCAGAGTGAAGCTAAAGCA 1239
DB 1138 CTATGGAACTACCGACATGCTCTTCTATTTTATCTGTCCAAATGTGAGATTGCAACCA 1197
QY 1240 GAAATGTGACCTTTTGGCTCTTCAACGAAA 1272
DB 1198 GAAAGCTGAGAAAAGCATGCGGCTTTTGGGAAA 1230

```

RESULT 9

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US-09-206-344A-13
; Sequence 13, Application US/09206344A
; Patent No. 6432668
; GENERAL INFORMATION:
; APPLICANT: Christoph Reinhard
; APPLICANT: David Pot
; APPLICANT: Alfat Kassem
; APPLICANT: Tasha Marendach
; APPLICANT: Lewis T. Williams
; TITLE OF INVENTION: HUMAN CYCLIN-DEPENDENT KINASE (hPPTAIRE)
; FILE REFERENCE: 200103.445 / 1429.002
; CURRENT APPLICATION NUMBER: US/09/206,344A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-206-344A-13

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Query Match          33.3%; Score 436.2; DB 4; Length 1549;
Best Local Similarity 65.0%; Pred. No. 4,3e-134;
Matches 645; Conservative 0; Mismatches 348; Indels 0; Gaps 0;

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QY 280 AGCTCCCTTTGGGCGAGCTCATCTTGAAGTTGAGAGAGCTGGAGGCTCT 339
DB 451 AGTCCCAATTGGAAAAGCTGACTCATATGAAAAGCTGAGAAAAGCTAGGGAGAGATCT 510
QY 340 TATGCCAGATTTCAGAGGATTAGAGAAATTAATGACACACTAGGCTTTAAAAGTC 399
DB 298 TATGCTACATATACAAAGGAAAAGGATAATGGAAAGTTGTAAGCTCTGAAGGTG 570
QY 511 TATGCTACATATACAAAGGAAAAGGATAATGGAAAGTTGTAAGCTCTGAAGGTG 570
QY 400 ATCAGCATGATCAGAGAGAGAGTCCATTATACAGTATCCGAGAAAGCTTCTCTCTG 459
DB 571 ATCAGGCTGAGAGAGAGAGAGGACACCTTTCACAGCTATCAGGAGGAGCTTCTTTTA 630
QY 460 AAGGTTTGAACATGCGCAATATTGCTCTGATGACATTAATCCACCAAGAGACA 519
DB 631 AAAAGACTTAAACATGCTTACATAGTCTTACTTCAATGACATTCATCAACAAAGAGAG 690
QY 520 CTGACATGCTTTTGAATATCATGACACAGAGCTGGCCGAGTATGCTCAGATCCA 579
DB 691 CTGACATGCTTTGTAATATGTCACACTGATTTTATGTCAGTACATGAGCAAGACCTT 750
QY 580 GAGAGGCTTCATCTCATTAATGTGACATTTTCAATGTTTCAACTTTTGGGGGCTGGCG 639
DB 751 GGGGGGCTGACATCCAGATTAATGTGAAGTGTTTTATTTACAGTGTCTCGAGTCTGTCT 810
QY 640 TACAATCCACCAACAGGCTTTCACAGGAGCTTGAAGAACTTGAATTTACTCATCGT 699
DB 811 TACATCCACCAAGCTTATATTTTGAACAGAGACCTGAAAACCAAGAACTTCTGATCAGT 870
QY 700 CACCTGGAGAGCTCAAACTGGCTGATTTTGTGCTTGGCCCGGGCCAAAGCTCATTTCCAGC 759

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Db 871 GACAGCGGGAGTTAAAGCTGACGATTTGGCTTTCAGAACGAAATCCCTCCTAGC 930
 QY 760 CAGACATCTCTTCAAGAGTCTGACCTCTGTTACCGGCCCCCTGATGCTTTGCTGGA 819
 Db 931 CACACATCTCTCCAAAGAGTGTACCTTGTGTACAGACCTCAAGATGCTTTAGGC 990
 QY 820 GGCACGAAATATCTCTGAGCTGACATATGAGGCTGAGGCTGATCTTTATGAAAG 879
 Db 991 TCAACGAAATATCTCTGAGCTGACATATGAGGCTGAGGCTGATCTTTATGAAAG 1050
 QY 880 TTCAGGCTCAACCTTGTCTCTGAGGCTTCCAAATCTTGAACAGCTGAGAAATC 939
 Db 1051 ATCCAGAGAGTCTCTCTTTCAGGAAATGAAGATCTTACAGATCACTTGACGAAAT 1110
 QY 940 TGGAGCTGCTGAGAGTCTCTTCAAGAGATCTTGGCCGAGTCTCAAGCTACCTAAC 999
 Db 1111 TTTCTGCTTCTGGAACACCAATGAGGACACATGCTGAGATCTTATCTTACACATT 1170
 QY 1000 TACAATCCAGAAATGTTCCACCTGCTAGGCTCCGAGCTTCATGTTGCTGGAACAG 1059
 Db 1171 TTTAAGCCAGAAAGCTTTAACCCTGTAAGCTTTAAACCTTAGACAGATGAAATAG 1230
 QY 1060 CTGGAGGAGGCTCTGAGAGCTGAGAGCTGAGCTCCAGATGCTTAAAGGCTTTCCAGA 1119
 Db 1231 CTCAGCTATGTGAACCATGAGAGACCTGAGCTCCAGCTCTCAAGTCTTCAATGTTCCAAAG 1290
 QY 1120 GACCGGCTCTCGCCGAGAGAGCATTTGATGATTTATTCAGCCCTCCATCTCAG 1179
 Db 1291 AACAGACTGCTGGGACAGGCTGCTGAGCAGAGATTTATGATGACCTGCGGACAGG 1350
 QY 1180 CTGTACACACTTCTCTATGAGAGCTTTGTTTACAGTTTACAGAGTGAAGGCTTAAAGCA 1239
 Db 1351 CTATGGAACTCAACCACTGCTTCTTATTTTATCTGCTCCAAATGATGAGATTGCAACCA 1410
 QY 1240 GAAATGTGACCTTTGGGCTCTTACAGAAA 1272
 Db 1411 GAAAGCTGAGAAAGCATGCGGCTTTGGGAAA 1443

RESULT 10

US-09-620-312D-53

Sequence 53, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyang

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonhong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yungling

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Dornmac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt_fl_genes Version 1.0

SEQ ID NO 53

LENGTH: 2868
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (431)..(1924)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(2868)
 OTHER INFORMATION: n = a,t,c or g
 us-09-620-312D-53

Query Match 22.6%; Score 296.2; DB 4; Length 2868;
 Best Local Similarity 58.6%; Pred. No. 2,1e-87;
 Matches 555; Conservative 0; Mismatches 383; Indels 9; Gaps 2;

QY 289 TTTGGGCGAGCTCATCTTACTTTGAACCTGAGAAAGCTGGTGAAGGCTCTTATGCGACA 348
 Db 905 TTTGGGAACTGAGACCTTACATTAAGCTGACAACTGGGAGGATCACTATGCCACC 964
 QY 349 GTTTACAAAGGGATTAAGCAAAATTAATGACAATAGTGGCTTTTAAAGTCATGACATG 408
 Db 965 GTCTACAAAGGCAAAAGCAAGCTCAAGACAACTTGTGGCACTCAAGAGATCAAGACTG 1024
 QY 409 AATGCAAGAGAGAGTCCCATTTACAGTATCCGAGAAAGCTTCTCTGAAAGGCTTTG 468
 Db 1025 GAACATGAAGAGGGGCAACCTGCAACCGCATCCGGGAAGTGTCCCTGCTCAAGAACCTC 1084
 QY 469 AAACATGCCAATATTTGTGCTCTGATGACATATTCACACCAAGAGACATGACATTG 528
 Db 1085 AAACAGGCCAATATGTTAGCTTACATGACATTTATCCACGAGAGAGTCCCTCACCTT 1144
 QY 529 GTTTTGAATATATGACACACAGACCTGGCCAGTATATGTCTCAGCATTCAGAGAGGCTT 588
 Db 1145 GTCTTTGAGTACTGGAAGAGACCTGAAAGCAGTACCTGATGACGTGGGAAATCATC 1204
 QY 589 CATCTCATATATGACACTTTTCAATGTTTCACTTTTGGGGGCTGGCTGATCATCCAG 648
 Db 1205 AACATGACACAGTAACTGTTCTGTTCCAGCTGCTCCGGGCTGGCTGATCTCCAG 1264
 QY 649 CACCAACAGTCTTCAACAGGAGCTGAAACCTGAAACTTACTCATCATGACCTGAGGA 708
 Db 1265 CGGCAAGAGTCTTCAACCGAGATCTCAAGCCCAAGCTCTCATCAACAGAGGGA 1324
 QY 709 GAGCTCAAACTGCTGATTTTGTCTTGGCCCGGCAAGTCCATTCAGCCAGACATAC 768
 Db 1325 GAGCTCAAGCTGCTGACTTTGGCTGGCCGAGCAAGTCAATCCAAACAAAGACATAC 1384
 QY 769 TCTTCAGAAAGTGTGACCTCTGTGTAACGGCCCCCTGATGCTTTGGGAGCCACTGAA 828
 Db 1385 TCCAAATGAGTGTGTAACCTGTGTACCGGCCCCCTGACATCTCTGGGTCCACGGAC 1444
 QY 829 TATTCCTGAGCTGACATATAGGGGTGAGGCTGACATCTTATTAATGATGTTCCAGGT 888
 Db 1445 TACTCAGCTCAGATTTGACATGTGGGTGTGGCTGACATCTTATGAGATGCTCACAGGC 1504
 QY 889 CAACCTTGTCTCTGAGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGAGGTG 948
 Db 1505 CGTCCCTCTTCC---GGGCTCCACGGTGAAGGAAAGCTACATTTATCTTCGGTATC 1561
 QY 949 CTGGAGTCTCTTACAGAGATTTCTGGCCGGAGAGTCTCAAGCTTCACTTACATCAATCA 1008
 Db 1562 TTAGGAACCCCACTGAGAGAGCTGGCCAGG-----CATCTGTCCAAACAGAGAGTTC 1615
 QY 1009 GAATGTTCCCACTGAGCTGAGGCTGAGGCTTCAATGTTGTGTGAACAGAGCTGGAGAG 1068
 Db 1616 AAGACATACACTTACCTCAAGTACGAGGCTGAGGCTTTTGAAGCAGACCCGACTT 1675
 QY 1069 GTTCTGAAGCTGAAGAGCTGGCTCCAGATGCTTAAAGGCTTTCCAGAGACCGGCTC 1128
 Db 1676 GATAGCAGAGGGGCGAGCTCTCTCAACAGGCTTGAAGGTTGAAGGTTGAAGTGAATC 1735
 QY 1129 TCCGCCCAAGAAAGCATTTGTTATGATTTTCAAGGCCCTGCGCATCTCAGCTGATCAG 1188

Db 1736 TCCGACAGAGATGCCATGAACATCCATCTTCTCAGTCTGGGGAGCGGATCCACAA 1795
Qy 1189 CTTCTGATGAGAGCTTTGTTTACAGTTTCAGAGTGAAGCTAA 1235
Db 1796 CTTCTGACACTCTTCCATATTTGACATTAAGAGATTCAGCTACA 1842

RESULT 11

US-09-016-434-1283
; Sequence 1283, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1242 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g297101
; US-09-016-434-1283

Query Match 22.3%; Score 291.8; DB 4; Length 1242;
Best local Similarity 58.2%; Pred. No. 3,4e-86;
Matches 572; Conservative 0; Mismatches 402; Indels 9; Gaps 3;

Qy 289 TTTGGGCGACCCCTCATCTTGAAGTGGAGAGCTGGTGAAGGCTTTTNGGACA 348
Db 130 TTTGGGAAATGGAACATACGTGAACCTGACAACTGGAGAGGGACCTTANGCCACA 189
Qy 349 GTTTACAGGGAGATTGACAAATTAATGACAACTAGTGGCTTTAAAGTCATCAGCATG 408
Db 190 GTCTTCAAGGGCCGACAACTGACGGAACCTTGTGGCCCTGAAAGAGATCCGGCTG 249
Qy 409 AATGACAGAGAGAGTCCATTTTACAGCTATTCGAGAGAGCTTCTCTGAAAGGTTTG 468
Db 250 GAGCAGCAGAGAGAGGAGCGCCCTGACATGCGATCCGAGAGGTGTCTGTGTAAGAACCTG 309
Qy 469 AAACATGCCAATATTTGTGCTCTGATGACATATTCACACAAAGAGACATGACATTTC 528

Db 310 AAGCAGCCCAATATTTGTATACCTTGATACCTCATCCACAGATGCGTCTCACCGT 369
Qy 529 GTTTTGAATATGACACACAGACCTGGCCAGTATATGTCTCAGCATTCAGAGAGGCTT 588
Db 370 GTTTTGAATATGACACAGATGACCTGAAGCAGTATGAGACCACTGTGGAACTCATG 429
Qy 589 CATCTCATATATGTAGACTTTTCAATTTTCACTTTTGGCGGGCGTGGCATTCAC 648
Db 430 AGCATGCAACAGCTAAATTTTCATGTTTCAAGCTGCTCCGGGCGTGGCTTACTGTAC 489
Qy 649 CACCAACAGTCTTTCACAGGAGCTGAAACCTGAACTTCACTTATCATGATCAGCTGGGA 708
Db 490 ACCCGAAGATCTCTCACCGGAGCTGAAGCCGAGAACCTGCTCATCAAGAGAGGGGG 549
Qy 709 GAGCTCAACAGTGTGATTTTGTCTTGGCCCGGGCCAGATCATTTCCAGCCAGCATAC 768
Db 550 GAGCTGAAGCTGGCGGACTTTGGAAGTGGCCAGGGCCAGTCAAGTCCCAAGACCTTAC 609
Qy 769 TCTTCAGAGTGTGACCTCTGTGTAACCGGCCCTGATGCTTGTGGAGGCCACTGA 828
Db 610 TCCATGAGGTGTGACCTCTGTGTAACGGCCCGCATGCTGTGAGATCCAGAG 669
Qy 829 TATCTCTGAGCTGACATATGAGGTGACAGCTGATCTTATTTGAATGTTCCAGGAT 888
Db 670 TACTCCACCCCATTTGCTATGTGGGGCGTGGCTGATCAGTACAGATGGCCACAGGG 729
Qy 889 CAACCTTTGTTCTTGGGGGTTTCCAACTCTTGAACAGCTGAGAAATCTGGAGAGT 948
Db 730 AGGCCCTCTTCTCC---GGGCTCCAGTCAAGGAGGAGCTGACCTCATCTTTGGCCTC 786
Qy 949 CTGGAGTCCCTACAGAGATATCTGGCCGGAGTCTCAAGCTACCTAATCAATCA 1008
Db 787 CTGGGAGCCCAAGAGAGAGCTGGCCGGCGTACCGCTTCTTGAAGTTCCGACAC 846
Qy 1009 GAATGTTCCCACTGCTACGCTCGAAGCTTCAATGTTGTGTAAGAGAGCTGGAGAG 1068
Db 847 TACAGCTTC--CTGTCTACCTCCGCGAGCC---GCTCATCAACAGCGCCAGGTTG 900
Qy 1069 GTTCTGAAGTGAAGAGCTGGCCCTCCAGATGCTTAAAGCTTTCCAGAGACCGCTC 1128
Db 901 GATACGAGATGCGATCACCCTCTGAGAGCCGTCTGTATGAATCCAAAGATGCGATG 960
Qy 1129 TCCGCCAGAGAGCACTTTGATGATATTTACAGGCGCTGCTCAGCTGATCAG 1188
Db 961 TAGAGAGGCTGCTGATGATCTTCTTCCGCTCTTGGAGAGCTGTGACCGAG 1020
Qy 1189 CTTCTGATGAGAGCTTTTGTATCAAGTTTCAGAGTGAAGCTTAAAGCAGAAATGTGT 1248
Db 1021 CTTGAAGACATGCTTCATCTTCTCCGAAAGGATCAGCTCCAGAAAGACCGAGC 1080
Qy 1249 GACCTTTTGGCTCTTACCAAA 1271
Db 1081 TACCGAGGCTTGGCTTCCAGCA 1103

RESULT 12

US-08-154-915-1
; Sequence 1, Application US/08154915
; Patent No. 5618669
; GENERAL INFORMATION:
; APPLICANT: Beach, David
; APPLICANT: Xiong, Yue
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,915
FILING DATE: 19-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 13..888
US-08-154-915-1

Query Match 16.5%; Score 216.2; DB 1; Length 1089;
Best Local Similarity 57.1%; Pred. No. 4,1e-61;
Matches 414; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

QY 307 TACTTGAACTTGAGAGCTGGGTGAGGCTTTATGCGACAGTTTACAGAGGGATTAGC 366
DB 22 TACGAGAACTGGAAGATTGGGAGGACCTACGAACTGTGTTCAAGGCCAAGAAC 81
QY 367 AGAATTAATGACACATAGTGGCTTTAAAGTATCAGCATGAATGACAGGAA--GGA 423
DB 82 CGGAGACCTCATGAGATGCTGCTTAAACGGGTGAGGCTGATGCATGATGAGGAT 141
QY 424 GTCCCATTTACAGACTTCGAGAGAGCTTCTCTCGAAGGGTTTGAACATGCAATATT 483
DB 142 GTGCCAGATTCCGCCCTCCGGAGATCTGCTTACTCAAGAGCTGAAGCAAGAACATC 201
QY 484 GTGCTCTCATGACATTAATCCACACAAAGACACATGACATTCGTTTTTGAATCATG 543
DB 202 GTGAGGCTTCATGAGCTCTGCGACAGCAGCAAGAACTGACTTTGTTTTGAATTTCTG 261
QY 544 CACACAGACCTGGCCAGTATATGTTCAGCATCCAGAGGGCTTATCTCTAATATGTC 603
DB 262 GACACAGACCTGAAGAGTATTTGACAGTTCATGAGGAGCTCATCTCGATTTGTA 321
QY 604 AGACTTTTATGTTTCAACTTTTGGCGGGCTGGCGTACATCCACCAACACGTTCTT 663
DB 322 AAGTATTTCTCTTCAAGTACTTAAGAGGCTGGATTCTGTATAGCCGCAATGTGCTA 381
QY 664 CACAGGAGCTTGAACCTCAGAACTTACTATCAGTACCTGGAGAGCTCAAACTGGCT 723
DB 382 CACAGGAGCTTGAAGCCCGCAGAACTGTATTAACAGAAATGGGAGCTGAATTTGGCT 441
QY 724 GATTTTGGTCTTGCCCGGGCCAAAGTCATTTCCAGCAGACATATCTTCAAGATGCTG 783

DB 442 GATTTTGGCTCTGAGACCTTTTGGGATTTCCCGTCCGTGTTACTAGCTAAGTGTGTC 501
QY 784 ACCCTCTGTACCGGCCCCCTGATGCTTTGCTGGAGCCACTGAATATTTCTGTAGCTG 843
DB 502 ACACGTGTGTACCGCCACCGGATGCTTTGGGGCCAAAGCTGTACTCAAGTCCATC 561
QY 844 GACATATGGGGTGCAGAGCTGATCTTTTATTTGAATGTTCCAGAGGTCAACCTTTTCT 903
DB 562 GACATGTGTGTCAGCCGGCTGATCTTTTGAAGCTGGCCAAATGCTGGGGCGGCTCTTTT 621
QY 904 GGGGTTTCCACATCTCTTGAACAGCTGGAGAAATCTGGAGAGTGTGGAGTCCCTACA 963
DB 622 CCGGCAATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681
QY 964 GAGATATCTTGGCCGGAGCTTCCAGCTACCTTAACCTAATCAAGATGTTCCACTG 1023
DB 682 GAGAGACAGTGGCCCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 741
QY 1024 CCTAC 1028
DB 742 GCCAC 746

RESULT 13
US-08-464-517-37
Sequence 37, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 13..888

US-08-464-517-37

Query Match 16.5%; Score 216.2; DB 2; Length 1089;
Best Local Similarity 57.1%; Pred. No. 4.1e-61;
Matches 414; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

QY 307 TACTTGAACCTTGGAGAAAGCTGGGTGAAAGGCTCTTATGCGACATTTTACAAAGGGATTAAC 366
DB 22 TACGAGAACTGGAAGAAAGATTTGGGAGGACCTTACGAACTGTGTTCAGAGGCCAAAAAC 81
QY 367 AGAATAAATGCAACAATACTAGTGGCTTTTAAAGTATCATGAGATGATGAGAGAA---GGA 423
DB 82 CGGAGAGCTCATGAGATCGTGGCTCTTAAACGGGTGAGGCTGATGACATGATGAGGGT 141
QY 424 GTCCCATTTACAGCTATCGGAGAAAGCTTCTCTCTGAAAGGTTTGAACATGCGAAATT 483
DB 142 GTCCGAGTTCCTCCCTCCCGGAGATCTGCTCTCAAGAGCTGAAGACCAAGAACATC 201
QY 484 GTGCTCCTGATGATCAATTAATCCACACCAAGAGACATGATTCGTTTGTGAAATACATG 543
DB 202 GTACAGCTTATATACCTCTGCAAGAGACAGAAAGCTGATTTGTGAAATCTGT 261
QY 544 CACACAGACCTGGCCAGATATATGCTCAAGATCCAGAGGCTTATCTCTCAATATGTC 603
DB 262 GACCAAGACCTGAAGAAGTATTTGAACATGCAATGCTGATCTGATCTGAGATTGTA 321
QY 604 AGACTTTTCACTTTTCACTTTTGGGGGCTGGCTGATCCACCAACACAGTTCTT 663
DB 322 AAGTCATTCCTCTTCAGCTACTTAAAGGCTGGGATTCGTCTATGACCGCAATGTGCTA 381
QY 664 CACAGGAGACCTGAAACCTTCAAGATTAATCTATCATGATCACTGGGAGGCTCAAACTGGCT 723
DB 382 CACAGGAGACCTGAAAGCCCAAGACCTGCTATTAACAGAAATGGGAGCTGAATTTGGCT 441
QY 724 GATTTTGTCTTGGCCCGGAGCAAGTCATTTCCAGCAGACATATCTTTCAGAAAGTCGTG 783
DB 442 GATTTTGTCTTGGCTGAGGCTTTGGGATTTCCGTCCTGTTACTCAGTGAGGTGGTC 501
QY 784 ACCCTGCTGTAACCGGCCCCCTGATGCTTTGCTGGAGCCCACTGAATATCTCTTGAGCTG 843
DB 502 AACCTGTGTGACCGCCACCGAGATGCTCTTTGGGCGCAAGCTGATCAACGTCATC 561
QY 844 GACATATGAGGAGTGCAGAGCTGATCTTATTAAGAAATGTTCCAGGGCTCAACCTTTGTTTCT 903
DB 562 GACATGTGTGACCGGCTGATCTTTGCAAGAGCTGGCAATGCTGGGCGCTCTTTT 621
QY 904 GGGGTTTCCAACTCTTGAACAGCTGAGAAATGTGGAGGTGCTGGAGTCCCTACA 963
DB 622 CCGGCAATGATGTCCATGACCACTTGAAGAGATCTTCCACTGCTGGGAGAGCCACC 681
QY 964 GAGGATATTTGGCCGGAGTCTCAAGCTAACCTTAATCAATCCAGAAATGTTCCACTG 1023
DB 682 GAGGAGCAAGTGGCCCTTATGACCAAGCTGCCAGACTAATAGCCCTATCCGATGTACCG 741
QY 1024 CCTAC 1028
DB 742 GCCAC 746

RESULT 14
US-08-246-361A-37
Sequence 37, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mathew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 13..888

US-08-246-361A-37

Query Match 16.5%; Score 216.2; DB 2; Length 1089;
Best Local Similarity 57.1%; Pred. No. 4.1e-61;
Matches 414; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

QY 307 TACTTGAACCTTGGAGAAAGCTGGGTGAAAGGCTCTTATGCGACATTTTACAAAGGGATTAAC 366
DB 22 TACGAGAACTGGAAGAAAGATTTGGGAGGACCTTACGAACTGTGTTCAGAGGCCAAAAAC 81
QY 367 AGAATAAATGCAACAATACTAGTGGCTTTTAAAGTATCATGAGATGATGAGAGAA---GGA 423
DB 82 CGGAGAGCTCATGAGATCGTGGCTCTTAAACGGGTGAGGCTGATGACATGATGAGGGT 141
QY 424 GTCCCATTTACAGCTATCGGAGAAAGCTTCTCTGAAAGGTTTGAACATGCGCAATTT 483
DB 142 GTCCGAGTTCCTCCCTCCCGGAGATCTGCTTACTCAAGAGCTGAAACCAAGAAACATC 201
QY 484 GTGCTCCTGATGATCAATTAATCCACACCAAGAGACATGATTCGTTTGTGAAATACATG 543
DB 202 GTACAGCTTATATACCTCTGCAAGAGACAGAAAGCTGATTTGTGAAATCTGT 261
QY 544 CACACAGACCTGGCCAGATATATGCTTCAGATCCAGAGGCTTATCTCATATATGTC 603
DB 262 GACCAAGACCTGAAGAAGTATTTGACAGTTGCAATGATGATGATCTGAGATTGTA 321
QY 604 AGACTTTTCACTTTTCACTTTTGGGGGCTGGCTGATCCACACCAACAGATCTT 663
DB 322 AAGTCATTCCTCTTCAGCTACTTAAAGGCTGGGATTCGTCTATGACCGCAATGTGCTA 381
QY 664 CACAGGAGACCTGAAACCTCAGAACTTACTCATGATCACTGGAGAGCTCAAACTGGCT 723
DB 382 CACAGGAGACCTGAAGCCCAAGACCTGCTATTAACAGAAATGGGAGCTGAATTTGGCT 441
QY 724 GATTTTGTCTTGGCCCGGAGCAAGTCATTTCCAGCAGACATATCTTTCAGAAAGTCGTG 783
DB 442 GATTTTGTCTTGGCTGAGGCTTTGGGATTTCCGTCCTGTTACTCAGCTGAGGTGGTC 501

QY 784 ACCCTCTGATACCGCCCTTATGCTTCTGGAGCACTGATATATCTCTGAGCTG 843
 Db 502 AACCTGTGTACCGCCGACCGATGTCCTTTGGGCGCAAGCTGATCTCAAGTCCATC 561
 QY 844 GACATATGGGAGGCGAGCTGATCTTATTTGAATGTTCCAGGATCAACCTTTGTTCT 903
 Db 562 GACATGTGTACCGCCGCTGATCTTGTGCAAGAGCTGCAATGCTGGGCGGCTTTT 621
 QY 904 GGGGTTTCCACATCTCTGAAAGCTGAGAAATCTGGAGGTCGCTGGAGTCCCTACA 963
 Db 622 CCGGGAATGATGTGATGATGACAGTTGAGAGGATCTTCCGACTGCTGGGAGCGCCACC 681
 QY 964 GAGGATCTTGGCCGGGAGTCTCCAACTAATCTAATCAATCAGAAATGTTCCACTG 1023
 Db 682 GAGGAGCACTGGCCCTTATGACCAAGCTGCCAGACTAATAGCCCTATCCGATGTAACCG 741
 QY 1024 CCTAC 1028
 Db 742 GCCAC 746

RESULT 15

US-08-463-772-37

Sequence 37, Application US/08463772

Patent No. 6066501

GENERAL INFORMATION:

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,772

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mathew P. Vincent

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MII-004C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1089 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 13..888

US-08-463-772-37

Query Match 16.5%; Score 216.2; DB 3; Length 1089;
 Best Local Similarity 57.1%; Pred. No. 4,1e-61;
 Matches 414; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

QY 307 TACTTGAACCTTGGAGAGCTGGGTGAGGCTTTATGACACAGTTTACAAAGGATTTAGC 366
 Db 22 TACGAGAACTGAGAAAGATTGGGAGGACACTGAGAACTGTGTCAAGGCCAAAGAAC 81
 QY 367 AGAATTAATGACAACTAGTGGCTTTAAAGTATCAGATGATGACAGAGAA--GGA 423
 Db 82 CCGGAGACTCATGATGATGCTGCTTAAACGGGTGAGGCTGGATGACATGATGAGGCT 141
 QY 424 GTCCATTACAGCTATCCGAGAGCTTCTCTGAAAGGTTTGAATGCAATATT 483
 Db 142 GTCCGAGTTCCGCTCCGGAGATCTGCTTACTCAAGAGCTGAAGCAAGAACATC 201
 QY 484 GTGCTCTCGATGACATTAATCCACCAAGAGACACTGACATTCGTTTTTGAATCATG 543
 Db 202 GTACAGCTTCATGACCTCTGACACAGGACCAAGAGCTGATCTTTGATTTCTGT 261
 QY 544 CACACAGACCTGAGCCAGTATATGTCAGCATCCAGAGGAGCTTCATCTCAATATGTC 603
 Db 262 GACAGAGACTGAGAAATGATTTTGAAGTTGCAATGATGAGCTGATCTGATGATGTA 321
 QY 604 AGACTTTTATGTTTCAATTTTGGGGGCTGGGCTATATCCACCAACACCTTCTT 663
 Db 322 AAGTCAATTCCTTTCAGCTACTTAAAGGGCTGGGATTTGTCTATGACGCAATGTGCTA 381
 QY 664 CACAGGAGCTGAGAACTCAGAACTTACTCATGATGACCTGGAGAGGCTCAAACTGGCT 723
 Db 382 CACAGGAGCTGAGAACTCAGAACTTACTCATGATGACCTGGAGAGGCTGAAATTTGGCT 441
 QY 724 GATTTTGTCTTGGCCCGGAGCAAGTCCATTCACAGCAGACATCTTTCAGAAATGCTG 783
 Db 442 GATTTTGGCTGTGCTGAGCTTTGGGATTTCCGTCGCTGTTACTCACTGAGGTGTC 501
 QY 784 ACCCTCTGATACCGGCCCTGATGCTTGTGAGAGCCACTGAAATATCTCTGAGCTG 843
 Db 502 AACCTGTGTACCGCCGACCGATGTCCTTTGGGCGCAAGCTGATCTCAAGTCCATC 561
 QY 844 GACATATGGGAGGCGAGCTGATCTTATTTGAATGTTCCAGGATCAACCTTTGTTCT 903
 Db 562 GACATGTGTACCGCCGCTGATCTTTTGAAGAGCTGCGCAATGCTGGGCGGCTCTTTT 621
 QY 904 GGGGTTTCCACATCTCTGAAAGCTGAGAAATCTGGAGGTCGCTGGAGTCCCTACA 963
 Db 622 CCGGGAATGATGTGATGATGACAGTTGAGAGGATCTTCCGACTGCTGGGAGCGCCACC 681
 QY 964 GAGGATCTTGGCCGGGAGTCTCCAACTAATCTAATCAATCAGAAATGTTCCACTG 1023
 Db 682 GAGGAGCACTGGCCCTTATGACCAAGCTGCCAGACTAATAGCCCTATCCGATGTAACCG 741
 QY 1024 CCTAC 1028
 Db 742 GCCAC 746

Search completed: December 27, 2004, 11:08:27
 Job time : 70.1305 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 17:40:11 ; Search time 2501.82 Seconds
(without alignments) 19051.434 Million cell updates/sec

Title: US-10-786-065-4

Perfect score: 1308

Sequence: 1 atgggtcaagcgtcgtgc.....agttacgaatcgtcgtga 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	687	52.5	804	4	BI755983	603030316
2	652.4	49.9	766	2	BE562611	601336446
3	592.8	45.3	602	6	CD636753	560150098
4	591.6	45.2	598	6	CD636752	560150017
5	583.2	44.6	601	6	CD636760	560150897
6	580.8	44.4	600	6	CD636754	560150097
7	578.6	44.2	602	6	CD636748	560149737
8	574.2	43.9	602	6	CD636751	560150018
9	573.6	43.9	596	6	CD636758	560150257
10	570.4	43.6	598	6	CD636740	560149017
11	566.6	43.3	602	6	CD636757	560150258
12	565.8	43.3	602	6	CD636759	560150894
13	564.2	43.1	601	6	CD636746	560149253
14	560	42.8	602	6	CD636755	560150178
15	557.2	42.6	587	6	CD636750	560149817
16	557.2	42.6	598	6	CD636756	560150177
17	536.4	41.0	586	6	CD636749	560149817
18	534.6	40.9	600	6	CD636739	560149018
19	520.6	39.4	603	6	CD636742	560149093
20	514.8	39.4	600	6	CD636741	560149098
21	512.4	39.2	538	6	CD636744	560149170
22	512.4	39.2	599	6	CD636747	560149738
23	500.2	38.2	623	4	BM539173	BM50512.9
24	481	36.8	481	1	AA436054	zuo1c12.r

25	476	36.4	499	5	BX283916	BX283916
26	472.4	36.1	586	6	CD636745	CD636745
27	444.6	34.0	660	4	BD326162	BD326162
28	388.2	29.7	540	9	CG523756	CG523756
29	370.2	28.3	3067	3	AK087398	AK087398
30	367	28.1	2435	3	AK083269	AK083269
31	348.2	26.6	745	6	CB518516	CB518516
32	346.2	26.5	580	4	BI345276	BI345276
33	340.8	26.1	471	4	BO720115	BO720115
34	333.4	25.5	471	3	AK051283	AK051283
35	332	25.4	468	4	BG772738	BG772738
36	327.4	25.0	729	6	CB525597	CB525597
37	325.4	24.9	1322	9	AY406869	AY406869
38	325.2	24.9	879	5	BO220223	BO220223
39	323.6	24.7	731	6	CF536868	CF536868
40	319.4	24.4	762	6	CB523552	CB523552
41	318.2	24.3	1290	9	AY406870	AY406870
42	318	24.3	633	6	CB522451	CB522451
43	316.8	24.2	598	5	BU265800	BU265800
44	316.4	24.2	786	7	CN537781	CN537781
45	314.8	24.1	929	5	BU464167	BU464167

ALIGNMENTS

RESULT 1
BI755983
LOCUS 603030316F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5200755 5',
DEFINITION mRNA sequence.
ACCESSION BI755983
VERSION BI755983.1 GI:15747561
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 804)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1502 row: p column: 04
High quality sequence stop: 797.
Location/Qualifiers

FEATURES
source 1..804
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5200755"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains; Age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 52.5%; Score 687; DB 4; Length 804;

Best Local Similarity 97.5%; Pred. No. 2.5e-196;
Matches 740; Conservative 0; Mismatches 15; Indels 4; Gaps 4;

QY 1 ATGGGTCAAGAGCTGTGTGCAAGAGCTGTACAGCTGTGATGACGTGTCTACATTGTCA 60
Db ATGGGTCAAGAGCTGTGTGCAAGAGCTGTACAGCTGTGATGACGTGTCTACATTGTCA 104
QY 61 GAGGAGGGGAGGACACACAGCTGTGAGAGAGTCAAGCTGTGACACACAGAGGCTGGCTTC 120
Db GAGGAGGGGAGGACACACAGCTGTGAGAGAGTCAAGCTGTGACACACAGAGGCTGGCTTC 164
QY 121 AAGCTAACAGACCTTAAAGAGCATGTCTCATGACTTCACTTACCCCAAGGACTT 180
Db AAGCTAACAGACCTTAAAGAGCATGTCTCATGACTTCACTTACCCCAAGGACTT 224
QY 181 CAAGTCCCGCTGCCCAGAAATTCAAGAGTAAAGGCCAGAGTAACAGTATGTTTT 240
Db CAAGTCCCGCTGCCCAGAAATTCAAGAGTAAAGGCCAGAGTAACAGTATGTTTT 284
QY 241 CAGGAAGAGATTTGAGGCAAGGTTTTCACTGAGAGAGAGCTCCCTTTTGGGGCAGCC 300
Db CAGGAAGAGATTTGAGGCAAGGTTTTCACTGAGAGAGAGCTCCCTTTTGGGGCAGCC 344
QY 301 TCATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGAGGG 360
Db TCATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGAGGG 404
QY 361 ATTACAGAAATAAATGAGCAACACTAGTGGCTTTAA-AGTCATCAGCATGATGCAAGAGA 419
Db ATTACAGAAATAAATGAGCAACACTAGTGGCTTTAA-AGTCATCAGCATGATGCAAGAGA 464
QY 420 AAGAGTCCCATTTTACAGCTATCCGAGAGCTTCTCTGAGAGGTTTGAACATGCCAA 479
Db AAGAGTCCCATTTTACAGCTATCCGAGAGCTTCTCTGAGAGGTTTGAACATGCCAA 524
QY 480 TATTGCTCTGTCATGA-CATATCCACACCAAGACACTGACATTGGTTTTGAAT 538
Db TATTGCTCTGTCATGA-CATATCCACACCAAGACACTGACATTGGTTTTGAAT 584
QY 525 TATTGCTCTGTCATGACATATCAACCAAGACACTGACATTGGTTTTGAAT 584
Db TATTGCTCTGTCATGACATATCAACCAAGACACTGACATTGGTTTTGAAT 644
QY 539 AC-ATGCAACAGACCTGGGCCAGTATATGTCTCAGCATTCAGAGAGGCTTCACTCTCAT 597
Db AC-ATGCAACAGACCTGGGCCAGTATATGTCTCAGCATTCAGAGAGGCTTCACTCTCAT 644
QY 598 AATGTGAGCTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAC 657
Db AATGTGAGCTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAC 704
QY 645 AATGTGAGCTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAC 704
Db AATGTGAGCTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAC 764
QY 658 GTTCTTCAAGGAGCTGAAACCTCAGAACTTATCATCATGCTCACT-GGGAGAGCTCAA 716
Db GTTCTTCAAGGAGCTGAAACCTCAGAACTTATCATCATGCTCACT-GGGAGAGCTCAA 764
QY 717 ACTGCTGATTTTGTGCTTGGCCGGGCAAGTCAATTC 755
Db ACTGCTGATTTTGTGCTTGGCCGGGCAAGTCAATTC 803

RESULT 2
BS62611 766 bp mRNA linear EST 15-AUG-2000
LOCUS 60136446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5',
DEFINITION mRNA sequence.
ACCESSION BS62611
VERSION BS62611.1 GI:9806331
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Query Match 49.9%; Score 652.4; DB 2; Length 766;
Best Local Similarity 97.6%; Pred. No. 7.7e-186;
Matches 736; Conservative 0; Mismatches 11; Indels 7; Gaps 7;

QY 123 GCTAACAGACTTAAAGAGCATCATGTTCCATGACTTCACTTACACCCAGGGACTTCA 182
Db GCTAACAGACTTAAAGAGCATCATGTTCCATGACTTCACTTACACCCAGGGACTTCA 77
QY 183 AGCTGCCGTGCGGAGGTTCAAGATTAAGGCGAGAGTAACAGTATGTTTCA 242
Db AGCTGCCGTGCGGAGGTTCAAGATTAAGGCGAGAGTAACAGTATGTTTCA 136
QY 243 GGAAGAGATCTGAGGCAAGGTTTTCACTGAGAGAGAGCTCCCTTTTGGGGCAGCTC 302
Db GGAAGAGATCTGAGGCAAGGTTTTCACTGAGAGAGAGCTCCCTTTTGGGGCAGCTC 195
QY 303 ATCTTACTTGAACCTTGAAGAGCTGGTGAAGGCTTTATGCGACAGTTTCAAGGGGAT 362
Db ATCTTACTTGAACCTTGAAGAGCTGGTGAAGGCTTTATGCGACAGTTTCAAGGGGAT 255
QY 363 TAGCAGAAATAATGAGCAACACTAGTGGCTTTAAAGTCATCAGATGAGAGAGAGG 422
Db TAGCAGAAATAATGAGCAACACTAGTGGCTTTAAAGTCATCAGATGAGAGAGAGG 315
QY 423 AGTCCATTTACAGCTATCCGAGAGCTTCTCTCTGGAAGGTTTGAACATGCCAATAT 482
Db AGTCCATTTACAGCTATCCGAGAGCTTCTCTCTGGAAGGTTTGAACATGCCAATAT 375
QY 483 TGTGCTCTGTCATGACATATTCACACCAAGAGCACTGACATTCGTTTTGAATATAT 542
Db TGTGCTCTGTCATGACATATTCACACCAAGAGCACTGACATTCGTTTTGAATATAT 434
QY 543 GCACACAGACCTGGGCCAGTATATGTCTCAGATCAGAGAGGCTTCACTCCATTAATGT 602
Db GCACACAGACCTGGGCCAGTATATGTCTCAGATCAGAGAGGCTTCACTCCATTAATGT 494
QY 603 CAGACTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAGCTTCT 662
Db CAGACTTTTCACTGTTTCACTTTTGGGGGCTTGGCTTATCCACCAACAGCTTCT 554
QY 663 TCACAGGAGACTGAAACCTCAGAACTTATCTCATGCTGAGAGAGCTCAAACTGGC 722
Db TCACAGGAGACTGAAACCTCAGAACTTATCTCATGCTGAGAGAGCTCAAACTGGC 614
QY 723 TGATTTTGTGCTGCGGGGCAAGTCAATTCAGGCAAGCATCTTTCAGAAAGTGAT 782

ORIGIN

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://Image.lnl.gov
Plate: LNC386 row: 12
High quality sequence stop: 714.
Location/Qualifiers
1. 766
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3690395"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_44"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
BclRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."


```

Db      615 TGAATTTGATCTTGGCCCGGGCC-AGTCCATTTCCACCGCAGACATCTTTCAGAACTCGT 673
Qy      783 GACCTCTGTGATACCGGCCCCCTGTATCTTGTCTGGAGCAGCAATATTCCTAGCT 842
Db      674 GAACCTCTGTGTA-CGGCCCCCTGTATGC-TTGTCTGGAGCAGCAATATTCCTAGCT 731
Qy      843 GGACATATGGGGTGCAGGCTGCATCTTTATTGA 876
Db      732 GGACCTATGGGGTGCAGCTGTCTTATTATGCA 765

RESULT 3
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LOCUS      CD636753      602 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 56015009H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD636753
VERSION     CD636753.1 GI:40285020
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 602)
AUTHORS     Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE       Circular rapid amplification of cDNA ends for high-throughput
            Genomics 84 (1), 205-210 (2004)
JOURNAL     Contact: Fu GK
COMMENT      Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
            Location/Qualifiers
                source          1..602
                               /organism="Homo sapiens"
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                               /db_xref="taxon:9606"
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Best Local Similarity 99.7%; Pred. No. 8.3e-168;
Matches 594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

410 ATGCAGAGGAGAGATCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTGA 469
Db      6 AGCGAGAGAGAGAGATCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTGA 65
Qy      470 AACATGCCAATATTGTGCTCTGCATGACATATTCACACCAAGAGACATGACATTG 529
Db      66 AACATGCCAATATTGTGCTCTGCATGACATATTCACACCAAGAGACATGACATTG 125
Qy      530 TTTTGAATACATGACACAGACCTGGGCCAGTATATGTCTCAGCATCCAGAGGGCTTC 589
Db      126 TTTTGAATACATGACACAGACCTGGGCCAGTATATGTCTCAGCATCCAGAGGGCTTC 185
Qy      590 ATCTCATATATGTCAGACTTTTCATGTTTCACTTTGGGGGGCTGGGGTACATCAC 649
Db      186 ATCTCATATATGTCAGACTTTTCATGTTTCACTTTGGGGGGCTGGGGTACATCAC 245
Qy      650 ACCAACACGTTTTCACAGGAGCCTGAAACCTCAGAACTTACTCATCACTGACCTGGAG 709
Db      246 ACCAACACGTTTTCACAGGAGCCTGAAACCTCAGAACTTACTCATCACTGACCTGGAG 305
Qy      710 AGCTCAAACTGGCTGATTTTGGTCTTGGCCGGGCAAGTCCATTCAGACCCAGACTACT 769
Db      306 AGCTCAAACTGGCTGATTTTGGTCTTGGCCGGGCAAGTCCATTCAGACCCAGACTACT 365
Qy      770 CTTCAGAAAGTCTGACCTCTGTGATCCGGCCCCCTGTATCTTGTCTGGAGCCACTGAAT 829
Db      366 CTTCAGAAAGTCTGACCTCTGTGATCCGGCCCCCTGTATCTTGTCTGGAGCCACTGAAT 425

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Qy      830 ATTCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTGAAATGTTCCAGGTC 889
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Qy      890 AACCTTGTCTCTGGGGTTTCCACATCTTGAACAGCTGGAGAAATCTGGAGAGTGC 949
Db      486 AACCTTGTCTCTGGGGTTTCCACATCTTGAACAGCTGGAGAAATCTGGAGAGTGC 545
Qy      950 TGGAGTCCCTACAGAGATACCTTGGCCGGAGTCTCCAGTACTCACTAACAAT 1005
Db      546 TGGAGTCCCTACAGAGATACCTTGGCCGGAGTCTCCAGTACTCACTAACAAT 601

RESULT 4
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LOCUS      CD636752      598 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 56015001J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD636752
VERSION     CD636752.1 GI:40285019
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 598)
AUTHORS     Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE       Circular rapid amplification of cDNA ends for high-throughput
            Genomics 84 (1), 205-210 (2004)
JOURNAL     Contact: Fu GK
COMMENT      Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
            Location/Qualifiers
                source          1..598
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                               /db_xref="taxon:9606"
                               /clone_1fb="FLP"
                               /note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match      45.2%; Score 591.6; DB 6; Length 598;
Best Local Similarity 99.3%; Pred. No. 1.9e-167;
Matches 594; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

408 GAATGCAAGAGAGAGATCCCATTTACAGCTATCCGAGAGCTTCTCTCTGAAGGTTT 467
Db      598 GAGCCAGAGAGAGAGATCCCATTTACAGCTATCCGAGAGCTTCTCTCTGAAGGTTT 539
Qy      468 GAAATGCCAATATTGTGCTCTGCATGACATATTCACACCAAGAGACATGACATT 527
Db      538 GAAATGCCAATATTGTGCTCTGCATGACATATTCACACCAAGAGACATGACATT 479
Qy      528 CGTTTGAATACATGACACAGACCTGGCCAGTATATGTCTCAGATCCAGAGGGCT 587
Db      478 CGTTTGAATACATGACACAGACCTGGCCAGTATATGTCTCAGATCCAGAGGGCT 419
Qy      588 TATCTCTATATATGTCAGACTTTTCATGTTTCACTTTGGGGGGCTGGGGTACATCA 647
Db      418 TATCTCTATATATGTCAGACTTTTCATGTTTCACTTTGGGGGGCTGGGGTACATCA 359
Qy      648 CCACCAACGTTTTCACAGGAGCCTGAAACCTCAGAACTTACTCATCACTGACCTGGAG 707
Db      358 CCACCAACGTTTTCACAGGAGCCTGAAACCTCAGAACTTACTCATCACTGACCTGGAG 299
Qy      708 AGAGCTCAAACTGGCTGATTTTGGTCTTGGCCGGGCAAGTCCATTCAGACCCAGACTA 767
Db      298 AGAGCTCAAACTGGCTGATTTTGGTCTTGGCCGGGCAAGTCCATTCAGACCCAGACTA 239
Qy      768 CTTCAGAAAGTCTGACCTCTGTGATCCGGCCCCCTGTATCTTGTCTGGAGCCACTGA 827

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Db	238	CTCTTCAGAAAGTCGTGACCCCTCTGGTACCGGCCCTCTGATCTCTTTCGCTGGAGGCACCTGA	179
Qy	828	ATATTTCTCTGAGCTGACATATATGGGGTGCAGGCTGCATCTTTATTTGAAATGTTCCAGG	887
Db	178	ATATTTCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAAATGTTCCAGG	119
Qy	888	TCAACCTTTGTTTCTCTGGGGTTTCCAAATCCTTGAAACAGCTGAGAAATCTGGAGGT	947
Db	118	TCAACCTTTGTTTCTCTGGGGTTTCCAAATCCTTGAAACAGCTGAGAAATCTGGAGGT	59
Qy	948	GCTGGAGATCCCTTCAGAGATCTTGGCGGGGAGTCTTCCAAGTACTTAATCTAAAT	1005
Db	58	GCTGGAGATCCCTTCAGAGATCTTGGCGGGGTTCTTCCAAGTACTTAATCTAAAT	1

RESULT 5			
CD636760			
LOCUS	CD636760	601 bp	mRNA
DEFINITION	56015089J1	FLP Homo sapiens cDNA, mRNA sequence.	linear
Accession	06027820		
			EST 12-JAN-2004

VERSION	CD636760.1	GI:40285027
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE
1 (bases 1 to 601)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE	Circular rapid amplification of cdna ends for high-throughput
AUTHORS	extension cloning of partial genes
JOURNAL	Genomics 84 (1), 205-210 (2004)

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES	LOCATION/Qualifiers
source	1. .601

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/organism="Homo sapiens"
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Query March	44.6%;	Score 583.2;	DB 6;	Length 601;
Best Local Similarity	99.5%;	Pred. No. 6.8e-165;		
Matches 585;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY	410	ATGAGAGGAGAGAGAGTCCCATTTTACAGTATCCGAGAAAGCTTCTCTCTGAAAGGTTTGA	463
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QY	470	AACATGCAATATATGTGCTCCTGATGACATATATCCACCAAGAGACATGACATTGG	529
Db	66	AACATGCAATATATGTGCTCCTGATGACATATATCCACCAAGAGACATGACATTGG	125
QY	530	TTTTTGATATCATGACACACAGACCCTGGCCAGTATATGTCTCAGCATCAGAGGGCTTC	589
Db	126	TTTTTGATATCATGACACACAGACCCTGGCCAGTATATGTCTCAGCATCAGAGGGCTTC	185
QY	590	ATCCTCATATATGTCAGACTTTTTCATGTTTCAACTTTTGGCGGGGCTGGCGTATCCACC	649
Db	186	ATCCTCATATATGTCAGACTTTTTCATGTTTCAACTTTTGGCGGGGCTGGCGTATCCACC	245
QY	650	ACCACACAGTCTTTCACAGGGAAGCTGAAGACTCAGAACTTCTCATCAGTCACTCGGGAG	709
Db	246	ACCACACAGTCTTTCACAGGGAAGCTGAAGACTCAGAACTTCTCATCAGTCACTCGGGAG	305
QY	710	AGCTCAAACTGGCTGATTTTGGCTGCTGGCCGGGGCAAGTCCATTCGAGCGACATATCT	769
Db	306	AGCTCAAACTGGCTGATTTTGGCTGCTGGCCGGGGCAAGTCCATTCGAGCGACATATCT	365

OY	770	TTGTGAAGTCTGTACCTCTGTGTATCGGAGCCCGCTGATAGCTTGTGTGGAGACATGAT	829
Db	366	CTTAGAAGTGTACCCCTGTGTATCGGCCCCCTGATGCTTTGTGTGGAGCACTGAT	425
OY	830	ATTCTCTGAGCTGAGACATATGGGGTGCAGGCTCATCTTATTTGAAATGTTCCAGGGTC	889
Db	426	ATTCTCTGAGCTAGACATATGGGGTGCAGGCTGATCTTATTTGAAATGTTCCAGGGTC	485
OY	890	AACTTTGTTCCTGTGGGTTTCCAAACATCTTTGAACAGCTGGAGAAAATCTGGGAGGTGC	949
Db	486	AACTTTGTTCCTGTGGGTTTCCAAACATCTTTGAACAGCTGGAGAAAATCTGGGAGGTGC	545
OY	950	TGGGAGTCCCTACAGAGATACCTTGGCCGGAGTCTCCAACTACTTA	997
Db	546	TGGGAGTCCCTACAGAGATACCTTGGCCGGAGTCTCCAACTACTTA	593

RESULT 6				
CD636754/c				
LOCUS	CD636754	600 bp	mRNA	linear
DEFINITION	56105109J1 FLJP Homo sapiens cDNA, mRNA sequence.			EST 12-JAN-2004
Accession	CD636754			

VERSION	CD636754.1	GI:40285021
KEYWORDS	Est.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE

AUTHORS
TITLE

Circular rapid amplification of cDNA ends for high-throughput
Pu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
1 (bases 1 to 600)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

JOURNAL
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102
 Email: gfu@incyte.com.

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FEATURES
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    location/Qualifiers
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      /organism="Homo sapiens"
      /mol_type="mrna"
      /db_xref="taxon:9606"

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Query Match	44.4%	580.8	600

	Matches	533;	Conservative	0;	Mismatches	2;	Indels	1;	Gaps	2
Qy	410	ATGCAAGAGAAGAGTCCCATTTTACAGTATCCGAGAAGCTTCTCTCTGAAGGTTTGA	469							
Db	595	AGGCAAGAGAAGAGTCCCATTTTACAGTATCCGAGAAGCTTCTCTCTGAAGGTTTGA	536							
Qy	470	AACATGCCAATATTGTGCTCCTGCATGACATATTCACACCAAGAAGACATGACATTGC	529							
Db	535	AACATGCCAATATTGTGCTCCTGCATGACATATTCACACCAAGAAGACATGACATTGC	476							
Qy	530	TTTTTGAATACATGCACACAGACTGGCCCAATATGTCTCAGATCTCAGAGAGGCTTC	589							
Db	475	TTTTTGAATACATGCACACAGACTGGCCCAATATGTCTCAGATCTCAGAGAGGCTTC	416							
Qy	590	ATCCTCATATGTGAGACTTTTCATGTTTCAACTTTTGGGGGGCTGGGCTGATATCCACC	649							
Db	415	ATCCTCATATGTGAGACTTTTCATGTTTCAACTTTTGGGGGGCTGGGCTGATATCCACC	356							
Qy	650	ACCAACAAGTCTTTCACAGGGAGCTGAAACCTCGAATTACTATCATGTCACCTGGAG	709							
Db	355	ACCAACAAGTCTTTCACAGGGAGCTGAAACCTCGAATTACTATCATGTCACCTGGAG	296							
Qy	710	AGCTCAAACTGGCTGATTTTGTGCTTGGCCGGGCGAAGTCCATTCCAGCCAGACATACT	769							

Db 295 AGCTCAAGCTGCTGATTTTGGCTTGGCCGGGCGCAAGTCCATTCACAGCAGACTACT 236
Qy 770 CTTCAGAAAGTGTGACCTCTGTGTACCGGCCCCCTGATCTTGTCTGGAGCCACTGAAT 829
Db 235 CTTCAGAAAGTGTGACCTCTGTGTACCGGCCCCCTGATCTTGTCTGGAGCCACTGAAT 176
Qy 830 ATTCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAATGTTCCAGGGTTC 889
Db 175 ATTCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAATGTTCCAGGGTTC 116
Qy 890 AACCTTTGTTCTCTGGGGTTCCTCAACATCTTGAAGAGCTGAGAAATCTGGAGAGTGC 949
Db 115 AACCTTTGTTCTCTGGGGTTCCTCAACATCTTGAAGAGCTGAGAAATCTGGAGAGTGC 56
Qy 950 TGGAGTCCCTTACAGAGATTAATTGGCCGGAGTCTTCAAGCTAATACTAAT 1005
Db 55 TGGAGTCCCTTACAGAGATTAATTGGCCGGAGTCTTCAAGCTAATACTAAT 1

RESULT 7
CD636748/c 602 bp mRNA linear EST 12-JAN-2004
LOCUS CD636748 56014973J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636748.1 GI:40285015
ACCESSION CD636748.1 GI:40285015
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source 1..602
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 44.2%; Score 578.6; DB 6; Length 602;
Best Local Similarity 99.2%; Pred. No. 1.7e-163;
Matches 592; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 410 ATGCAGAGAGAGAGTCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTTGA 469
Db 597 AGCGAGAGAGAGAGTCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTTGA 538
Qy 470 AACATGCCAATATTGTGCTCTGCGATGACATATCCAGACC-AAAGAGACATGACATTC 528
Db 537 AACATGCCAATATTGTGCTCTGCGATGACATATCCAGACC-AAAGAGACATGACATTC 478
Qy 539 GTTTTGAATATGACACAGACCTGGCCAGATATATGCTCAGATCCAGAGGGCTT 588
Db 477 GTTTTGAATATGACACAGACCTGGCCAGATATATGCTCAGATCCAGAGGGCTT 418
Qy 589 CATCTCATATATGTCAGACTTTTCACTTTTCACTTTTGGGGGCTGGCGTACATCCAC 648
Db 417 CATCTCATATATGTCAGACTTTTCACTTTTCACTTTTGGGGGCTGGCGTACATCCAC 358
Qy 649 CACCAACAGCTTCTTACAGAGGACCTGAACCTGAACTTACTATCATGACACCTGGGA 708
Db 357 CACCAACAGCTTCTTACAGAGGACCTGAACCTGAACTTACTATCATGACACCTGGGA 298

Qy 709 GAGCTCAAACTGCTGATTTTGGCTTGGCCGGGCGCAAGTCCATTCACAGCAGACTAC 768
Db 297 GAGCTCAAACTGCTGATTTTGGCTTGGCCGGGCGCAAGTCCATTCACAGCAGACTAC 238
Qy 769 TCTTCAGAAAGTGTGACCTCTGTGTACCGGCCCCCTGATCTTGTCTGGAGCCACTGA 828
Db 237 TCTTCAGAAAGTGTGACCTCTGTGTACCGGCCCCCTGATCTTGTCTGGAGCCACTGA 178
Qy 829 TATCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAATGTTCCAGGGT 888
Db 177 TATCTCTGAGCTGACATATGGGGTGCAGGCTGCATCTTTATTTGAATGTTCCAGGGT 118
Qy 889 CAACCTTTGTTCTCTGGGGTTCCTCAACATCTTGAACAGCTGAGAAATCTGGAGAGTGC 948
Db 117 CAACCTTTGTTCTCTGGGGTTCCTCAACATCTTGAACAGCTGAGAAATCTGGAGAGTGC 58
Qy 949 CTGGAGTCCCTTACAGAGATTAATTGGCCGGAGTCTTCAAGCTAATACTAAT 1005
Db 57 CTGGAGTCCCTTACAGAGATTAATTGGCCGGAGTCTTCAAGCTAATACTAAT 1

RESULT 8
CD636751 602 bp mRNA linear EST 12-JAN-2004
LOCUS CD636751 56015001H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636751
ACCESSION CD636751
VERSION CD636751.1 GI:40285018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source 1..602
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 43.9%; Score 574.2; DB 6; Length 602;
Best Local Similarity 99.2%; Pred. No. 3.6e-162;
Matches 587; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 410 ATGCAGAGAGAGAGTCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTTGA 469
Db 6 AGCGAGAGAGAGAGTCCCATTTACAGCTATCCGAGAGCTTCTCTCGAAGGGTTTGA 65
Qy 470 AACATGCCAATATTGTGCTCTGCGATGACATATCCAGACC-AAAGAGACATGACATTC 529
Db 66 AACATGCCAATATTGTGCTCTGCGATGACATATCCAGACC-AAAGAGACATGACATTC 125
Qy 530 GTTTTGAATATGACACAGACCTGGCCAGATATATGCTCAGATCCAGAGGGCTT 589
Db 126 GTTTTGAATATGACACAGACCTGGCCAGATATATGCTCAGATCCAGAGGGCTT 185
Qy 590 ATCTCATATATGTCAGACTTTTCACTTTTCACTTTTGGGGGCTGGCGTACATCCAC 649
Db 186 ATCTCATATATGTCAGACTTTTCACTTTTCACTTTTGGGGGCTGGCGTACATCCAC 245
Qy 650 ACCAACAAGCTTCTTACAGAGGACCTGAACCTGAACTTACTATCATGACACCTGGAG 709

Db 246 ACCAACAAGCTTTCACAGGAGACCTGAACCTCAGAACCTTACCTACGACCTGGAG 305
Qy 710 AGCTCAACTGCTGATTTTGTCTTGTCCCGGCGCAAGTCATTTCCAGCAGACATCT 769
Db 306 AGCTCAACTGCTGATTTTGTCTTGTCCCGGCGCAAGTCATTTCCAGCAGACATCT 365
Qy 770 CTTCAGAAAGTCGATCCCTTGTGTACCGGCGCCCTGATGCTTGTGGAGGACATGAA 829
Db 366 CTTCAGAAAGTCGATCCCTTGTGTACCGGCGCCCTGATGCTTGTGGAGGACATGAA 425
Qy 830 ATTCTCTGAGCTGACATATGGGGTGGAGGCTGACGCTTATTTGAATGTCAGAGGTC 889
Db 426 ATTCTCTGAGCTGACATATGGGGTGGAGGCTGACGCTTATTTGAATGTCAGAGGTC 485
Qy 890 AACCTTTGTTCTCGGGGTTTCCAACTCTTGAACAGCTGAGAAAATCTGGAGAGTGC 949
Db 486 AACCTTTGTTCTCGGGGTTTCCAACTCTTGAACAGCTGAGAAAATCTGGAGAGTGC 545
Qy 950 TGGAGTCCCTACAGAGATCTTGGCCGGAGTCTCCAACTTAACTA 1001
Db 546 TGGAGTCCCTACAGAGATCTTGGCCGGAGTCTCCAACTTAACTA 596

RESULT 9
CD636758/c 596 bp mRNA linear EST 12-JAN-2004
LOCUS CD636758
DEFINITION 56015025J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636758
VERSION CD636758.1 GI:40285025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 596)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..596
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_11b="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 43.9%; Score 573.6; DB 6; Length 596;
Best Local Similarity 99.2%; Pred. No. 5.5e-162;
Matches 587; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 650 ACCAACAAGCTTTCACAGGAGCTGAACCTCAGAACTTACTATCACTACCTGGAG 709
Db 351 ACCAACAAGCTTTCACAGGAGCTGAACCTCAGAACTTACTATCACTACCTGGAG 292
Qy 710 AGCTCAACTGCTGATTTTGTCTTGTCCCGGCGCAAGTCATTTCCAGCAGACATCT 769
Db 291 AGCTCAACTGCTGATTTTGTCTTGTCCCGGCGCAAGTCATTTCCAGCAGACATCT 232
Qy 770 CTTCAGAAAGTCGATCCCTTGTGTACCGGCGCCCTGATGCTTGTGGAGGACATGAA 829
Db 231 CTTCAGAAAGTCGATCCCTTGTGTACCGGCGCCCTGATGCTTGTGGAGGACATGAA 172
Qy 830 ATTCTCTGAGCTGACATATGGGGTGGAGGCTGACGCTTATTTGAATGTCAGAGGTC 889
Db 171 ATTCTCTGAGCTGACATATGGGGTGGAGGCTGACGCTTATTTGAATGTCAGAGGTC 112
Qy 890 AACCTTTGTTCTCGGGGTTTCCAACTCTTGAACAGCTGAGAAAATCTGGAGAGTGC 949
Db 111 AACCTTTGTTCTCGGGGTTTCCAACTCTTGAACAGCTGAGAAAATCTGGAGAGTGC 52
Qy 950 TGGAGTCCCTACAGAGATCTTGGCCGGAGTCTCCAACTTAACTA 1001
Db 51 TGGAGTCCCTACAGAGATCTTGGCCGGAGTCTCCAACTTAACTA 596

RESULT 10
CD636740/c 598 bp mRNA linear EST 12-JAN-2004
LOCUS CD636740
DEFINITION 56014901J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636740
VERSION CD636740.1 GI:40285007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 598)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
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/clone_11b="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 43.6%; Score 570.4; DB 6; Length 598;
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Matches 587; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

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Db      413 ATCTCATATATGTCAGACCTTTTCATGTTTCACTTTTGGGGGCGCTGGGCTACATCCACC 354
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Db      353 ACCAACACGTTCTTCAAGAGACCTGAAAACCTGAGAACTTACTCATGCTACCTGGAG 294
Qy      710 AGCTCAAACTGGCTGATTTTGGCTTGGCCCGGGCCAAAGTCATTTCCAGCAACAATACT 769
Db      293 AGCTCAAACTGGCTGATTTTGGCTTGGCCCGGGCCAAAGTCATTTCCAGCAACAATACT 234
Qy      770 CTTCAGAACTGTCGACCTCTGCTGTCACGGCCCTGATGCTTGTGAGGACCACTGAAT 829
Db      233 CTTCAGAACTGTCGACCTCTGCTGTCACGGCCCTGATGCTTGTGAGGACCACTGAAT 174
Qy      830 ATTCCTCTGAGCTGACATATGAGGAGTCAGAGCTGATCTTTATTTGAAATGTTCCAGGGTC 889
Db      173 ATTCCTCTGAGCTGACATATGAGGAGTCAGAGCTGATCTTTATTTGAAATGTTCCAGGGTC 114
Qy      890 AACCTTTGTTTCTGGGGGTTTCCACATCTTGAACAGCTGAGAAAATCTGGGAGGTG 949
Db      113 AACCTTTGTTTCTGGGGGTTTCCACATCTTGAACAGCTGAGAAAATCTGGGAGGTG 54
Qy      950 TGGAGTCCCTACAGAGATACTTGGCCGGAGTCTCAAGCTAACCTAACAT 1005
Db      53 TGGAGTCCCTACAGAGATACTTGGCCGGAGTCTCAAGCTAACCTAACAT 1

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RESULT 11

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CD636757 602 bp mRNA linear EST 12-JAN-2004
LOCUS CD636757
DEFINITION 56015089H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636757
VERSION CD636757.1 GI:40285024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Vector: pDrive Cloning Vector"

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Query Match 43.3%; Score 566.6; DB 6; Length 602;
Best Local Similarity 99.0%; Pred. No. 7.4e-160;
Matches 591; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 410 ATGCAGAGAGAGAGTCCCATTTACAGCTATCCGAGAACTTCTCTCGAAGGGTTTGA 469
Db 6 AGGAGAGAGAGAGTCCCATTTACAGCTATCCGAGAACTTCTCTCGAAGGGTTTGA 65
Qy 470 AACATGCCAATATTTGCTCTCGATGACATATACACCAAGAGACATGACATTTGG 529
Db 66 AACATGCCAATATTTGCTCTCGATGACATATACACCAAGAGACATGACATTTGG 125
Qy 530 TTTTGAATATACATGACACAGACCTGGCCAGATATATGCTGACATCCAGAGGGCTTC 589
Db 126 TTTTGAATATACATGACACAGACCTGGCCAGATATATGCTGACATCCAGAGGGCTTC 185

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Qy 590 ATCTCATATATGTCAGACCTTTTCATGTTTCACTTTTGGGGGCGCTGGGCTACATCCACC 649
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Qy 650 ACCAACACGTTCTTCAAGAGACCTGAAAACCTGAGAACTTACTCATGCTACCTGGAG 709
Db 246 ACCAACACGTTCTTCAAGAGACCTGAAAACCTGAGAACTTACTCATGCTACCTGGAG 305
Qy 710 AGCTCAAACTGGCTGATTTTGGCTTGGCCCGGGCCAAAGTCATTTCCAGCAACAATACT 769
Db 306 AGCTCAAACTGGCTGATTTTGGCTTGGCCCGGGCCAAAGTCATTTCCAGCAACAATACT 364
Qy 770 CTTCAGAACTGTCGACCTCTGCTGTCACGGCCCTGATGCTTGTGAGGACCACTGAAT 829
Db 365 CTTCAGAACTGTCGACCTCTGCTGTCACGGCCCTGATGCTTGTGAGGACCACTGAAT 424
Qy 830 ATTCCTCTGAGCTGACATATGAGGAGTCAGAGCTGATCTTTATTTGAAATGTTCCAGGGTC 889
Db 425 ATTCCTCTGAGCTGACATATGAGGAGTCAGAGCTGATCTTTATTTGAAATGTTCCAGGGTC 484
Qy 890 AACCTTTGTTTCTGGGGGTTTCCACATCTTGAACAGCTGAG-AAAATCTGGGAGGTG 948
Db 485 AACCTTTGTTTCTGGGGGTTTCCACATCTTGAACAGCTGAGAAAATCTGGGAGGTG 544
Qy 949 CTGGAGTCCCTACAGAGATACTTGGCCGGAGTCTCAAGCTAACCTAACAT 1005
Db 545 CTGGAGTCCCTACAGAGATACTTGGCCGGAGTCTCAAGCTAACCTAACAT 601

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RESULT 12

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CD636759 602 bp mRNA linear EST 12-JAN-2004
LOCUS CD636759/c
DEFINITION 56015089H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636759
VERSION CD636759.1 GI:40285026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 43.3%; Score 565.8; DB 6; Length 602;
Best Local Similarity 97.8%; Pred. No. 1.3e-159;
Matches 584; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
Qy 410 ATGCAGAGAGAGTCCCATTTACAGCTATCCGAGAACTTCTCTCGAAGGGTTTGA 469
Db 597 AGGAGAGAGAGAGTCCCATTTACAGCTATCCGAGAACTTCTCTCGAAGGGTTTGA 538
Qy 470 AACATGCCAATATTTGCTCTCGATGACATATACACCAAGAGACATGACATTTGG 529
Db 537 AACATGCCAATATTTGCTCTCGATGACATATACACCAAGAGACATGACATTTGG 478
Qy 530 TTTTGAATATACATGACACAGACCTGGCCAGATATATGCTGACATCCAGAGGGCTTC 589

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Db 477 TTTTGAATACATGACACAGACCTGGCCAGATATATGCTCAGCATCCAGAGGGCTTC 418
Qy 590 ATCTCATATATGTCAGACTTTTTCATGTTTCACTTTTGGGGGCTGGGCTATCATCCACC 649
Db 417 ATCTCATATATGTCAGACTTTTTCATGTTTCACTTTTGGGGGCTGGGCTATCATCCACC 358
Qy 650 ACCAACAAGTTCTTTCAGAGGACCTTAAACCTCAGAACTTACTCATCAGCTCAGCTGGAG 709
Db 357 ACCAACAAGTTCTTTCAGAGGACCTTAAACCTCAGAACTTACTCATCAGCTCAGCTGGAG 298
Qy 710 AGCTCAACCTGAGCTGATTTTGTCTTGCCCGGGCCAAGTCATTTCCAGCAGACATACT 769
Db 297 AGCTCAACCTGAGCTGATTTTGTCTTGCCCGGGCCAAGTCATTTCCAGCAGACATACT 238
Qy 770 CTTCAGAAAGTGTGACCTCTGTTGATCCGGCCCCCTGATGCTTTGCTGGAGCCACTGAAT 829
Db 237 CTTCAGAAAGTGTGACCTCTGTTGATCCGGCCCCCTGATGCTTTGCTGGAGCCACTGAAT 178
Qy 830 ATTCCTCTGAGCTGACATATATGGGGTCAGAGCTGACATCTTATTTGAATGTTCCAGGGTC 889
Db 177 ATTCCTCTGAGCTGACATATATGGGGTCAGAGCTGACATCTTATTTGAATGTTCCAGGGTC 118
Qy 890 AACCTTGTCTTCTGAGGGTTTCCAAAT-CTTTGAACAGCTGAGAAATCTGGAGGTG 948
Db 117 AACCTTGTCTTCTGAGGGTTTCCAAAT-CTTTGAACAGCTGAGAAATCTGGAGGTG 58
Qy 949 CTGGAGATCCCTTACAGAGATACTTGGCGGGAGTCTCCAAAGCTTCAACTCAAT 1005
Db 57 CTGGAGATCCCTTACAGAGATACTTGGCGGGAGTCTCCAAAGCTTCAACTCAAT 1

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RESULT 13
CD636746/c 601 bp mRNA linear EST 12-JAN-2004
LOCUS 56014925J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636746
ACCESSION CD636746.1 GI:40285013
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
INCYTE Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers

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FEATURES
source
1. 601
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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Query Match 43.1%; Score 564.2; DB 6; Length 601;
Best Local Similarity 99.2%; Pred. No. 3.9e-159;
Matches 588; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Qy 412 GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
Db 593 GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
Qy 472 CATGCCAATATTTGCTCTGTCATGACATATTCACACCAAGAGACATGACATTCGTT 531
Db 533 CATGCCAATATTTGCTCTGTCATGACATATTCACACCAAGAGACATGACATTCGTT 475

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Qy 532 TTTGAATACATGACACAGACCTGGCCAGATATATGCTCAGCATCCAGAGGGCTTCAT 591
Db 474 TTTGAATACATGACACAGACCTGGCCAGATATATGCTCAGCATCCAGAGGGCTTCAT 415
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Db 174 TCCTCTGAGCTGACATATATGGGGTCAGAGCTGACATCTTATTTGAATGTTCCAGGGTC 115
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Db 114 CCTTGTCTTCTGAGGGTTTCCAAAT-CTTTGAACAGCTGAGAAATCTGGAGGTGCTG 55
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LOCUS 56015017H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636755
ACCESSION CD636755
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
INCYTE Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers

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Best Local Similarity 97.3%; Pred. No. 7.4e-158;
Matches 580; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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Db      66 AACATGCCAATCTGTGCTCTGTCATGACATTAATCCACACAAAGACATGACATTTG 125
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Qy      950 TGGGAGTCCCTACAGAGATCTTGGCCGGGAGTCTCCAGCTCACTTAACCTAACAAT 1005
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RESULT 15

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CD636750/c  CD636750 587 bp mRNA linear EST 12-JAN-2004
LOCUS 56014981J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636750
ACCESSION CD636750.1 GI:40285017
VERSION
KEYWORDS
SOURCE

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ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 587)
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 Genomics 84 (1), 205-210 (2004)

JOURNAL COMMENT Contact: Fu GK

INCYTE Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com

FEATURES

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 Location/Qualifiers
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 /note="Vector: pDrive Cloning Vector"

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Matches 570; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Qy      484 GTCTCTGTCATGACATTAATCCACACAAAGACATGACATTTGTTTGAATACATG 543
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Qy      784 ACCCTCTGCTACCGGCCCCCTGATGCTTTGCTGGAGCCACTGAATATTTCTGAGCTG 843
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignment)
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: geneseqn2003ds:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1308	100.0	1308	6	AA148891	AA148891 Human PTC
2	1308	100.0	1308	6	ACC79970	ACC79970 Human ser
3	1308	100.0	1584	9	ACC79968	ACC79968 Human ser
4	1308	100.0	1628	9	ACC79971	ACC79971 Human ser
5	1308	100.0	2250	12	ADJ96563	ADJ96563 Human cyc
6	1191	91.1	2140	11	AD122554	AD122554 Human dis
7	1186	90.7	1311	10	ADC30755	ADC30755 Human nov
8	1185.4	90.6	1534	9	ACC79969	ACC79969 Human ser
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11	887.6	67.9	1376	8	ABA00722	ABA00722 Human KRP
12	873	66.7	1828	12	ADM16422	ADM16422 DNA encod
13	821	62.8	888	10	ABE77160	ABE77160 Human pro
14	702.2	53.7	1077	4	AAFA4668	AAFA4668 Novel pro
15	702.2	53.7	1077	12	AD129366	AD129366 Human MAR
16	481	36.8	481	6	AA517061	AA517061 Human pro
17	481	36.8	481	10	AA61613	AA61613 Human pro
18	481	36.8	481	10	ABX14985	ABX14985 Human pro
19	439.6	33.6	4529	12	ADJ75962	ADJ75962 Marker ge
20	437.8	33.5	1372	2	AA86605	AA86605 Coding re
21	436.4	33.4	2424	2	AA86606	AA86606 Murine mp

22	436.2	33.3	4957	10	ADD89960	ADD89960 Human can
23	436.2	33.3	4957	11	ADN95587	ADN95587 Human BRC
24	436.2	33.3	4957	12	ADJ75096	ADJ75096 Marker ge
25	436.2	33.3	4957	12	ADQ17589	ADQ17589 Human sof
26	436.2	33.3	5161	12	ADQ22276	ADQ22276 Human sof
27	436.6	33.2	1410	6	AA153644	AA153644 DNA enco
28	329.2	25.2	2703	4	AB120823	AB120823 Drosophill
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41	296.6	22.7	1839	3	AAZ46142	AAZ46142 CDNA sequ
42	296.6	22.7	2580	4	AA158117	AA158117 Human pol
43	296.6	22.7	2858	4	AA18828	AA18828 Human kin
44	296.2	22.6	2363	4	AAK51826	AAK51826 Human pol
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ALIGNMENTS

RESULT 1	AA148891	strand: cDNA, 1308 BP.
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XX	AA148891	
AC	AA148891	
XX	AA148891	
DT	24-OCT-2002	(first entry)
XX	AA148891	
DE	Human PTC	family kinase splice form 2 coding sequence.
XX	Human	PTC
KW	Human	PTC
KM	uterus	endometrium adenocarcinoma; lung fibroblast; splice form;
KX	kidney	renal cell adenocarcinoma; gene therapy; gene; ss..
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
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FT		/*tag= a
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XX	XX	
PN	WO200261060-A2.	
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PD	08-AUG-2002.	
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PF	17-JAN-2002;	2002WO-US001106.
XX	XX	
PR	31-JAN-2001;	2001US-0265151P.
PR	09-MAR-2001;	2001US-00801861.
XX	XX	
PA	(PEKE)	PE CORP NY.
XX	XX	
PI	Yan C,	Ketchum K, Di Francesco V, Beasley EM;
XX	XX	
DR	WPI; 2002-608515/65.	
XX	XX	
PT	P-PSDB; AAO18614.	
PT	New human kinase peptide and nucleic acid molecule, useful for treating	
PT	disorders associated with abnormal expression of kinase protein, e.g.	
PT	adenocarcinoma of uterus or lung, in drug screening assays and	
XX	pharmacogenomic analysis.	
PS	Claim 4; Fig 1; 131p; English.	
XX	XX	

CC The present invention provides the protein, cDNA and gene sequences of
 CC two splice variants of a human Pfkfb1 kinase. The sequences are
 CC specifically expressed in the human testis, brain, uterus endometrium
 CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and
 CC can be used to treat related diseases. The present sequence is the cDNA
 CC of splice variant 2 of the invention

XX Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1308; DB 6; Length 1308;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

ACC79970
 ID ACC79970 standard; cDNA, 1308 BP.

AC79970;
 DT 09-SEP-2003 (first entry)

XX Human serine/threonine protein kinase encoding cDNA SEQ ID NO:8.

XX Human; serine/threonine protein kinase; kinase; enzyme; cytosolic;
 KW antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
 KW cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
 KW gynecological; uropathic; dermatological; gene therapy; cancer;
 KW diabetes; central nervous system disorder; CNS disorder; liver disease;
 KW respiratory disorder; chronic obstructive pulmonary disease; stroke;
 KW cardiovascular disorder; dermatological disorder; urological disorder;
 KW gastrointestinal disease; haematological disorder; Alzheimer's disease;
 KW musculoskeletal disorder; reproductive disorder; Parkinson's disease;
 KW neuropathic pain; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 1. 1308
 FT CDS /tag= a
 FT /product= "serine/threonine protein kinase"

XX WO2003046167-A1.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002MO-EP013268.

XX 27-NOV-2001; 2001US-0333131P.

XX (FARB) BAYER AG.

XX Koehler RH;

XX WPI, 2003-505196/47.

XX P-PSDB; ABR57361.

XX New polynucleotide encoding a serine/threonine protein kinase

PT polypeptide, useful for diagnosing, preventing or treating diseases
PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
or diabetes.

Disclousure; Fig 8; 196bp; English.

CC The present sequence encodes a human serine/threonine protein kinase (1).
CC (1) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian,
CC neurotropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic,
CC gastrotectinal, gynaecological, uropathic and dermatological
CC activities, and can be used in gene therapy. Serine/threonine protein
CC kinase polynucleotide and polypeptide sequences can be used in
CC diagnosing, preventing, ameliorating or treating diseases associated with
CC serine/threonine protein kinase dysfunction. They may also be used to
CC identify test compounds that may act, for example, as activators or
CC inhibitors at the enzyme's active site. The human serine/threonine
CC protein kinase and its fragments are also useful in raising specific
CC antibodies that can block the enzyme and effectively reduce its activity.
CC Human serine/threonine protein kinase sequences can be used in the
CC preparation of a medicament for modulating the activity of a serine/
CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
CC nervous system (CNS) disorder, a respiratory disorder (including chronic
CC obstructive pulmonary disease), a cardiovascular disorder, a
CC dermatological disorder, a gastrotectinal or liver disease, a
CC haematological disorder, a musculoskeletal disorder, a reproductive
CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
CC disease, Parkinson's disease, stroke or neuropathic pain
CC
SQ Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;

Query Match	100.0%	Score 1308;	DB 9;	Length 1308;
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DB 781 GTGACCTTGTGATCCGCGCCCTGATGCTTGTGAGACCACTGAATATTTCTGTAG 840					
QY 841 CTGAGATATGAGGAGTGCAGAGCTGCATCTTATTTGAATGTTCCAGGCTCAACTTGT 900					
DB 841 CTGAGATATGAGGAGTGCAGAGCTGCATCTTATTTGAATGTTCCAGGCTCAACTTGT 900					
QY 901 CTTGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGAGGCTGCGAGTCCCT 960					
DB 901 CTTGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGAGGCTGCGAGTCCCT 960					
QY 961 ACAGAGATATCTTGGCGGAGTCTTCAAGCTTCACTTCACTCAATCCAGATGTTTCCA 1020					
DB 961 ACAGAGATATCTTGGCGGAGTCTTCAAGCTTCACTTCACTCAATCCAGATGTTTCCA 1020					
QY 1021 CTGCGTACGCTCTGAGAGCTTATGTTTCTGAGAAAGCTGCGAGGCTTCTGAGCT 1080					
DB 1021 CTGCGTACGCTCTGAGAGCTTATGTTTCTGAGAAAGCTGCGAGGCTTCTGAGCT 1080					
QY 1081 GAAAGCTGCTGCTCCAGATGCTTAAAGGCTTCCAGAGACCGGCTCTCCGCCAGAA 1140					
DB 1081 GAAAGCTGCTGCTCCAGATGCTTAAAGGCTTCCAGAGACCGGCTCTCCGCCAGAA 1140					
QY 1141 GCACTTGTTCATGATTTATTTACAGCGCTGCTGCAATCTCAGCTGTACAGCTTCTGATGAG 1200					
DB 1141 GCACTTGTTCATGATTTATTTACAGCGCTGCTGCAATCTCAGCTGTACAGCTTCTGATGAG 1200					
QY 1201 GAGTCTTGTTTTACAGTTTCAAGAGTGAAGGCTTAAAGGCGCAAGATGTTGACCTTTTGGCC 1260					
DB 1201 GAGTCTTGTTTTACAGTTTCAAGAGTGAAGGCTTAAAGGCGCAAGATGTTGACCTTTTGGCC 1260					
QY 1261 TCCTACAGAAAGTCAACCAAGCCAGTTTACAGAAATGCTGTGA 1308					
DB 1261 TCCTACAGAAAGTCAACCAAGCCAGTTTACAGAAATGCTGTGA 1308					
RESULT 3					
ACCT9968					
ID	ACCT9968	standard;	cdna;	1584	BP.
XX	ACCT9968;				
DT	09-SEP-2003	(first entry)			
XX					
DE	Human serine/threonine protein kinase encoding cdna seq ID NO:4.				
KW	Human; serine/threonine protein kinase; kinase; enzyme; cytosolic;				
KW	antidiabetic; neuroprotective; neurotropic; antiparkinsonian; analgesic;				
KW	cerebroprotective; antiinflammatory; gastrotectinal; hepatotropic;				
KW	gynaecological; uropathic; dermatological; gene therapy; cancer;				
KW	diabetes; central nervous system disorder; CNS disorder; liver disease;				
KW	respiratory disorder; chronic obstructive pulmonary disease; stroke;				
KW	cardiovascular disorder; dermatological disorder; urological disorder;				
KW	gastrotectinal disease; haematological disorder; Alzheimer's disease;				
KW	musculoskeletal disorder; reproductive disorder; Parkinson's disease;				
KW	neuropathic pain; gene; ss.				
XX					
OS	Homo sapiens.				

FH	Key	Location/Qualifiers
FT	CDS	1..1308
FT		/tag= a
FT		/product= "serine/threonine protein kinase"
PN	MO2003046167-A1.	
PD	05-JUN-2003.	
XX		
XX	26-NOV-2002; 2002WO-BP013266.	
PF		
XX	27-NOV-2001; 2001US-0333131P.	
PR	(FARB) BAYER AG.	
PA	Koehler RH;	
PI		
XX	WPI; 2003-505196/47.	
DR	P-PsDB; ABR57359.	
XX		
PT	New polynucleotide encoding a serine/threonine protein kinase	
PT	polypeptide, useful for diagnosing, preventing or treating diseases	
PT	associated with serine/threonine protein kinase dysfunction, e.g. cancer	
PS	or diabetes.	
XX		
PS	Disclosure; Fig 4; 196pp; English.	
XX		
CC	The present sequence encodes a human serine/threonine protein kinase (I).	
CC	(I) has cyrostatic, antidiabetic, neuroprotective, antiparkinsonian,	
CC	neurotropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic,	
CC	gastrointestinal, gynaecological, uropathic and dermatological	
CC	activities, and can be used in gene therapy. Serine/threonine protein	
CC	kinase polynucleotide and polypeptide sequences can be used in	
CC	diagnosing, preventing, ameliorating or treating diseases associated with	
CC	serine/threonine protein kinase dysfunction. They may also be used to	
CC	identify test compounds that may act, for example, as activators or	
CC	inhibitors at the enzyme's active site. The human serine/threonine	
CC	protein kinase and its fragments are also useful in raising specific	
CC	antibodies that can block the enzyme and effectively reduce its activity.	
CC	Human serine/threonine protein kinase sequences can be used in the	
CC	preparation of a medicament for modulating the activity of a serine/	
CC	threonine protein kinase in a disease, e.g. cancer, diabetes, a central	
CC	nervous system (CNS) disorder, a respiratory disorder (including chronic	
CC	obstructive pulmonary disease), a cardiovascular disorder, a	
CC	dermatological disorder, a gastrointestinal or liver disease, a	
CC	haematological disorder, a musculoskeletal disorder, a reproductive	
CC	disorder, or a urological disorder. CNS disorders may include Alzheimer's	
CC	disease, Parkinson's disease, stroke or neuropathic pain	
XX		
SQ	Sequence 1584 BP; 418 A; 376 C; 387 G; 403 T; 0 U; 0 Other;	
	Query Match	100.0%; Score 1308; DB 9; Length 1584;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1308; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Dy	1 ATGGGTCAAGAGCTGTGTCGAAGAAGCTATACAGCCTTGATGAGTGTCTACTATTGTCCA	60
Db	1 ATGGGTCAAGAGCTGTGTCGAAGAAGCTATACAGCCTTGATGAGTGTCTACTATTGTCCA	60
Dy	61 GAGGAGGCAGAGGCACACAGCTGTTCGAGGAGTCAAGCTTGAGACCACGAGAGGCTCGTTCC	120
Db	61 GAGGAGGCAGAGGCACACAGCTGTTCGAGGAGTCAAGCTTGAGACCACGAGAGGCTCGTTCC	120
Dy	121 AAGCTTAAGACCTTAATAAAGAACATCATGTTTCATGACTTTCATTTCACCCCAGGGGACTT	180
Db	121 AAGCTTAAGACCTTAATAAAGAACATCATGTTTCATGACTTTCATTTCACCCCAGGGGACTT	180
Dy	181 CAAGTGCCTCCGTCACAGAGTTCACAAGAGTAAAGGCCACGAGATTAAGTAGATTGTTTT	240
Db	181 CAAGTGCCTCCGTCACAGAGTTCACAAGAGTAAAGGCCACGAGATTAAGTAGATTGTTTT	240
Dy	241 CAGGAAGAGATCTGAGGCAAGGTTTTTCAGTGGAGAAAGAGCTTCTTTTGGGGCACCC	300

Db	241	CAGGAAGAGATCTGAGGCAAGGTTTTCAGTGGAGAAAGACCTCTCTTTGGGGACCC	300
Qy	301	TCATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTCTTATGGACAATTACAAAGGG	360
Db	301	TCATCTTACTTGAACCTTGGAGAGCTGGGTGAAGGCTCTTATGGAGACGTTTACAAAGGG	360
Qy	361	ATTACAGAAATTAATGGAACAACTAAGTGGCTTTAAAGTCATCAGCATGAATGCAAGAA	420
Db	361	ATTACAGAAATTAATGGAACAACTAAGTGGCTTTAAAGTCATCAGCATGAATGCAAGAA	420
Qy	421	GGAGGCCATTTCACAGTATCCGAGAAGCTCTCTCCGAAAGGGTTGAAACATGCCAAT	480
Db	421	GGAGGCCATTTCACAGTATCCGAGAAGCTCTCTCCGAAAGGGTTGAAACATGCCAAT	480
Qy	481	ATTGTGCTTCGACGACATTAATCCACCAAAAGACCTGACATTCGTTTTGAATAC	540
Db	481	ATTGTGCTTCGACGACATTAATCCACCAAAAGACCTGACATTCGTTTTGAATAC	540
Qy	541	ATGCAACAAGACCTGGGCCAGTATATGTCAGATCCAGAGAGGCTTCATCCCATAT	600
Db	541	ATGCAACAAGACCTGGGCCAGTATATGTCAGATCCAGAGAGGCTTCATCCCATAT	600
Qy	601	GTCAAGACTTTTCATGTTTCAACTTTTGGGGGGCTGGCGTACATCCACCAACACGTT	660
Db	601	GTCAAGACTTTTCATGTTTCAACTTTTGGGGGGCTGGCGTACATCCACCAACACGTT	660
Qy	661	CTTCACAGGAGACTGAAACCTCACAACCTACTCATCACTGACCTGGAGAGACTAAACTG	720
Db	661	CTTCACAGGAGACTGAAACCTCACAACCTACTCATCACTGACCTGGAGAGACTAAACTG	720
Qy	721	GCTGATTTTGGTCTTGGCCCGGGCCAGTCCATTCCTCCACGACGACATCTCTTCAGAA	780
Db	721	GCTGATTTTGGTCTTGGCCCGGGCCAGTCCATTCCTCCACGACGACATCTCTTCAGAA	780
Qy	781	GTGACCCCTCTGATACCGGCCCCCTGATGCTTGTCTGGAGGCACTGAATATTTCTCTGAG	840
Db	781	GTGACCCCTCTGATACCGGCCCCCTGATGCTTGTCTGGAGGCACTGAATATTTCTCTGAG	840
Qy	841	CTGGAACATATGGGGTGCAGAGCTGATCTTTTATGAATGTTCCAGAGGCTCAACTTTGTTT	900
Db	841	CTGGAACATATGGGGTGCAGAGCTGATCTTTTATGAATGTTCCAGAGGCTCAACTTTGTTT	900
Qy	901	CTGGGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGGAGGTGCTGGAGTCCCT	960
Db	901	CTGGGGGTTTCCAAACATCTTGAACAGCTGAGAAATCTGGGAGGTGCTGGAGTCCCT	960
Qy	961	AACAGAGATCTTGGCGGGAGGCTCCAGGTACTCTAATCAATCCAGAAATGATCCCA	1020
Db	961	AACAGAGATCTTGGCGGGAGGCTCCAGGTACTCTAATCAATCCAGAAATGATCCCA	1020
Qy	1021	CTGCCTACGCTCGAAGCTTTCATGTTGTCTGAAACAGGCTGGGACAGGTTCTGAAGCT	1080
Db	1021	CTGCCTACGCTCGAAGCTTTCATGTTGTCTGAAACAGGCTGGGACAGGTTCTGAAGCT	1080
Qy	1081	GAAAGACCTGGGCTCCAGATGCTTAAAGGCTTCCAGAGACCGCGTCCCGCCAGAAA	1140
Db	1081	GAAAGACCTGGGCTCCAGATGCTTAAAGGCTTCCAGAGACCGCGTCCCGCCAGAAA	1140
Qy	1141	GCACCTGTTCATGATTTATTTACAGCGCCCTGCATCTAGCTGTACCAAGCTTCTCATGAG	1200
Db	1141	GCACCTGTTCATGATTTATTTACAGCGCCCTGCATCTAGCTGTACCAAGCTTCTCATGAG	1200
Qy	1201	GAGTCTTTGTTTAAAGTTTTCAGAGGTAGAGGCTTAAAGCCAGAAATGTGTGACTTTTGGCC	1260
Db	1201	GAGTCTTTGTTTAAAGTTTTCAGAGGTAGAGGCTTAAAGCCAGAAATGTGTGACTTTTGGCC	1260
Qy	1261	TCCTACCAAGAAAGGTCAACACCCAGCCAGTTTGAACAAATGCTGGTGA 1308	
Db	1261	TCCTACCAAGAAAGGTCAACACCCAGCCAGTTTGAACAAATGCTGGTGA 1308	

XX	DE	Human serine/threonine protein kinase encoding cDNA SEQ ID NO:9.
XX	XX	09-SEP-2003 (first entry)
XX	XX	ACC79971.
XX	XX	ACC79971 standard; cDNA; 1628 BP.
XX	XX	Human; serine/threonine protein kinase; kinase; enzyme; cytosolic; antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic; gastroprotective; antiinflammatory; gastrointestinal; hepatotropic; gynaecological; uropathic; dermatological; gene therapy; cancer; diabetes; central nervous system disorder; CNS disorder; liver disease; respiratory disorder; chronic obstructive pulmonary disease; stroke; cardiovascular disorder; dermatological disorder; urological disorder; gastrointestinal disease; haematological disorder; Alzheimer's disease; musculoskeletal disorder; reproductive disorder; Parkinson's disease; neuropathic pain; gene; 88.
XX	XX	Homo sapiens.
XX	XX	Key Location/Qualifiers
XX	XX	CDS 45..1352
XX	XX	/tag= a
XX	XX	/product= "serine/threonine protein kinase"
XX	XX	MO2003046167-A1.
XX	XX	05-JUN-2003.
XX	XX	26-NOV-2002; 2002MO-BP03260.
XX	XX	27-NOV-2001; 2001US-0333131P.
XX	XX	(FARB) BAYER AG.
XX	XX	Koehler RH;
XX	XX	WPI; 2003-505196/47.
XX	XX	P-PSDB; ABR57361.
XX	XX	New polynucleotide encoding a serine/threonine protein kinase polypeptide, useful for diagnosing, preventing or treating diseases associated with serine/threonine protein kinase dysfunction, e.g. cancer or diabetes.
XX	XX	Claim 1; Page 185-188; 196pp; English.
XX	XX	The present sequence encodes a human serine/threonine protein kinase (I). (1) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian, nootropic, cerebroprotective, analgesic, antiinflammatory, hepatotropic, gastrointestinal, gynaecological, uropathic and dermatological activities, and can be used in gene therapy. Serine/threonine protein kinase polynucleotide and polypeptide sequences can be used in diagnosing, preventing, ameliorating or treating diseases associated with serine/threonine protein kinase dysfunction. They may also be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. The human serine/threonine protein kinase and its fragments are also useful in raising specific antibodies that can block the enzyme and effectively reduce its activity. CC Human serine/threonine protein kinase sequences can be used in the preparation of a medicament for modulating the activity of a serine/threonine protein kinase in a disease, e.g. cancer, diabetes, a central nervous system (CNS) disorder, a respiratory disorder (including chronic obstructive pulmonary disease), a cardiovascular disorder, a dermatological disorder, a gastrointestinal or liver disease, a haematological disorder, a musculoskeletal disorder, a reproductive disorder, or a urological disorder. CNS disorders may include Alzheimer's disease, Parkinson's disease, stroke or neuropathic pain
XX	XX	Sequence 1628 BP; 429 A; 383 C; 400 G; 416 T; 0 U; 0 Other;
XX	XX	100.0%; Score 1308; DB 9; Length 1628;
XX	XX	Query Match

[illegible]

Db 1065 CTGCTACGCTCGAAGCTTCATGTTGTCGGAACAGGCTGGGAGGTTTCTGAAGCT 1124
QY 1081 GAAAGCTGCGCTCCAGATGCTAAAGAGGCTTTCCAGAGACGCGCTCCGCGCCAGAA 1140
Db 1125 GAAGACCTGCGCTCCAGATGCTAAAGAGGCTTTCCAGAGACGCGCTCCGCGCCAGAA 1184
QY 1141 GCACCTGTCATATTAATTTTCAGGCGCTCCGATCTTACGCTGTAACAGCTTCTGATGAG 1200
Db 1185 GCACTGTCATATTAATTTTCAGGCGCTCCGATCTTACGCTGTAACAGCTTCTGATGAG 1244
QY 1201 GAGCTTTGTTACAGTTTCAGAGTGAAGCTTAAAGCCAGAAATGTTGACCTTTTGAGCC 1260
Db 1245 GAGCTTTGTTACAGTTTCAGAGTGAAGCTTAAAGCCAGAAATGTTGACCTTTTGAGCC 1304
QY 1261 TCCTACCAAGAGTCCACCAAGCCCAAGTTTACCAATGCTGTGA 1308
Db 1305 TCCTACCAAGAGTCCACCAAGCCCAAGTTTACCAATGCTGTGA 1352

RESULT 5

ADJ96563
ID ADJ96563 standard; DNA; 2250 BP.

AC ADJ96563;

DT 06-MAY-2004 (first entry)

DE Human cyclin dependent kinase PFTAIR2 DNA SeqID 20.

XX Gene; ds; kinase; human; tyrosine protein kinase;
KW serine/threonine protein kinase; PK; STK; gene therapy; cancer;
KW immune-related disease; cardiovascular disease; brain;
KW neuronal associated disease; metabolic; inflammatory disorder;
KW cytosolic; neuroprotective; immunomodulator; antiinflammatory;
KW cyclin dependent kinase; PFTAIR2.

XX Homo sapiens.

OS 51.

PN MO2004006838-A2.

XX 22-JAN-2004.

PF 15-JUL-2003; 2003MO-US021730.

PR 15-JUL-2002; 2002US-0395632P.

PA (SUGEN-) SUGEN INC.

PI Whyte D, Manning G, Caenepeel S;

DR MPI; 2004-122753/12.

XX P-PSDB; ADJ96529.

PT New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.

XX Example 1; SEQ ID NO 20; 366bp; English.

XX This invention relates to a novel isolated, enriched or purified nucleic
XX acid molecule that encodes a kinase polypeptide. Specifically, it relates
XX to human tyrosine and serine/threonine protein kinases (PK's and STK's),
XX as well as protein kinase-like enzymes. The present invention describes
XX screening methods to identify agonists, antagonists and antibodies that
XX can be used to modulate the activity or function of the mammalian kinase
XX enzymes. As such, these compositions can be used for gene therapy
XX purposes to treat diseases or disorders including cancer, immune-related
XX diseases, cardiovascular disease, brain or neuronal associated disease,
XX metabolic and inflammatory disorders. Accordingly, they exhibit
XX cytosolic, neuroprotective, immunomodulator and antiinflammatory
XX activities. This polynucleotide sequence is a human kinase DNA sequence
XX of the invention.

XX Sequence 2250 BP; 616 A; 494 C; 531 G; 609 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1308; DB 12; Length 2250;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTCAAGAGCTGTGTGCAAAAGCTGACAGCTGTGATGAGCTGACCATTTGTC 60
Db 45 ATGGGTCAAGAGCTGTGTGCAAAAGCTGACAGCTGTGATGAGCTGACCATTTGTC 104
QY 61 GAGGAGGCGGAGGACACACAGCTGTGTGAGAGATGAGCTGACCAAGAGCTGTGTC 120
Db 105 GAGGAGGCGGAGGACACACAGCTGTGTGAGAGATGAGCTGACCAAGAGCTGTGTC 164
QY 121 AAGCTAACAGAGCTTAAAGAACATCATTTGTCATGACTTTCATTTCAAGGAGGACT 180
Db 165 AAGCTAACAGAGCTTAAAGAACATCATTTGTCATGACTTTCATTTCAAGGAGGACT 224
QY 181 CAAGTCCCGTGGCCGAGAGTTCAAGATTAAGAGCCACGAGATPACAGTATTTT 240
Db 225 CAAGTCCCGTGGCCGAGAGTTCAAGATTAAGAGCCACGAGATPACAGTATTTT 284
QY 241 CAGGAAAGAGATCTGAGGAGGCTTTTCACTGAGAGAAAGCTCCCTTTGGGCAAGC 300
Db 285 CAGGAAAGAGATCTGAGGAGGCTTTTCACTGAGAGAAAGCTCCCTTTGGGCAAGC 344
QY 301 TCATCTTACTTGAATTTGAGAGAGCTGGTGAAGGCTTTATGACAGTTTCAAGAGG 360
Db 345 TCATCTTACTTGAATTTGAGAGAGCTGGTGAAGGCTTTATGACAGTTTCAAGAGG 404
QY 361 ATTACAGATTAATGACACACTAGTGTGTTAAAGTCATCAGATGATGACAGAGAA 420
Db 405 ATTACAGATTAATGACACACTAGTGTGTTAAAGTCATCAGATGATGACAGAGAA 464
QY 421 GGAGTCCCATTTACAGACTATCCGAGAGAGCTTCTCTGAAGGGTTGAAACATCCAT 480
Db 465 GGAGTCCCATTTACAGACTATCCGAGAGAGCTTCTCTGAAGGGTTGAAACATCCAT 524
QY 481 ATTGTCTCTGTCATGACATTAATCCACCAAGAGACCTGACATTCGTTTGAATAC 540
Db 525 ATTGTCTCTGTCATGACATTAATCCACCAAGAGACCTGACATTCGTTTGAATAC 584
QY 541 ATGACACAGAGCTGGCCGAGATATGTCAGACATCCAGAGGCTTCATCTCATAT 600
Db 585 ATGACACAGAGCTGGCCGAGATATGTCAGACATCCAGAGGCTTCATCTCATAT 644
QY 601 GTGACATTTTCATGATTTCACTTTTGGGGGCTGGGCTGATCCACCAACACGTT 660
Db 645 GTGACATTTTCATGATTTTCATTTTGGGGGCTGGGCTGATCCACCAACACGTT 704
QY 661 CTTCACAGGAGCTGAAACCTCAGAACTTACTCATGATCAGCTGGAGAGCTCAACTG 720
Db 705 CTTCACAGGAGCTGAAACCTCAGAACTTACTCATGATCAGCTGGAGAGCTCAACTG 764
QY 721 GGTGATTTTGTGCTGGCCGAGGACAGTCCATTCACAGACATATCTTTCAAGATC 780
Db 765 GGTGATTTTGTGCTGGCCGAGGACAGTCCATTCACAGACATATCTTTCAAGATC 824
QY 781 GTGACCTCTGTGTAACGCGCCCTGTGATGCTTTGCTGGAGGACATGAAATATTCCTGAG 840
Db 825 GTGACCTCTGTGTAACGCGCCCTGTGATGCTTTGCTGGAGGACATGAAATATTCCTGAG 884
QY 841 CTGACATATGAGGAGTGAGGCTGACATCTTATTTGAATGTTCCAGAGGCAACTTTGTTT 900
Db 885 CTGACATATGAGGAGTGAGGCTGACATCTTATTTGAATGTTCCAGAGGCAACTTTGTTT 944
QY 901 CCTGGGGTTTCCACATCTTGAACAGCTGAGAGAAATCTGGAGGCTCTGGAGTCCCT 960
Db 945 CCTGGGGTTTCCACATCTTGAACAGCTGAGAGAAATCTGGAGGCTCTGGAGTCCCT 1004
QY 961 ACAGAGATTAATTTGGCCGAGAGTCTCCAAAGCTTAATCAATCCAGAAATGTTCCCA 1020

DB 1005 ACAGAGATACCTTGGCCGGAGTCTCCAGCTACCTACCTACCAATGCTTCCCA 1064
 QY 1021 CTGCTACCGCTTGAAGCTTCACTGTTGTCTGGAACAGGCTGGGCAAGGTTCTGAAGCT 1080
 DB 1065 CTGCTACCGCTTGAAGCTTCACTGTTGTCTGGAACAGGCTGGGCAAGGTTCTGAAGCT 1124
 QY 1081 GAAGACCTGGCTCCCAAGATGCTAAAGGCTTCCAGAGACCGGCTTCCGCGCCAGGAA 1140
 DB 1125 GAAGACCTGGCTCCCAAGATGCTAAAGGCTTCCAGAGACCGGCTTCCGCGCCAGGAA 1184
 QY 1141 GCACCTGTCATGATTAATTTACAGCGCCCTGCTCATCTCAGCTGATACAGCTTCTGATGAG 1200
 DB 1185 GCACCTGTCATGATTAATTTACAGCGCCCTGCTCATCTCAGCTGATACAGCTTCTGATGAG 1244
 QY 1201 GACCTTTGTTTACGATTTTCAGAGAGTGAAGCTTAAAGCCAGAAATGTGTGACCTTTTGGCC 1260
 DB 1245 GAGCTTTGTTTACGATTTTCAGAGAGTGAAGCTTAAAGCCAGAAATGTGTGACCTTTTGGCC 1304
 QY 1261 TCCTACAGAAAGTCAACCAAGCCAGCCAGCTTACGAAATGCTGTGA 1308
 DB 1305 TCCTACAGAAAGTCAACCAAGCCAGCTTACGAAATGCTGTGA 1352

RESULT 6

ADL22554
 ID ADL22554 standard; cDNA, 2140 BP.

AC ADL22554;
 XX

DT 20-MAY-2004 (first entry)
 XX

DE Human disease detection and treatment (MDPT) cDNA - SEQ ID 3.
 XX

KW disease detection; MDPT; antiarteriosclerotic; antipsoriatic; cytostatic;
 cell signalling; arteriosclerosis; psoriasis; cancer; human; ss; gene.
 XX

OS Homo sapiens.
 XX

PN WO2003062379-A2.
 XX

PD 31-JUL-2003.
 XX

PF 14-JAN-2003; 2003MO-US001363.
 XX

PR 17-JAN-2002; 2002US-0349413P.
 XX

PR 17-JAN-2002; 2002US-0349946P.
 XX

PA (INCY-) INCYTE GENOMICS INC.
 XX

PI Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL,
 PI Yu JY, Tuason O, Yap PE, Ameshey SR, Dam TC, Liu TF, Gerstein EH,
 PI Peralta CH, Lewis SA, Chen AJ, Marwaha R, Lan RX, Urashka MB,
 PI Kristnam SR, Kolluru V, Panesar IS;
 XX

DR MPI; 2003-853443/79.
 XX

DR P-PSDB; ADL22658.
 XX

PT New isolated disease detection and treatment polynucleotide for
 PT diagnosing or treating conditions associated with cell signalling e.g.
 PT arteriosclerosis, psoriasis, and cancer.
 XX

PS Claim 1; SEQ ID NO 3; 411bp; English.
 XX

CC The invention relates to a novel isolated disease detection and treatment
 CC (MDPT) DNA polynucleotide. The polynucleotide of the invention
 CC demonstrates antiarteriosclerotic, antipsoriatic and cytostatic
 CC activities and may be useful in a composition for detecting the
 CC expression of a disease detection and treatment molecule polynucleotide.
 CC The molecules of the invention may be utilised to diagnose or treat
 CC conditions, diseases or disorders associated with cell signalling, such
 CC as arteriosclerosis, psoriasis and cancer. The current sequence is that
 CC of a human MDPT cDNA of the invention.
 XX

SO Sequence 2140 BP; 601 A; 485 C; 493 G; 561 T; 0 U; 0 Other;

Query Match 91.1%; Score 1191; DB 11; Length 2140;

Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1239; Conservative 0; Mismatches 0; Indels 8; Gaps 4;

QY 70 GAGGCAACAAGCTGTGGAGAGTCAAGCTGAGACCAAGGAGGCTGCTCAAGCTAAACA 129
 DB 1 GAGGCAACAAGCTGTGGAGAGTCAAGCTGAGACCAAGGAGGCTGCTCAAGCTAAACA 60
 QY 130 GACCTAAAGAAAGCATCATGTTCCATGATCACTTATTTCAACCCAGGGGACTTCAAGCTGCG 189
 DB 61 GACCTAAAGAAAGCATCATGTTCCATGATCACTTATTTCAACCCAGGGGACTTCAAGCTGCG 120
 QY 190 CGTGCCAGAAAGTTCAAGAGTAAAGGCGACGAGTAAACAGTATGTTTTCAGAGAGAG 249
 DB 121 CGTGCCAGAAAGTTCAAGAGTAAAGGCGACGAGTAAACAGTATGTTTTCAGAGAGAG 180
 QY 250 GATCTGAGGCAAGGTTTTCAGTG-----GAGGAAGAGCTCTTTTGGGGCAGCCTCAT 304
 DB 181 GATCTGAGGCAAGGTTTTCAGTGAGAGCAAGAGAGAGCTCTTTTGGGGCAGCCTCAT 240
 QY 305 CTTAATTGAAGCTTGAAGAGTGGGTGAAGGCTCTTATGCAACAAGTTTCAAGGGGATTA 364
 DB 241 CTTAATTGAAGCTTGAAGAGTGGGTGAAGGCTCTTATGCAACAAGTTTCAAGGGGATTA 300
 QY 365 GCAGAAATAATGAGCAACTAGTGGCTTTAAAGTCATCGATGAATGAGAGAGAGAG 424
 DB 301 GCAGAAATAATGAGCAACTAGTGGCTTTAAAGTCATCGATGAATGAGAGAGAGAG 360
 QY 425 TCCCATTTACAGCTATCCGAGAGGCTTCTCTCTGTAAGGGTTGAAACATGCCCAATTTG 484
 DB 361 TCCCATTTACAGCTATCCGAGAGGCTTCTCTCTGTAAGGGTTGAAACATGCCCAATTTG 420
 QY 485 TGCTCTGTGATGACATTAATCCACACCAAGAGACATGATCTGTTTGAATACATGC 544
 DB 421 TGCTCTGTGATGACATTAATCCACACCAAGAGACATGATCTGTTTGAATACATGC 480
 QY 545 ACACAGAGCTGGCCAGATATATGCTCAGCATCCAGAGAGGCTTCAATCTCATATATGCA 604
 DB 481 ACACAGAGCTGGCCAGATATATGCTCAGCATCCAGAGAGGCTTCAATCTCATATATGCA 540
 QY 605 GACTTTTCACTGTTTCACTTTGCGGGGCTGGCGGTACATCCACACCC-AAACAGTTCTT 663
 DB 541 GACTTTTCACTGTTTCACTTTGCGGGGCTGGCGGTACATCCACACCC-AAACAGTTCTT 600
 QY 664 CACAGGAGCTGAAAGCTCAGAACTTACTCATCATGATCACTGGAGAGGCTCAAACTGGCT 723
 DB 601 CACAGGAGCTGAAAGCTCAGAACTTACTCATCATGATCACTGGAGAGGCTCAAACTGGCT 660
 QY 724 GATTT-TGGTCTTGGCCGGGCCAAGTCCATTCCAGCCAGACATATCTTCAAGAGTGT 782
 DB 661 GATTTGTGCTTGGCCGGGCCAAGTCCATTCCAGCCAGACATATCTTCAAGAGTGT 720
 QY 783 GACCTCTGTGACCGGCCCCCTGATGCTTGTCTGGAGGCACTGAATATTTCTCTGAGCT 842
 DB 721 GACCTCTGTGACCGGCCCCCTGATGCTTGTCTGGAGGCACTGAATATTTCTCTGAGCT 780
 QY 843 GGAACATATGAGGAGTGAAGGCTGATCTTTATGAATGTTCCAGGGGCAACTTTGTTTCC 902
 DB 781 GGAACATATGAGGAGTGAAGGCTGATCTTTATGAATGTTCCAGGGGCAACTTTGTTTCC 840
 QY 903 TGGGGTTTTCACATCTTGAACAGCTGAGAGAAATCTGGAAGGTGCTGGAGTCCCTTAC 962
 DB 841 TGGGGTTTTCACATCTTGAACAGCTGAGAGAAATCTGGAAGGTGCTGGAGTCCCTTAC 900
 QY 963 AAGAGATATTTGGCGGGAGGTCTCCAGAGTACTTAACTTCAATCCAGAAATGTTTCCACT 1022
 DB 901 AAGAGATATTTGGCGGGAGGTCTCCAGAGTACTTAACTTCAATCCAGAAATGTTTCCACT 960
 QY 1023 GCCTACGAGCTGAGAGGCTTCAATGTTGTCTGAGAAAGGCTGGGAGAGGTTCTGAAGCTGA 1082
 DB 961 GCCTACGAGCTGAGAGGCTTCAATGTTGTCTGAGAAAGGCTGGGAGAGGTTCTGAAGCTGA 1020

QY 1083 AGACCTGGCTCCGAGATGCTAAAGCTTTCCAGAGACCGGCTCTCCGCCAGGAAG 1142
DB 1021 AGACCTGGCTCCGAGATGCTAAAGCTTTCCAGAGACCGGCTCTCCGCCAGGAAG 1080
QY 1143 ACTTGTCATGATTAATTTAGAGCCCGCTGCATCTCAGTGTACAG-CTTCTGATGAG 1201
DB 1081 ACTTGTCATGATTAATTTAGAGCCCGCTGCATCTCAGTGTACAGACTTCCGATGAG 1140
QY 1202 AGCTTTGTTTACAGTTTCAGAGGTAGAGCTTAAGCCAGAAATGTGTACCTTTGAGCT 1261
DB 1141 AGCTTTGTTTACAGTTTCAGAGGTAGAGCTTAAGCCAGAAATGTGTACCTTTGAGCT 1200
QY 1262 CCACACGAAAGGTACACCCAGCCAGTTTACGAAATGCTGTGA 1308
DB 1201 CCTACGAAAGGTACACCCAGCCAGTTTACGAAATGCTGTGA 1247

RESULT 7
ADG30755
ID ADG30755 standard; cDNA; 1311 BP.
XX
AC ADG30755;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:837.
XX
XX Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; noctropic;
KW neuroprotective; antinaemic; anticoagulant; thrombolytic; vulnerary;
KW anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002MO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T,
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
XX MPI; 2003-371981/35.
DR P-SDB; ADG31726.
XX
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Claim 1; SEQ ID NO 837; 1185bp; English.
XX
XX The invention relates to 971 novel human cDNA sequences (ADG29919-
CC ADG30889) and the polypeptides they encode (ADG30890-ADG31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or

CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADG31861-ADG32627) and the polypeptides encoded by the contigs (ADG32628
CC -ADG33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIGO at
CC ftp.wigo.int/pub/published_pcl_sequences.
XX

SQ Sequence 1311 BP; 332 A; 328 C; 329 G; 322 T; 0 U; 0 Other;

Query Match 90.7%; Score 1186; DB 10; Length 1311;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

Matches 1186; Conservative 0; Indels 0;

QY 123 GCTAACAGACCTTAAGAAAGCATGCTTCATGATCTTCACTTCAACCCAGGGGACTTCA 182
DB 72 GCTAACAGACCTTAAGAAAGCATGCTTCATGATCTTCACTTCAACCCAGGGGACTTCA 131
QY 183 AGCTGCCGTGCCCGCAGAACTTCAAGATTAAGGCCAGGATTAACAGTATGTTTCA 242
DB 132 AGCTGCCGTGCCCGCAGAACTTCAAGATTAAGGCCAGGATTAACAGTATGTTTCA 191
QY 243 GGAAGAGATCTGAGGCGAGGCTTTCAGTGGAGGAAGCCCTCTTTGGGGAGCCTC 302
DB 192 GGAAGAGATCTGAGGCGAGGCTTTCAGTGGAGGAAGCCCTCTTTGGGGAGCCTC 251
QY 303 ATCTTACTTGAATCTGAGAACTGGGTGAAGGCTCTTATGCGACATTTAACAAGGGAT 362
DB 252 ATCTTACTTGAATCTGAGAACTGGGTGAAGGCTCTTATGCGACATTTAACAAGGGAT 311
QY 363 TAGCAGATTAATGACAACTATGTCCTTTAAAGTCATCAGATGAATGCAAGGAAG 422
DB 312 TAGCAGATTAATGACAACTATGTCCTTTAAAGTCATCAGATGAATGCAAGGAAG 371
QY 423 AGTCCCATTTAAGCATATCCGAGAAAGCTCTCCCTGGAAGGGTTGGAACATGCCAATAT 482
DB 372 AGTCCCATTTAAGCATATCCGAGAAAGCTCTCTCTGGAAGGGTTGGAACATGCCAATAT 431
QY 483 TGTGCTCTGATGATCATATATCCAGAAAGCACTGATTCGTTTGGATATACAT 542
DB 432 TGTGCTCTGATGATCATATATCCAGAAAGCACTGATTCGTTTGGATATACAT 491
QY 543 GCAACAGACCTGGCCCAATATATGTTGAGATCCAGAGGGCTTCATCTCATATAT 602
DB 492 GCAACAGACCTGGCCCAATATATGTTGAGATCCAGAGGGCTTCATCTCATATAT 551
QY 603 CAGACTTTTCATGTTTCACTTTGGGGGCTGGGCTATCCACCAACACAGCTTCT 662
DB 552 CAGACTTTTCATGTTTCACTTTGGGGGCTGGGCTATCCACCAACACAGCTTCT 611
QY 663 TCACAGGAGCTGAACCTCAGAACTTACTCATCATGCTCCTGGAGAGCTCAAACTGCG 722
DB 612 TCACAGGAGCTGAACCTCAGAACTTACTCATCATGCTCCTGGAGAGCTCAAACTGCG 671
QY 723 TGAATTTGCTCTGCTCCGGGCAAGTCAATTCACGACGACATATCTTCAAGAGTCT 782
DB 672 TGAATTTGCTCTGCTCCGGGCAAGTCAATTCACGACGACATATCTTCAAGAGTCT 731

QY 783 GACCTCTGTGTACCGGCCCCCTGATGCTTGTGCGAGGACCTGAATATTCTCTGAGCT 842
 DB 732 GACCCCTGTGTACCGGCCCCCTGATGCTTGTGCGAGGACCTGAATATTCTCTGAGCT 791
 QY 843 GGACATATGGGTGACGAGCTGATCTTTATTTGAAATGTTCCAGGGGCAACTTTGTTTCC 902
 DB 792 GGAATATGGGTGACGAGCTGATCTTTATTTGAAATGTTCCAGGGGCAACTTTGTTTCC 851
 QY 903 TGGGGTTTCCAACTCTTTGAAACAGCTGAGAAATCTGAGAGTGTGAGAGTCCCTAC 962
 DB 852 TGGGGTTTCCAACTCTTTGAAACAGCTGAGAAATCTGAGAGTGTGAGAGTCCCTAC 911
 QY 963 AGAGATATCTTGGCCGGAGTCTCCAGAGTACTTAACTCAATCCAGATGTTTCCCACT 1022
 DB 912 AGAGATATCTTGGCCGGAGTCTCCAGAGTACTTAACTCAATCCAGATGTTTCCCACT 971
 QY 1023 GGCTACGCTCGAGGCTTCTGTTGTCTGAAACAGGCTGGGAGGGGTTCTGAAAGCTGA 1082
 DB 972 GGCTACGCTCGAGGCTTCTGTTGTCTGAAACAGGCTGGGAGGGGTTCTGAAAGCTGA 1031
 QY 1083 AGACCTGGCTTCCAGAGTCTTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGAGAC 1142
 DB 1032 AGACCTGGCTTCCAGAGTCTTAAAGGCTTTCCAGAGACCGGCTCTCCGCCAGAGAC 1091
 QY 1143 ACTTGTCTATGATTTATTTTCAAGGCGCTGCTGCTGATCTGATCTGATGATAGA 1202
 DB 1092 ACTTGTCTATGATTTATTTTCAAGGCGCTGCTGCTGATCTGATCTGATGATAGA 1151
 QY 1203 GCTTTTGTATAGTTTCAAGAGTGAAGGCTTAAAGCAGAAATGTGTGACCTTTGGGCTTC 1262
 DB 1152 GCTTTTGTATAGTTTCAAGAGTGAAGGCTTAAAGCAGAAATGTGTGACCTTTGGGCTTC 1211
 QY 1263 CTACAGAAAGGTCAACCCAGCCCAAGTTTAGCAAAATGCTGTGTA 1308
 DB 1212 CTACAGAAAGGTCAACCCAGCCCAAGTTTAGCAAAATGCTGTGTA 1257

RESULT 8

ACC79969
ID ACC79969 standard; cDNA, 1534 BP.

AC C79969;

DT 09-SEP-2003 (first entry)

DE Human serine/threonine protein kinase nucleotide sequence SEQ ID NO:5.

XX Human; serine/threonine protein kinase; kinase; enzyme; cytosolic;
 XX antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
 XX cerebroprotective; antiinflammatory; gastrointestinal; hepatotropic;
 XX gynaecological; uropathic; dermatological; gene therapy; cancer;
 XX diabetes; central nervous system disorder; CNS disorder; liver disease;
 XX respiratory disorder; chronic obstructive pulmonary disease; stroke;
 XX cardiovascular disorder; dermatological disorder; urological disorder;
 XX gastrointestinal disease; haematological disorder; Alzheimer's disease;
 XX musculoskeletal disorder; reproductive disorder; Parkinson's disease;
 XX neuropathic pain; gene; ss.

OS Homo sapiens.

PN WO2003046167-A1.

PD 05-JUN-2003.

PF 26-NOV-2002; 2002WO-EP013268.

PR 27-NOV-2001; 2001US-033313P.

PA (FARB) BAYER AG.

PI Koehler RH;

DR WPI; 2003-505196/47.

XX New polynucleotide encoding a serine/threonine protein kinase
 PT polypeptide, useful for diagnosing, preventing or treating diseases
 PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
 PT or diabetes.
 XX
 PS Disclosure; Fig 5; 196pp; English.
 CC
 CC The present sequence represents a human serine/threonine protein kinase
 CC (I) related nucleotide sequence from the present invention. (I) has
 CC cytosolic, antidiabetic, neuroprotective, antiparkinsonian, nootropic,
 CC cerebroprotective, analgesic, antiinflammatory, hepatotropic,
 CC gastrointestinal, gynaecological, uropathic and dermatological
 CC activities, and can be used in gene therapy. Serine/threonine protein
 CC kinase polynucleotide and polypeptide sequences can be used in
 CC diagnosing, preventing or treating diseases associated with
 CC serine/threonine protein kinase dysfunction. They may also be used to
 CC identify test compounds that may act, for example, as activators or
 CC inhibitors at the enzyme's active site. The human serine/threonine
 CC protein kinase and its fragments are also useful in raising specific
 CC antibodies that can block the enzyme and effectively reduce its activity.
 CC Human serine/threonine protein kinase sequences can be used in the
 CC preparation of a medicament for modulating the activity of a serine/
 CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
 CC nervous system (CNS) disorder, a respiratory disorder (including chronic
 CC obstructive pulmonary disease), a cardiovascular disorder, a
 CC dermatological disorder, a gastrointestinal or liver disease, a
 CC haematological disorder, a musculoskeletal disorder, a reproductive
 CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
 CC disease, Parkinson's disease, stroke or neuropathic pain
 CC
 XX
 SQ Sequence 1534 BP; 407 A; 362 C; 365 G; 400 T; 0 U; 0 Other;
 Query Match 90.6%; Score 1185.4; DB 9; Length 1534;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 122 AGCTAACAGACCTTAAAGAGCATGTTCCATGATCTTCACTTTCAACCCAGGGGACTTC 181
 DB 72 ATCTAACAGACCTTAAAGAGCATGTTCCATGATCTTCACTTTCAACCCAGGGGACTTC 131
 QY 182 AAGCTGCCCGTCCAGAAAGTCAAGAGTAAAGCCAGAGTAAAGTGAATGTTTTC 241
 DB 132 AAGCTGCCCGTCCAGAAAGTCAAGAGTAAAGCCAGAGTAAAGTGAATGTTTTC 191
 QY 242 AGAAGAGGATCTGAGCGAGGTTTCAAGTGAAGAGGCTCCCTTTTGGGGCAGCCT 301
 DB 192 AGAAGAGGATCTGAGCGAGGTTTCAAGTGAAGAGGCTCCCTTTTGGGGCAGCCT 251
 QY 302 CATCTTACTTGAACCTTGAAGAGTGGGTGAAGGCTTTATCGACAGTTTCAAGGGGA 361
 DB 252 CATCTTACTTGAACCTTGAAGAGTGGGTGAAGGCTTTATCGACAGTTTCAAGGGGA 311
 QY 362 TTAGAGAAATTAATGACAACTAGGCTTTAAAGTATCGATGCAATGAGAGGAAG 421
 DB 312 TTAGAGAAATTAATGACAACTAGGCTTTAAAGTATCGATGCAATGAGAGGAAG 371
 QY 422 GAGTCCCATTTACAGCTATCCGAGAGGCTTCTCTCTGAGAGGGTTGAAACATGCAATA 481
 DB 372 GAGTCCCATTTACAGCTATCCGAGAGGCTTCTCTCTGAGAGGGTTGAAACATGCAATA 431
 QY 482 TTGTCTCTCTGATGATATATCAACCAAGAGCACTGACATTCGTTTTGAAATCA 541
 DB 432 TTGTCTCTCTGATGATATATCAACCAAGAGCACTGACATTCGTTTTGAAATCA 491
 QY 542 TGCACAGACCTGGCCAGATATAGTCTCAGATCTCAGAGGGGCTTATCTCTCAATATG 601
 DB 492 TGCACAGACCTGGCCAGATATAGTCTCAGATCTCAGAGGGGCTTATCTCTCAATATG 551
 QY 602 TCAGACTTTTCAATGTTTCAACTTTTGGCGGGGCTGCGGTACATCCACCAACCAAGCTTC 661
 DB 552 TCAGACTTTTCAATGTTTCAACTTTTGGCGGGGCTGCGGTACATCCACCAACCAAGCTTC 611

QY	662	TTCAAGGGA	CTGAA	CTTCAAG	CTTATCAT	AGTCA	CCCTGG	AAGGCT	CAAA	CTGG	721		
Db	612	TTCAAGGGA	CTTGA	AACTCAG	AACTTATCAT	AGTCA	CCCTGG	AAGGCT	CAAA	CTGG	671		
QY	722	CTGATTTT	TGCTTG	CCCGGG	CAAGTCC	ATTC	CCAGC	CAGACAT	ACTT	CAGAGT	CG	781	
Db	672	CTGATTTT	TGCTTG	CCCGGG	CAAGTCC	ATTC	CCAGC	CAGACAT	ACTT	CAGAGT	CG	731	
QY	782	TGACCCCT	TGGTAC	CCGGCCCC	CTGATG	CTTTGCT	TGGGAG	CCACTG	AAATAT	TCTCTG	TGAGC	841	
Db	732	TGACCCCT	TGGTAC	CCGGCCCC	CTGATG	CTTTGCT	TGGGAG	CCACTG	AAATAT	TCTCTG	TGAGC	791	
QY	842	TGACATAT	TGGGGT	GCAGAGCT	GCATCTTT	ATTGA	ATTTCC	AGGGTCA	ACTTTG	TTCTTC		901	
Db	792	TGACATAT	TGGGGT	GCAGAGCT	GCATCTTT	ATTGA	ATTTCC	AGGGTCA	ACTTTG	TTCTTC		851	
QY	902	CTGGGGTT	TTCCAA	CACTCTT	GAACAG	CTGAG	AGAAAT	CTGGAG	GTGCTG	GGAGTCC	CTA	961	
Db	852	CTGGGGTT	TTCCAA	CACTCTT	GAACAG	CTGAG	AGAAAT	CTGGAG	GTGCTG	GGAGTCC	CTA	911	
QY	962	CAGAGGAT	ACTTGG	CGCGGAG	CTCC	CAAGCTA	CCCTA	CTAC	ATAC	ATCC	AAATGG	TTCCAC	1022
Db	912	CAGAGGAT	ACTTGG	CGCGGAG	CTCC	CAAGCTA	CCCTA	CTAC	ATAC	ATCC	AAATGG	TTCCAC	971
QY	1022	TGCTTAC	GCCTCG	AAGCCTT	CATGTTG	TC	TGGA	ACAGGCT	GGGAGG	TTCT	CCTGA	AGCTG	1081
Db	972	TGCTTAC	GCCTCG	AAGCCTT	CATGTTG	TC	TGGA	ACAGGCT	GGGAGG	TTCT	CCTGA	AGCTG	1031
QY	1082	AAGACT	CTGGCT	CCCA	CAATGCT	AAAGGCTT	TTCC	AGAG	CCGGCT	CTCC	CGCC	CAGAG	1141
Db	1032	AAGACT	CTGGCT	CCCA	CAATGCT	AAAGGCTT	TTCC	AGAG	CCGGCT	CTCC	CGCC	CAGAG	1091
QY	1142	CACATGTT	TCATGAT	TTATTT	CAGCGCCT	CGCATCT	CAGCTG	TAA	CAGGCTT	CC	TGATG	AG	1201
Db	1092	CACATGTT	TCATGAT	TTATTT	CAGCGCCT	CGCATCT	CAGCTG	TAA	CAGGCTT	CC	TGATG	AG	1151
QY	1202	AGTCTTTG	TTTACAG	TTTCAG	GAAGGCT	TAAAGC	CAAGAA	TGTGT	GAACCT	TTT	TGAGCT		1261
Db	1152	AGTCTTTG	TTTACAG	TTTCAG	GAAGGCT	TAAAGC	CAAGAA	TGTGT	GAACCT	TTT	TGAGCT		1211
QY	1262	CCCTAC	CGAAAGT	CA	CCACC	CAAGCC	CGCTT	TA	GAATGCT	GGTGA		1308	
Db	1212	CCCTAC	CGAAAGT	CA	CCACC	CAAGCC	CGCTT	TA	GAATGCT	GGTGA		1258	

```

QY 482 TTGTGCTCTGTCATGATATATCCACACCAAGAGACCTGACATTCGTTTTGAATAC 541
DB 432 TTGTGCTCTGTCATGATATATCCACACCAAGAGACCTGACATTCGTTTTGAATAC 491
QY 542 TGCACACAGACCTGGCCAGATATATGCTCAGATCCAGAGAGGCTTCATCTCATATAG 601
DB 492 TGCACACAGACCTGGCCAGATATATGCTCAGATCCAGAGAGGCTTCATCTCATATAG 551
QY 602 TCAGACTTTTCATGTTTCAACTTTTGGGGGCTGGGCTGATCAATCAACCAACAGCTTC 661
DB 552 TCAGACTTTTCATGTTTCAACTTTTGGGGGCTGGGCTGATCAATCAACCAACAGCTTC 611
QY 662 TTCACAGGAGACCTGAAACCTCAGAACTTACTCATCATCTGCGAGAGCTCAAACTGG 721
DB 612 TTCACAGGAGACCTGAAACCTCAGAACTTACTCATCATCTGCGAGAGCTCAAACTGG 671
QY 722 CTGATTTTGGTCTGGCCGGGCGCAAGTCCATTCACGCGCAGATACCTTCAGAAAGTCG 781
DB 672 CTGATTTTGGTCTGGCCGGGCGCAAGTCCATTCACGCGCAGATACCTTCAGAAAGTCG 731
QY 782 TGACCTCTGTGACCGGCGCCCTGATGCTTGTGCGAGGCACTGAATATTCCTCTGAGC 841
DB 732 TGACCTCTGTGACCGGCGCCCTGATGCTTGTGCGAGGCACTGAATATTCCTCTGAGC 791
QY 842 TGGACATATGGGGTGCAGGCTGATCTTTATGTAATGTTCCAGGGTCAACTTTGTTTC 901
DB 792 TGGACATATGGGGTGCAGGCTGATCTTTATGTAATGTTCCAGGGTCAACTTTGTTTC 851
QY 902 CTGGGGTTTCCAACTCTTTGAAACAGCTGAGAAATCTGGGAGGCTGGGAGTCCCTA 961
DB 852 CTGGGGTTTCCAACTCTTTGAAACAGCTGAGAAATCTGGGAGGCTGGGAGTCCCTA 911
QY 962 CAGAGATATCTTGCCCGGAGTCTCCAAAGCTACTAATCAATCCAGATGTTTCCAC 1021
DB 912 CAGAGATATCTTGCCCGGAGTCTCCAAAGCTACTAATCAATCCAGATGTTTCCAC 971
QY 1022 TGGCTACGCTTGAAGCTTCATGTTGTCTGAAACAGGCTGGGAGGTTCTGAAAGCTG 1081
DB 972 TGGCTACGCTTGAAGCTTCATGTTGTCTGAAACAGGCTGGGAGGTTCTGAAAGCTG 1031
QY 1082 AAGACCTGGCTCCAGATGCTTAAAGGCTTCCAGAGACCGGCTCCGCCCAAGAA 1141
DB 1032 AAGACCTGGCTCCAGATGCTTAAAGGCTTCCAGAGACCGGCTCCGCCCAAGAA 1091
QY 1142 CACTTGTGATGATTTATTTCAAGGCGCCCTGCACTCAGCTGTACAGCTTCCTGATGAG 1201
DB 1092 CACTTGTGATGATTTATTTCAAGGCGCCCTGCACTCAGCTGTACAGCTTCCTGATGAG 1151
QY 1202 AGCTTTGTTTACAGTTTCAAGAGTGAAGGCTAAAGCCAGAAATGTGTGACTTTTGCCCT 1261
DB 1152 AGCTTTGTTTACAGTTTCAAGAGTGAAGGCTAAAGCCAGAAATGTGTGACTTTTGCCCT 1211
QY 1262 CCTACAGAAAGGTCAACACCCAGCCAGTTTGAAGAAATGCTGGTGA 1308
DB 1212 CCTACAGAAAGGTCAACACCCAGCCAGTTTGAAGAAATGCTGGTGA 1258

```

RESULT 10

ID AAL48889 standard; cDNA; 2203 BP.

XX AAL48889;

XX 24-OCT-2002 (first entry)

XX Human p15^{cat} family kinase splice form 1 coding sequence.

XX Human: p15^{cat} family kinase; kinase; enzyme; testis; brain; cytosolic;
 KW uterine endometrium adenocarcinoma; lung fibroblast; splice form;
 KW kidney renal cell adenocarcinoma; gene therapy; gene; ss.

OS Homo sapiens.

```

XX Key Location/Qualifiers
FH 5'UTR e1..117
FT /tag= a
FT CDS 118..1149
FT /tag= b
FT /product= "kinase"
FT 3'UTR 1149..2203
FT /tag= c
PN MO200261060-A2.
PN 08-AUG-2002.
XX 17-JAN-2002; 2002MO-US001106.
XX 31-JAN-2001; 2001US-0265151P.
PR 09-MAR-2001; 2001US-00801861.
XX (PEKE ) PE CORP NY.
XX PA
XX PI Yan C, Ketchum K, Di Francesco V, Beasley EM;
XX DR WPI: 2002-608515/65.
XX P-PSDB; AAO18613.
XX PT New human kinase peptide and nucleic acid molecule, useful for treating
XX PT disorders associated with abnormal expression of kinase protein, e.g.
XX PT adenocarcinoma of uterus or lung, in drug screening assays and
XX PT pharmacogenomic analysis.
XX PS Claim 4; Fig 1; 131pp; English.
XX CC The present invention provides the protein, cDNA and gene sequences of
XX CC two splice variants of a human p15cat family kinase. The sequences are
XX CC specifically expressed in the human testis, brain, uterus endometrium
XX CC adenocarcinoma, lung fibroblasts, kidney renal cell adenocarcinoma, and
XX CC can be used to treat related diseases. The present sequence is the cDNA
XX CC of splice variant 1 of the invention
XX SQ Sequence 2203 BP; 657 A; 460 C; 538 G; 548 T; 0 U; 0 Other;

Query Match 77.1%; Score 1009; DB 6; Length 2203;
Best Local Similarity 100.0%; Pred. No. 2.4e-312; Mismatches 0; Gaps 0;
Matches 1009; Conservative 0; Indels 0;

QY 1 ATGGGTCAAGAGCTGTGTGCAAGAAGCTGTACAGCTGATGAGCTGCTACCATTTGTC 60
DB 118 ATGGGTCAAGAGCTGTGTGCAAGAAGCTGTACAGCTGATGAGCTGCTACCATTTGTC 177
QY 61 GAGGAGGAGGAGGACACAGCTGTGAGAGTCAAGCTGAGACCAAGAGGCTGCGTTC 120
DB 178 GAGGAGGAGGAGGACACAGCTGTGAGAGTCAAGCTGAGACCAAGAGGCTGCGTTC 237
QY 121 AAGCTTACAGACCTTAAAGAGATCATATGTCATGACTTCAATTTACCCAGGAGACTT 180
DB 238 AAGCTTACAGACCTTAAAGAGATCATATGTCATGACTTCAATTTACCCAGGAGACTT 297
QY 181 CAAGCTGCCGCTGCCAGAAAGTTCAAGAGTAAAGGCCAGAGTAAAGATGATTTGTTT 240
DB 298 CAAGCTGCCGCTGCCAGAAAGTTCAAGAGTAAAGGCCAGAGTAAAGATGATTTGTTT 357
QY 241 CAGGAAGAGATCTGAGCAGAGGTTTTCAGTGAAGAGAGAGCTCCCTTTTGGGGAGCC 300
DB 358 CAGGAAGAGATCTGAGCAGAGGTTTTCAGTGAAGAGAGAGCTCCCTTTTGGGGAGCC 417
QY 301 TCATCTTACTTGAACCTTGAAGAGCTGGGTGAAGGCTTAAAGCCACATTTAAAGGGG 360
DB 418 TCATCTTACTTGAACCTTGAAGAGCTGGGTGAAGGCTTAAAGCCACATTTAAAGGGG 477
QY 361 ATTAGCAAAATTAATGACAACATGAGGCTTTAAAGTCAATGAGATGAATGACAGAGAA 420
DB 478 ATTAGCAAAATTAATGACAACATGAGGCTTTAAAGTCAATGAGATGAATGACAGAGAA 537

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QY 421 GGAGTCCCATTTTACAGCTATCCGAGAGCTTCTCTCTGTAAGGTTTGAACATGCCAAT 480
DB 538 GGAGTCCCATTTTACAGCTATCCGAGAGCTTCTCTCTGTAAGGTTTGAACATGCCAAT 597
QY 481 ATTGTGCTCTGATGATGATATCCACCAAGAGACATGACATTCGTTTTTGAATAC 540
DB 598 ATTGTGCTCTGATGATGATATCCACCAAGAGACATGACATTCGTTTTTGAATAC 657
QY 541 ATGCACACAGACCTGGCCAGATATATGTCATGATCAGAGAGGCTTCAATCCTCATAT 600
DB 658 ATGCACACAGACCTGGCCAGATATATGTCATGATCAGAGAGGCTTCAATCCTCATAT 717
QY 601 GTGAGATTTTTCATGTTTTCATTTTGGGGGCTGGCCGATACATCCACCAACAGCTT 660
DB 718 GTGAGATTTTTCATGTTTTCATTTTGGGGGCTGGCCGATACATCCACCAACAGCTT 777
QY 661 CTTACACAGGAGACCTGAACCTCAGAACTTACTCATGATCAGTCCGGAGAGCTCAACCTG 720
DB 778 CTTACACAGGAGACCTGAACCTCAGAACTTACTCATGATCAGTCCGGAGAGCTCAACCTG 837
QY 721 GCTGATTTTGTCTTGGCCGGGCAAGTCCATTTCCAGCCAGACATATCTTTCAGAACTC 780
DB 838 GCTGATTTTGTCTTGGCCGGGCAAGTCCATTTCCAGCCAGACATATCTTTCAGAACTC 897
QY 781 GTGACCTCTGTGATACCGGCCCCCTGATGCTTTGTGGAGCCCATGAAATTTCTCTGAG 840
DB 898 GTGACCTCTGTGATACCGGCCCCCTGATGCTTTGTGGAGCCCATGAAATTTCTCTGAG 957
QY 841 CTGACATATATGGGGTGAGGCTGATCTTATTTGAATTTTCCAGGGTCAACCTTTGTTT 900
DB 958 CTGACATATATGGGGTGAGGCTGATCTTATTTGAATTTTCCAGGGTCAACCTTTGTTT 1017
QY 901 CTTGGGGTTTCCAAATCTTTTGAACAGCTGGAAGAAAATCTGGAGGTTCTGGAGTCCCT 960
DB 1018 CTTGGGGTTTCCAAATCTTTTGAACAGCTGGAAGAAAATCTGGAGGTTCTGGAGTCCCT 1077
QY 961 ACAGAGGATCTTGGCCGGGAGTCTCCAACTACTCAATCAATCAATCCAG 1009
DB 1078 ACAGAGGATCTTGGCCGGGAGTCTCCAACTACTCAATCAATCAATCCAG 1126

RESULT 11
ABA00722 standard; cDNA; 1376 BP.
AC ABA00722;
XX 04-MAR-2003 (first entry)
DT Human KPP-7 cDNA, Incyte ID No. 7494145CB1.
XX
DE
XX
XX Gene; kinase; phosphatase; KPP; cell proliferation; arteriosclerosis;
XX attherosclerosis; cirrhosis; hepatitis; reproduction; infertility;
XX paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;
XX primary thrombocytopenia; cancer; development; renal tubular acidosis;
XX anaemia; mental retardation; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; epilepsy; Sjogren's syndrome; uveitis; asthma;
XX menstrual cycle; autoimmune; inflammation; rheumatoid arthritis; AIDS;
XX diabetes mellitus; contact dermatitis; Crohn's disease; allergy;
XX Graves' disease; Hashimoto's thyroiditis; Goodpasture's syndrome; gout;
XX multiple sclerosis; osteoarthritis; irritable bowel syndrome;
XX Reiter's syndrome; mouse; PPTAIRE kinase; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 298..1263
FT /tag= a
FT /product= "KPP-7"
XX
XX WO200290530-A2.
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XX
PD 14-NOV-2002.
XX
XX
PF 16-JAN-2002; 2002WC-US001369.
XX
XX 18-JAN-2001; 2001US-0263083P.
XX 23-FEB-2001; 2001US-0271117P.
XX 23-FEB-2001; 2001US-0271205P.
XX 16-MAR-2001; 2001US-0276859P.
XX 23-MAR-2001; 2001US-0278504P.
XX 23-MAR-2001; 2001US-0278522P.
XX 29-MAR-2001; 2001US-0280266P.
XX 29-MAR-2001; 2001US-0280510P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Lee EA, Walla NK, Baughn MR, Ison CH, Gururajan R, Arvien C;
XX Yao MG, Jackson JL, Tang TY, Yue H, Tran B, Ding L, Lu DM;
XX Lal PG, Warren BA;
XX
XX MPI; 2003-111972/10.
XX P-PSDB; AAG79729.
XX
XX New human kinases and phosphatases and polynucleotides, useful for
XX diagnosing, treating or preventing autoimmune or inflammatory disorders
XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
XX cancer or hepatitis.
XX
XX Claim 5; Page 144; 144pp; English.
XX
XX The sequences given in ABA00716-23 encode human kinases and phosphatases
XX (KPP). The KPP polypeptides, polynucleotides, and agonists and
XX antagonists to them, are useful for diagnosing, treating or preventing
XX disorders associated with aberrant expression of KPP, particularly cell
XX proliferative disorders (e.g. arteriosclerosis, attherosclerosis,
XX cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia
XX vera, psoriasis, primary thrombocytopenia or cancer), developmental
XX disorders (e.g. renal tubular acidosis, anaemia or mental retardation),
XX neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
XX epilepsy), reproductive disorders (e.g. infertility or a disruption in
XX the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS,
XX allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
XX disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
XX gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
XX multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
XX syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
XX bacterial, fungal, parasitic, protozoan or helminthic infections. They
XX are also useful in the assessment of the effects of exogenous compounds
XX on the expression of nucleic acid and amino acid sequences of proteins
XX associated with KPP. The protein encoded by this sequence is homologous
XX to mouse PPTAIRE kinase
XX
XX
XX Sequence 1376 BP; 374 A; 321 C; 342 G; 339 T; 0 U; 0 Other;
XX
XX Query Match 67.9%; Score 887.6; DB 8; Length 1376;
XX Best Local Similarity 99.6%; Pred. No. 1.7e-273;
XX Matches 890; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 122 ACCTAACAGACCTTAAGAAGCATGTTCCATGATCTTCAATTCACCCAGGAGCTTC 181
XX |
XX 266 ACTTAACAGACCTTAAGAAGCATGTTCCATGATCTTCAATTCACCCAGGAGACTTC 325
XX |
QY 182 AAGCTGCCCGTCCCAAGAAAGTTCAAGAGTAAAGGCCACAGAGTAAAGTATTTTTC 241
XX |
DB 326 AAGCTGCCCGTCCCAAGAAAGTTCAAGAGTAAAGGCCACAGAGTAAAGTATTTTTC 385
XX |
QY 242 AGGAAGAGATCTGAGGAGAGGTTTTCAGTGAAGGAAGAGCTCCCTTTGGGGAGGCT 301
XX |
DB 386 AGGAAGAGATCTGAGGAGAGGTTTTCAGTGAAGGAAGAGCTCCCTTTGGGGAGGCT 445
XX |
QY 302 CATCTTACTTGAACCTTGGAAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGAGGA 361
XX |
DB 446 CATCTTACTTGAACCTTGGAAGAGCTGGGTGAAGGCTTTATGCGACAGTTTCAAGAGGA 505
XX |
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